

```
OY 398 GCGCCCGGGGCTCCG-----GGAGAGAAAGCGGCGGAGGCGG 439
      |||||
Db 62 LeuProGlyLeuAlaGlyAspHisGlyIuLeuGlyIuLysGlyAspAlaGlyIlePro 81
      |||||
OY 440 GGACTGCGC-----GGACTCGAGAGGACCCCGCGAGAGAGCGGAGACC 490
      |||||
Db 82 GlyIleProGlyLysValGlyProLysGlyProValGlyProLysGlyAlaProGlyPro 101
      |||||
OY 491 GCGGGGCGCCCGGCGCT-----GCCGGGAGTCTCGGTCTCCGCGATCCGC 541
      |||||
Db 102 ProGlyProArgGlyProLysGlyLysSerGlyLysPyrLysAlaThrGlnLysValAla 121
      |||||
OY 542 TTCAGCGCGCAGCGCTCCGAGAGCGGCGGCTCCCGCTCGACGACACCCCTGCGCTTC 601
      |||||
Db 122 PheSerAlaLeuAlaGlyThrValAsnSerAlaLeuArgProAsnGlnAla---IleArgPhe 140
      |||||
OY 602 GACCGCGTGTGTGACGAGCAGGACGACATTACGAGCGCGTACCGCGCAGCTTCACCTGC 661
      |||||
Db 141 GlutylValIleThrAsnValAsnAspAsnTyrGluProArgSerGlyLysPheThrCys 160
      |||||
OY 662 CAGGTGCTGGGGTCTACTTCCGCTCCATGCGCACCGTCTACCGGGCCAGCTGCAG 721
      |||||
Db 161 LysValProGlyLeuTyrPheThrTyrHisAlaSer---SerArgGlyAsnLeuCys 179
      |||||
OY 722 TTGTATCTGTGAGAGATGCG-----GAATCATTCGCTCTTC----- 760
      |||||
Db 180 ValAsnIleValArgGlyArgAspArgAspArgMetGlnLysValLeuThrPheCysAsp 199
      |||||
OY 761 -----TTCACGTTTTCGGGGGCGGCGCCCAAGCCAGCCTCGCTCGTGGGG 805
      |||||
Db 200 TyrAlaGlnAsnThrPheGlnVal-----ThrThrGly 210
      |||||
OY 806 GGGGCCATGTGTGAGCTGTGAGCCTGAGAGCAACAGTGTGGTGCAG---GTGGGTGGGT 862
      |||||
Db 211 GlnValValLeuLysLeuGlnGlnGlnValAlaHisLeuGlnAlaThrAspLysAsn 230
      |||||
OY 863 GACTACATTGGCATCTATGCCAGCATCAAGACAGACAGACACCTTCCTCGGATTTCTGGTG 922
      |||||
Db 231 SerLeuLeuGlyValGlnGlyAla-----AsnSerIlePheThrGlyPheLeuLeu 247
      |||||
OY 923 TACTCCGAC 931
      |||||
Db 248 PheProAsp 250
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Search completed: June 21, 2003, 16:07:42  
Job time : 63.5 secs

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Db 409 PheProGlyProLysGlyGlyLeuVal---GlyProGlnGlyProProGlyPro 427
Qy 217 TGCCAGGCGATGAGGCGCACTCCGCTGCTGCTGCTGCTGCGGCGGCGGCGGCC 276
Db 428 LysGlyLysProGlyLeuGlnGlyPheProGlyLysProGlyPheLeuGlyGlyValGly 447
Qy 277 CCCACTGGACGACACAGATCCCGACCT----- 306
Db 448 ProProGlyMetArgGlyPheProGlyProIleGlyProLysGlyGlnGlyGly 467
Qy 307 -----CTGCCCGGGGACCGCGGCTT----- 336
Db 468 GlyValProGlyLeuProGlyVal---ProGlyLeuGlyProLysGlyGlyProGly 487
Qy 337 GCGGCGGCGCATGCGAGCCAG-----GGCTTCCGCGGCGGCGGCGGCGGCGG 387
Db 487 eProGlyAspGlnGlyLeuGlnGlyProProGlyIleProGlyIleGlyLysProSerGly 507
Qy 388 CCGGAGCGGCGCGCGCGCGCGCGGAGAAAGCGGAGCGGCGGCGGCGGAGCTGCG 447
Db 507 yProIleGlyProProGlyIleProGlyProLysGlyGlyProGlyLeuProGlyPro 527
Qy 448 G----- 448
Db 527 oGlyPheProGlyIleGlyLysProGlyValAlaGlyLeuGlnGlyProProGlyLysPr 547
Qy 449 -----GCACTTCCAGGCGGAGCGCGGCGGCGGAGAGCGGCGGCGGCGGCG 498
Db 547 oGlyAlaLeuGlyProGlnGlyGlnProGlyLeuProGlyProProGlyProProGlyPr 567
Qy 499 CACCGGCGCT----- 508
Db 567 oProGlyProAlaValMetProProthProProProGlnGlyLysLysLeuProAs 587
Qy 509 -----GCCGGGAGGCGTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 561
Db 587 pMetGlyLeuGlyIleAspGlyValLysProProGlnAlaThrGlyAlaLysGlyLys 607
Qy 562 GAGCGGCGGCGCT-----CC 576
Db 607 sAsnGlyGlyProAlaValGlyMetProAlaPheThrAlaGlyLeuThrAlaProPhePr 627
Qy 577 GCGGCTGAGCGACCTTCCGCTTCCAGCGCGGCTGCTGAGAGCGGAGCGGAGCATTA 636
Db 627 oProValGlyLysProValLysPheAsnLysLeuLeuLysAsnGlyLysGlnAsnLys 647
Qy 637 CGCGGCTGAGCGAGTCACTGCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTG 696
Db 647 nProGlnThrGlyIlePheThrGlyValProGlyValLysLysPheAlaLysLys 667
Qy 697 CACCGCTTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 754
Db 667 lHisCysLysGlyGlyLysAsnValThrValAlaLeuPheLysAsnValLysProValMet 687
Qy 755 -TCTTCTTCCAGTTTTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 813
Db 687 rTrpTrpAspGlyLysLysLysGlyPheLeuAspGlnAla-----SerLysSerAlaVal 705
Qy 814 GGTAGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 873
Db 705 lLeuLeuLeuArgProGlyLysAspArgValPheLeuGlnMetProSerGlyGlnAlaLys 725
Qy 874 CACTATGCGAGCATCAAGACAGACAGACACTTCTCGGATTCCTGCTGCTGCTGCTG 925
Db 725 yLeuTyAlaGlyGlnTyAlaHisSerSerPheSerGlyTyLeuLeuTy 742

```

## RESULT 12

S23779  
collagen alpha 1(VIII) chain - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
C:Accession: S23779  
R:Muragaki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, B.R.; Nishimura, Y.

Eur. J. Biochem. 207, 895-902, 1992  
A:Title: Alpha-1(VIII)-collagen gene transcripts encode a short-chain collagen polype  
A:Reference number: S23779; MUID:92362626; PMID:1499564  
A:Accession: S23779  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-743 <MUR>  
A:Cross-references: EMBL:X66976; NID:950493; PIDN:CAA47387.1; PID:G1359953  
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homolog  
F:616-742/Domain: complement C1q carboxyl-terminal homology <C1Q>

## Alignment Scores:

Pred. No.:	5,02e-18	Length:	743
Score:	408.50	Matches:	119
Percent Similarity:	42.51%	Conservative:	40
Best Local Similarity:	31.82%	Mismatches:	123
Query Match:	16.08%	Indels:	92
		Gaps:	12

US-09-944-944-41 (1-1377) x S23779 (1-743)

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Qy 70 GGCAGGCGCAGGCGGCGGCGGCGGAGAACCGCGGCGGCTGAGACACCA----- 123
Db 372 GlyProArgGlyGlyLysGlyProIleGlyAlaProGlyMetGlyLysProProGlyGly 391
Qy 124 ACTGAGGCTCCGAGTACGAGC-----GCCCGAAGAGGCGCATCGGAGCGGGA 177
Db 392 ProGlyLeuProGlyIleProGlyProMetGlyProProGlyAlaIleGlyPheProGly 411
Qy 178 -----GGGGGACTGCGAGAGACCCCGGCGGCTCCGCGGCTCCGCGGCGGCGG 225
Db 412 ProLysGlyGlnGlyValVal---GlyProGlnGlyProProGlyProLysGlyLys 430
Qy 226 TATGAGCGCATCTCTGCTGCTGCTGCTGCTGCGGCGGCGGCGGCGGCGGCGGCGG 285
Db 431 ProGlyLeuGlnGlyPheProGlyLysProGlyPheLeuGlyGlyValGlyProProGly 450
Qy 286 CGACACACAGATCCCGACCT-----CTGCC 312
Db 451 MetArgLysLeuProGlyProIleGlyProLysGlyGlnGlyGlnHisLysGlyLeuPro 470
Qy 313 GGGGACCCCGGCGGCTTCCAGGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 372
Db 471 GlyLeu---ProGlyValProGlyLeuGlnGlyProLysGlyGlnProGlyLysProGlyAs 490
Qy 373 CGATGCGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 432
Db 490 pGlnGlyLeuGlnGlyProProGlyIleProGlyIleValGlyProSerGlyProIleGly 510
Qy 433 GAGGCGGAGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 466
Db 510 yProProGlyIleProGlyProLysGlyGlnProGlyLeuProGlyProProGlyPhePr 530
Qy 466 ----- 466
Db 530 oGlyValGlyLysProGlyValAlaGlyLeuHisGlyProProGlyLysProGlyAlaLe 550
Qy 467 -GGGCGCGAGAGAG-----GGGAGACCGGCGGCGGCGGCGGCGGCGGCGGCGG 516
Db 550 uGlyProGlnGlyGlnProGlyLeuProGlyProProGlyProProGlyProProGlyPr 570
Qy 517 GTGCTGCTGCTCCGCGA----- 535
Db 570 oProAlaValMetProThrProSerProGlnGlyGlyLysLeuProAspMetGlyLeuG 590
Qy 536 -----TCGCGCTTACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 556
Db 590 yIleAspGlyValLysThrProHisAlaGlyLysLysGlyLysHisGlyLysPr 610
Qy 557 -----TCCGAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 588
Db 610 oAlaTyrgLysMetProAlaPheThrAlaGlyLeuThrValProPheProProValGlyAl 630

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Db      585 gsergllylephethcysylsileproglylletytrpheserlythnvalnlsva 605
Qy      703 STACSGGGGCGAGCTGAGTTGATGTCGTGAGAAATGSC---GAATCATTGCCCTTT 759
Db      605 llysglythnlsvalatrrvalglyleutytrlysasnglythnprothmettytrnly 625
Qy      760 STTCAGATTTTGGGGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 819
Db      625 larsglutyserlyserlytytleuasnrlala-----SerGlyserlallemetgl 643
Qy      820 GCTGGAGACCTGAGACCACTGTGGTGCAGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 879
Db      643 yleutrglwnasrplnvaltrpleuglnleuproasnrlaglsuasnlyleuty 663
Qy      880 TGGCAGATCAAGACAGACACTTCCGGATTTCTGGTG 922
Db      663 rterserglutytrvalnhsrserpheserlythnleuval 677

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## RESULT 6

A34246 collagen alpha 1(VIII) chain precursor - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C>Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C/Accession: A34246  
 R:Yamauchi, N.; Benya, P.D.; van der Rest, M.; Nishimura, Y.  
 J. Biol. Chem. 264, 16022-16029, 1989  
 A>Title: The cloning and sequencing of alpha1(VIII) collagen cDNAs demonstrate that type  
 omains similar to those of type x collagen.  
 A:Reference number: A34246; MUID:89380199; PMID:2476437  
 A:Accession: A34246  
 A:Molecule type: mRNA  
 A:Residues: 1-744 <YAM>  
 A:Cross-references: GB:05042; NID:9164895; PIDN:AAA1204.1; PID:9164896  
 C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>  
 F:118-571/Region: interrupted helical  
 F:572-744/Region: carboxyl-terminal nonhelical  
 F:617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>

Alignment Scores:

Pred. No.:	Length:	744
Score:	426.50	125
Percent Similarity:	42.21%	Conservative: 43
Best Local Similarity:	31.41%	Mismatches: 130
Query Match:	16.79%	Indels: 100
DB:	1	Gaps: 12

US-09-944-944-41 (1-1377) x A34246 (1-744)

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Qy      22 GGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 81
Db      349 Gllvalgllylproglylphetroglylproglyllyllyllyllyllyllyllyl 368
Qy      82 GGGGCGC-----TGCGCGGCGGAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Db      369 GllAlAlleuglylproatrglyllyllyllyllyllyllyllyllyllyllyllyl 388
Qy      121 CCA-----ACTGGAGGGCTCCGAGTAGAGGAGC-----GCCCGAAGAGGAGCCATCGG 168
Db      389 Proglylgluprogllyleuprogllylprogllylprogllylprogllyllyllyllyl 408
Qy      169 GAGCCCGGGA-----GGGGGAGCTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 216
Db      409 Phetroglylproglyllyllyllyllyllyllyllyllyllyllyllyllyllyllyl 427
Qy      217 TGGCAGCGCATAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 276
Db      428 llygllylgluprogllyllyllyllyllyllyllyllyllyllyllyllyllyllyl 447
Qy      277 CCCACTGGAGCAGACAGATGCCAGAGCT----- 306

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Db      448 ProProDlylLeaAglyleuProglProglleuProlyselgluAlaGlnlslys 467
Qy      307 ---STGCGGGGAGACCCGCGCTGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 363
Db      468 GlllyleuProDlyleu-ProDlylAlProgllyleuLeuGlyllyllyllyllyllyl 487
Qy      364 GCGGCGGCGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 423
Db      487 eProgllylAsrlnslyleuInlnlylProvrogllylProgllylLehlnlylProsegl 507
Qy      424 CGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 466
Db      507 yProglleuProProDlylLeuProglProglyllyllyllyllyllyllyllyllyl 527
Qy      466 ----- 466
Db      527 ogllyrPhetrogllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyl 547
Qy      467 -----GGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 507
Db      547 ogllylAlleuInlylProglInlnlylInlnlyllyllyllyllyllyllyllyllyl 567
Qy      508 TGGCGGCGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 538
Db      567 oProgllyrProAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAl 587
Qy      539 -----GCTTGAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 561
Db      587 pmetgllyleuInlylLeasrlyllyllyllyllyllyllyllyllyllyllyllyllyl 607
Qy      562 GAGCCGCGGCGCT-----CC 576
Db      607 saanglyllylProAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAl 627
Qy      577 GCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 636
Db      627 oProvalgllylAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAl 647
Qy      637 CGCGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 656
Db      647 nProglInlnlylLehethrlyllyllyllyllyllyllyllyllyllyllyllyllyl 667
Qy      697 CAGCGTGTACCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 754
Db      667 lnsCyslylgllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyl 687
Qy      755 -TCCTTCTTCAGTCTTTTTCGGGGGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 813
Db      687 rthnlyllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyllyl 705
Qy      814 GGTGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 873
Db      705 llyleuLeuAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAl 725
Qy      874 CATCTATGCGCAGCATCAAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAC 925
Db      725 yleutrylAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAlAl 742

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## RESULT 7

JC4708 gelatin-binding 28k protein precursor - human  
 N:Alternate names: adipose specific collagen-like factor  
 C:Species: Homo sapiens (man)  
 C>Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 20-Sep-1999  
 C/Accession: JC4708; J04944  
 R:Meda, K.; Okubo, K.; Shimomura, T.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.  
 Biochem. Biophys. Res. Commun. 221, 286-289, 1996  
 A>Title: cDNA cloning and expression of a novel adipose specific collagen-like factor  
 A:Reference number: JC4708; MUID:96224171; PMID:8619847  
 A:Accession: JC4708  
 A:Molecule type: mRNA  
 A:Residues: 1-244 <MAE>



QY 458 -----GGGACCCCGGCGCGAGAGAGCG-----GGACCCGC 492  
 Db 483 yProProGlyProProGlyProLysAsnSerGlyLeuProGlyLeuProGlyPro 503  
 QY 493 GGGGCCACCGGGCTCCGGGAGTGGTGGCT----- 529  
 Db 503 oGlyProProGlyProProGlyInsThrLeProGlyGlyTyrValLysGlyLuse 523  
 QY 529 ----- 529  
 Db 523 rAtGluLeuSerGlyMetSerPheMetLysAlaGlyAlaAsnGlnAlaLeuThrGly 543  
 QY 530 -CCGCGATCCGCTTCAGCCGCAAGCCGCGAGAGCGGGCTCCGCGCTGTGACGC 588  
 Db 543 tProValSerAlaPheThrValLeuSerLysAlaTyr-----ProGlyAlaThrVa 561  
 QY 589 ACCCTTCCTTCGACCGCGCTGTGTGAACAGACAGCATTAACAGCGCTACCGG 648  
 Db 561 lProIleLysPheAspLysIleLeuTyrAsnArgGlnGlnIleTyrAspProAlaGlyThrG 581  
 QY 649 CAAGTTACCTGGCAGGCTGGGCTACTACTGCGGCTCATGCGACCGCTACCG 708  
 Db 581 yIlePheThrCysArgGlyLeuProGlyLeuTyrTyrPheSerTyrHisValHisAlaLysG 601  
 QY 709 GCGCAGCGCTCAGTTGATCTGTGAAGAAATGGCAATCCATTGCC--TCTTTCTTCA 765  
 Db 601 yThrAsnValAlaLysValAlaLeuTyrLysAsnGlySerProValMetTyrThrTyrAspG 621  
 QY 766 GTTTTGGGGGGGGGCGCAAGCCCTCGCTCTCGGGGGCGGCGCATGGAGAGCTGGA 825  
 Db 621 uTyrGlnLysGlyTyrLeuAspGlnAla-----SerGlySerAlaValIleAspLeuMe 639  
 QY 826 GCGTCGAGCAACGTTGGTGTGAGTGTGGTGTGACTACATTCATTCATTCGAC 885  
 Db 639 tGluAsnAspGlnValThrPheGlnLeuProAsnSerGlnSerAsnLysLeuTyrSerSe 659  
 QY 886 CATCAGACAGACAGACATTCCTCCGATTCTG 919  
 Db 659 rGluTyrValHisSerSerPheSerGlyPheLeu 670

## RESULT 4

S13301  
 collagen alpha 1(X) chain precursor - bovine  
 C:Species: Bos primigenius taurus (cattle)  
 C:Date: 21-Nov-1993 #sequence\_revision 23-Feb-1996 #text\_change 13-Aug-1999  
 C:Accession: S13301  
 R:Thomas, J.T.; Kwan, A.P.L.; Grant, M.E.; Boot-Handford, R.P.  
 Biochem. J. 273, 141-148, 1991  
 A:Title: Isolation of cDNAs encoding the complete sequence of bovine type X collagen. Ex  
 A:Reference number: S13301; MUID:9113131; PMID:1703407  
 A:Accession: S13301  
 A:Molecule type: mRNA  
 A:Residues: 1-674 <TPH>  
 A:Cross-references: EMBL:X53556; NID:9263; PIDN:CAA37624.1; PID:9264  
 C:Genetics:  
 A:Gene: COL10A1  
 C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology  
 C:Keywords: collid coll; extracellular matrix; glycoprotein; homotrimer  
 F:1-18/Domain: signal sequence #stratus predicted <SIG>  
 F:19-674/Product: collagen alpha 1(X) chain #status predicted <MAT>  
 F:347-673/Domain: complement C1q carboxyl-terminal homology <CIQ>

## Alignment Scores:

Pred. No.:	7,37e-21	Length:	674
Score:	454.00	Matches:	122
Percent Similarity:	44.93%	Conservative:	42
Best Local Similarity:	33.42%	Mismatches:	116
Query Match:	17.87%	Indels:	85
DB:	2	Gaps:	13

US-09-944-944-41 (1-1377) x S13301 (1-674)

QY 46 GAGCGAAGCAGACTGGGT-----GACGCGAGGCGAGGGCGCGCTGGCG 93

Db 320 GlyValLysGlyGlnGlnGlyProAlaGlyHisProGlyGlnAlaGly-----LeuPro 337  
 QY 94 GGAAGAAGCGCGGGCTCGAGACACACCACTGAGAGGTCCGAGTAGAGAGCCCGC 153  
 Db 338 GlyProSerGlyAsnMetGly-----ProGlnIleProLysGlyIleProGlyAsnPro 355  
 QY 154 AAGGAGGCCATCGGGGAGCGGGGAGGAGCTCCGAGAGGCC-----CGG 201  
 Db 356 -----GlyLeuProGlyProLysGlyLuseGlyMetGlyProValGlyProAlaGly 371  
 QY 202 CGTCGCGGCTCCCGGCTCCAGCGCTATAGAGCC-----ACTCCGCTCCGCTGCTCT 255  
 Db 372 AsnProGlyAlaLysGlyGlnArgGlySerSerGlyLeuAsnAspGlyLysProGlyTyrPro 391  
 QY 256 GGGCTTCGCGCGCGCTCCGCCCTCCAGACAGACACAGATCCCAAGCT----- 306  
 Db 392 GlyGluProGlyLeuAsnGlyProLysGlyAsnProGlyLeuProGlyProLysGlyAsp 411  
 QY 307 -----CTGGCCGGGCGACCGCGCTTCAGAGCGAGCGCGGCGCACCATGCGAGCGG 360  
 Db 412 ProGlyIleAlaGlySer-ProGlyLeuProGlyProValGlyProAlaGlyAlaLysG 431  
 QY 361 CTTCGCGGCGCGCGATGCGCGAGCGCGCGAGCGCGCGCGCGCGCTCCGAGAGAA 420  
 Db 431 yValProGlyHisAsnGlyGlnAlaGlyProArgGlyValProGlyIleProGlyThrAr 451  
 QY 421 AAGCGAGGGGGGAGCGCGGAGCTGCGC----- 448  
 Db 451 gGlyProIleGlyProProGlyIleProGlyPheProGlySerLysGlyAspValGlyTh 471  
 QY 449 -----GGACC 453  
 Db 471 rProGlyProProGlyProAlaGlyIleAlaValLysGlyLeuAsnGlyProThrGlyPr 491  
 QY 454 TCGAGGGAGCCCGCGCGCGAGAGAGCG-----GGACCGCGCG 495  
 Db 491 oProGlyProProGlyProArgGlyAsnAlaGlyGluProGlyLeuProGlyProProG 511  
 QY 496 GCGCAGCGGCGCTCCGCGGAGTGTGCTGGCT----- 529  
 Db 511 yProProGlyProProGlyGlnValAlaLeuProGluAspPheValLysAlaGlyGlnAr 531  
 QY 530 -----CCGCGATCCGCTTCAGCGCAA 552  
 Db 531 gProPheValSerAlaAsnGlnGlyValThrGlyMetProValSerAlaPheThrVal 551  
 QY 553 GCGCTCCGAGAGCGGGTGCCTCCGCTGAGCGACCCCTTGCGCTGACCGCGTGT 612  
 Db 551 eLeuSerLysAlaTyr-----ProAlaIleGlyThrProIleProPheAspLysIle 569  
 QY 613 GGTCAAGCAGGAGGAGATATACAGCGCGCGCGAGCAATTCACCTCCAGAGCGCTGG 672  
 Db 569 uTyrAsnLysGlnGlnIleHisThrAspProArgGlyThrGlyLeuPheThrLysLysIleProG 589  
 QY 673 GGTCTACTACTTCGCGCTCCATGCGACCGCTACCGGCGCAAGCTTCGAGTTGATCTGT 732  
 Db 589 yIleTyrTyrPheSerGlyHisIleHisValLysGlyThrHisAlaThrValGlyLeuTyr 609  
 QY 733 GAGAGATGCGAATCATTCGCC--TCTTTCTTCAGTTTTCGGGGGTGGCCCAAGCC 789  
 Db 609 rLysAsnGlyThrProValMetTyrThrTyrAspGlyTyrLysGlyLysLysAspG 629  
 QY 790 AGCTCCGCTTCGCGGGGCGCGCATGCGAGCGCTGAGCGCGAGGACCAATTCGGGCGCA 849  
 Db 629 nAla-----SerGlySerAlaValIleAspLeuThrGluAsnAspGlnValThrPheG 647  
 QY 850 GGTGGGTGTGGTACATTCGACATTCATTCATTCAGCATGACATGACAGACAGACACTTCTC 909  
 Db 647 nLeuProAsnAlaGlySerAsnGlyLeuTyrSerProGlyTyrValHisSerPheSe 667  
 QY 910 CGGATTTCTGCTG 922

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Db      361 SerProGlySer-----AspGlyLysProGlyTyrProGlyLysProGly 395
QY      250 GCTCTGGGCGTGGGCGCGGCTCGCCCATGAGCAGACAGATCCAGGCTGTG 309
      ||||| |||
Db      396 LeuAspGlyProGlyGlyAsnProGlyLeuProGlyProGlyGlyAspProGlyVal-- 414
QY      310 CCCGGGCGACCCCGGCTTTCAGGACCGCGGCGACCATGATGCGAGCGGCTTCCGGG 369
      ||| ||||| ||||| |||
Db      415 -GlyGlyProGlyLeuProGlyProGlyProGlyValGlyProAlaGlyAlaGlyLysGlyMetProGly 434
QY      370 CCGCATGGCCCGGACGCGCGGCGAGCGCGCGCGGCTCCGGGAGAGAAAGCGGAGG 429
      ||| ||||| ||||| ||||| |||||
Db      434 YHisAsnGlyLysGlyAlaGlyProGlyGlyAlaProGlyLysProGlyTyrArgGlyProGly 454
QY      430 CGGAGAGCGCGGACTGCGC----- 448
      ||| ||||| |||||
Db      454 eGlyProProGlyLysProGlyPheProGlySerLysGlyAspProGlySerProGlyPyr 474
QY      449 -----GGACCTCGAGGGA 462
      ||||| |||
Db      474 ProGlyProAlaGlyIleAlaThrLysGlyLeuAsnGlyProThrGlyProProGlyPyr 494
QY      463 CCCCGGCGCGCGAGAGAGCGC-----GGACCGCGGCGCGCCACCGG 504
      ||||| ||||| ||||| ||||| |||||
Db      494 ProProGlyProArgGlyHisSerGlyLysProGlyLeuProGlyProGlyProGlyProGly 514
QY      505 GCGTCGCGGAGAGTCTCGTGCT----- 529
      ||||| ||||| |||||
Db      514 YProProGlyGlnAlaValMetProGlyLysPheLysAlaGlyGlnAlaGlyProSerLys 534
QY      530 -----CCGCGATCCGCTT 543
      ||||| ||||| |||||
Db      534 UserGlyThrProLeuValSerAlaAsnGlnGlyValThrGlyMetProValSerAlaPhe 554
QY      544 CAGCCCGCAAGCGCTCCGAGAGCGCGGCTGCTCCGCTGACGACACCTTCCCTTGA 603
      ||| ||||| ||||| ||||| |||||
Db      554 eThrValIleLeuSerLysAlaTyr-----ProAlaIleGlyThrProIleProPheAs 572
QY      604 CCGGCTGCTGGTGAAGCAGAGGACATTACGACCGCGTACCGGCGCAAGTTCACCTGCA 663
      ||||| ||||| ||||| ||||| |||||
Db      572 PylsIleLeuTyrAsnAlaGlnGlnHisTyrAspProArgThrGlyLysPheThrCysAl 592
QY      664 GGTGCTGGGCTTACTACTTCCGCGTCCATGCCACCGCTTACCGGCGCGCTGCTGACT 723
      ||||| ||||| ||||| ||||| |||||
Db      592 nIleProGlyLysTyrPheSerTyrHisValHisValLysGlyThrHisValTyrPva 612
QY      724 TGATGTGGTGAAGATGGCGATCCATGCTCC--TCTTCTTCGAGTTTTCGGGGG 780
      ||| ||||| ||||| ||||| |||||
Db      612 IgIleuTyrLysAsnGlyThrProValMetLysThrTyrAspGlyTyrThrLysGlyTyr 632
QY      781 GCCCAAGCAGCGCTGCTCGGGGGGCGCATGTGTGAGGCTGAGAGCTGAGAGCAAGT 840
      ||| ||||| ||||| ||||| |||||
Db      632 rLeuAspGlnAla-----SerGlySerAlaIleIleAspLeuThrGlnAsnAspGlnVa 650
QY      841 GTGGTGCAAGTGGGTGGGTGACTACATGGAATGACCATGACCATGACCATGACAGAG 900
      ||||| ||||| ||||| ||||| |||||
Db      650 lTyrPheGlnLeuProAlaGlnSerAlaGlnLysSerSerGlyTyrValHisSe 670
QY      901 CACCTTCCGAGATTTCGTC 922
      ||||| ||||| ||||| |||||
Db      670 rSerPheSerGlyPheLeuVal 677

RESULT 3
S23297
collagen alpha 1(X) chain precursor - chicken
N:Alternate names: type X collagen
C:Species: Gallus gallus (chicken)
C:Date: 07-Oct-1994 #sequence revision 10-Nov-1995 #text change 13-Aug-1999
C:Accession: S23297; A31896; S65594; S77711; I50218
R:Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; Luvallie, P.; McC
maguch, N.; Olsen, B.R.
In Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pre
A:Title: The molecular biology of collagens with short triple-helical domains.

```

```

A:Reference number: S22243
A:Accession: S23297
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-674 <NIN>
R:Luvallie, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.
J. Biol. Chem. 263, 18378-18385, 1988
A:Title: The type X collagen gene. Intron sequences split the 5'-untranslated region
A:Reference number: A31896; MUID:89054019; PMID:2461368
A:Accession: A31896
A:Molecule type: mRNA
A:Residues: 1-75 <LUV>
R:Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linzenmayer, T.; Olsen, B.R.
J. Biol. Chem. 261, 5041-5050, 1986
A:Title: The developmentally regulated type X collagen gene contains a long open read
A:Reference number: I50218; MUID:86168227; PMID:3082876
A:Accession: S65594
A:Molecule type: DNA
A:Residues: 'T', '9', 'D', '11-12', 'EDGMKLYLEPTM', '30-31', 'TCKSGRAFTYMILONVMDLYSSHT', '48-89',
629, 'POAVLSLWSMTKCGSSCOIONMVSIPLMFTILSOVSYLKSNMPLMS' <NINI>
A:Cross-references: EMBL:M13496; NID:g211699; PIDN:AAA48736.1; PID:g211700
A:Accession: S77711
A:Molecule type: protein
A:Residues: 104-112, 'X', '114-117, 453-466 <NIN2>
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homolog
C:Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyprol
F:1-18/Domain: signal sequence #status predicted <SIG>
F:547-673/Domain: complement C1q carboxyl-terminal homology <C1Q>
F:453/455/Modified site: hydroxyproline (Pro) #status experimental
F:611/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 6,386-21 Length: 674
Score: 455.00 Matches: 120
Percent Similarity: 45.45% Conservative: 40
Best Local Similarity: 34.09% Mismatches: 111
Query Match: 17.91% Indels: 81
DB: 2 Gaps: 13

US-09-944-944-41 (1-1377) x S23297 (1-674)
QY      28 GGAAGAGGAGCGCGGAGGAGGAGCAACGACTGGGTGAC--GGCAGGGGAGGGGCG 84
      ||||| |||
Db      346 GlyGlnAsnGlyLeuProGlyProLysGlyAspMetGlyProValGlyProAlaGlyPro 364
QY      85 GCGTGGCGGAGAGAGCGCGGCGGCTGAGAGCACCACTGAGGGTCCGGGATACG 144
      ||||| |||
Db      365 --PheProGlyAlaLysGlyLysArgGlyLeuPro-----GlyLeuAsp 378
QY      145 AGCGCCCGGAAGAGGAGCATGCGGAGGAGCGGAGGAGTGCAGAGAGACCCCG-- 201
      ||| ||||| ||||| ||||| |||||
Db      379 GlyLysPro-----GlyTyrProGlyGlnGlnGlyLeuProGlyProLysGly 394
QY      202 -----CGTGGGCTCCCGGTCCAGCGCTATGAGCCACTCTGCTGCTGCT 252
      ||||| |||
Db      395 HisProGlyLeuProGlyGlnLysSerThrGlyHisAlaGlyPro---ProGlyLeu 413
QY      253 CTTGGGCTTGGCGCGCGGCTCGCCCACTGGAGCACAAGAATCCCAAGCTGTGCC 312
      ||||| |||
Db      414 ProGlyProValGly-----ProGlnGlyValLys 423
QY      313 GGGGACCGCGGCTTCCAGGACGCGGCGGCGACCATGACAGCGCTTGGCGGCGG 372
      ||| ||||| ||||| ||||| |||||
Db      424 GlyVal-ProGlyIleAsnGlyLysProGlyProArgGlyProSerGlyIleProGlyI 443
QY      373 CGATGGCGCGAGCGCGCGAGCGCGCGCGGCTCCGGAGAGAAAGCGAGGCGG 432
      ||| ||||| ||||| ||||| |||||
Db      443 eArgGlyProIleGlyProProGlyMetProGlyAlaProGlyAlaLysGlyLysAlaG 463
QY      433 GAGCGCGGAGCTGCGGAGCTCGA----- 457
      ||||| ||||| ||||| ||||| |||||
Db      463 yAlaProGlyLeuProGlyProAlaGlyIleAlaThrLysGlyLeuArgGlyPrometG 483

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 21, 2003, 15:50:16 ; Search time 42.5 seconds

6229.511 Million cell updates/sec

Title: US-09-944-944-41

Sequence: 1 gactagtctcttgagtc.....aaaaaaaaaaaaaaaa 1377

### Scoring table:

Xgapop	10.0	,	Xgapext	0.5
Ygapop	10.0	,	Ygapext	0.5
Fgapop	6.0	,	Fgapext	7.0
Delop	6.0	,	Delext	7.0

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 566448

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Command line parameters:

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-O/cgcn2.1/USPRO.spool/US09944944/runat.13062003.154847.22811/app.query.fasta_1.1543
-DB=PIR.73-QUERY=fastan-SUFFIX=rrp-MINMATCH=0.1-LOOPEL=0-LOOPEXT=0
-UNITS=bits-START=1-END=1-MATRIX=bloms62-TRANS=hungan0.cbl-LIST=45
-DOCALIGN=200-THR.SCORE=pct-THR.MAX=100-THR.MIN=0-ALIGN=15-MODE=LOCAL
-OUTFM=plo-NO.EXT=ext-HEAPSIZ=500-MINLEN=0-MAXLEN=200000000
-USER=US09944944.ecgn.1.1.37.ernal.13062003.145847.22811-NCPU=6-ICPU=3
-NO.MMAP-LARGEOBURY-NEG.SCORES=0-WAIT-DSBLOCK=100-LONGIOS
-DEV.TIMEOUT=120-MARK.TIMEOUT=30-THREADS=1-XGAPOP=10-XGAPEXT=0.5-FGAPOP=6
-FGAPEXT=7-YGAPOP=10-YGAPEXT=0.5-DELOP=6-DELXT=7
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Database : .
PIR_73: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *
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**Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	1207	47.5	219	2	T14782	hypothetical prot
2	458	18.0	680	1	CGH01D	collagen alpha 1(X)
3	455	17.9	674	2	S23297	collagen alpha 1(X)
4	454	17.9	674	2	S13301	collagen alpha 1(X)
5	446	17.6	680	2	S31216	collagen alpha 1(X)
6	426.5	16.8	744	1	A34246	collagen alpha 1(V)
7	424	16.7	244	2	UC4708	gelatin-binding 28
8	422.5	16.6	744	1	S23298	collagen alpha 1(V)
9	417.5	16.4	635	2	A57131	collagen alpha 2(V)
10	412	16.2	26	2	S29328	collagen subcomp
11	409.5	16.1	744	2	S15435	collagen alpha 1(V)
12	408.5	16.1	743	1	S23779	collagen alpha 1(V)
13	399	15.7	245	1	C1H0C	complement subcomp
14	362	14.3	253	1	C1H0B	complement subcomp

15	360.5	14.2	253	2	A51958	collagen precursor
16	357	14.1	423	2	A55797	collagen precursor
17	351	13.8	253	2	I45560	collagen precursor
18	328	12.9	1049	1	CG8075	collagen alpha 1(I)
19	322	12.7	1464	1	CGH015	collagen alpha 1(I)
20	318.5	12.5	1042	1	CGCH15	collagen alpha 1(I)
21	314.5	12.4	1419	2	A41182	collagen alpha 1(I)
22	314.5	12.4	1487	2	B41182	collagen alpha 1(I)
23	314	12.4	245	1	C1HD0A	collagen alpha 1(I)
24	314	12.4	245	2	S19018	collagen alpha 1(I)
25	311	12.2	1670	1	CGH03B	collagen alpha 1(I)
26	308	12.1	1418	2	T45467	collagen alpha 1(I)
27	306.5	12.1	886	2	I50694	collagen alpha 1(I)
28	302	11.9	636	2	S41067	collagen alpha 1(I)
29	302	11.9	1464	2	S59856	collagen alpha 1(I)
30	301.5	11.9	1487	1	CGH06C	collagen alpha 1(I)
31	300.5	11.8	1486	1	B40333	collagen alpha 1(I)
32	300	11.8	1466	1	CGH07L	collagen alpha 1(I)
33	299	11.8	673	1	CGB06C	collagen alpha 1(I)
34	299	11.8	964	1	CGCH2S	collagen alpha 2(I)
35	298.5	11.8	779	1	CGB01S	collagen alpha 1(I)
36	298.5	11.8	888	2	S28791	collagen alpha 1(I)
37	298	11.7	1453	2	S21626	collagen alpha 1(I)
38	298	11.7	1843	2	S18803	collagen alpha 1(I)
39	297	11.7	1549	2	I48103	collagen alpha 1(I)
40	297	11.7	1806	1	CGH01E	collagen alpha 1(I)
41	295.5	11.6	671	1	CGRT1S	collagen alpha 1(I)
42	295.5	11.6	730	2	A36226	collagen alpha 1(I)
43	294	11.6	1373	1	A43291	collagen alpha 2(I)
44	293.5	11.6	1027	2	S28774	collagen alpha 2(I)
45	291.5	11.5	402	1	CG8025	collagen alpha 2(I)

## ALIGNMENTS

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RESULT 1
T14782
hypothetical protein DKFP586B0621.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000
C:Accession: T14782
R:Ottewill, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to The Protein Sequence Database, August 1999
A:Reference number: Z18184
A:Accession: T14782
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <OTY>
A:Cross-references: EMBL:AL110261.
A:Experimental source: adult uterus; clone DKFP586B0621
C:Genetics:
A>Note: DKFP586B0621.1
C:Superfamily: complement C1q carboxyl-terminal homology

Alignment Scores:
Pred. No.:          9, 37e-68      Length:           219
Score:             1207.00         Matches:          219
Percent Similarity: 100.00%        Conservative:     0
Best Local Similarity: 100.00%    Mismatches:       0
Query Match:       47.52%         Indels:           0
DB:                2              Gaps:             0

US-09-944-944-41 (1-1377) x T14782 (1-219)

QY 299 CCCAGCGCTGTCCCGGGGACGCCGCGGCTTCACGAGCACGSCGGGSCAACATGAGCAACCAG 355
|||||
Db 1 ProSerLeucySProGlyHisProGlyLeuProGlyThrProGlyHisHisGlySerGln 20
|||||

QY 359 GGCTTGCCGGGCCGCGATGGCGCGACGGGCGCGACGGCGCGCGCGCGCGGCGCTCCGGGAAG 418
|||||
Db 21 GlyLeuProGlyAlaGArgPGLyAlaGArgPGLyAlaGArgPGLyAlaProGlyAlaProGlyGlu 40
|||||

419 AAAGCGAGGCGCGGAGCGCGGAGACTGCCGGGAACTCSAGAGGGAGCCCCGGGCGCGAGGA 478

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GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 13, 2003, 16:01:52 ; Search time 48 Seconds

(without alignments)  
\$41.261 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325

Sequence: 1 MRPLVLLLLGLAAGSPPLD.....DSFGSLVYSQWHSPPVFA 243

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 408643 seqs, 106915682 residues

Total number of hits satisfying chosen parameters: 408643

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published\_Applications\_AA:\*

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1: /cgn2_6/ptodata/1/pubpaa/US08_NEM_PUB pep: *
2: /cgn2_6/ptodata/1/pubpaa/PTC_NEM_PUB pep: *
3: /cgn2_6/ptodata/1/pubpaa/US06_NEM_PUB pep: *
4: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB pep: *
5: /cgn2_6/ptodata/1/pubpaa/US07_NEM_PUB pep: *
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep: *
7: /cgn2_6/ptodata/1/pubpaa/PTC_PUBCOMB pep: *
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep: *
9: /cgn2_6/ptodata/1/pubpaa/US09_NEM_PUB pep: *
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11: /cgn2_6/ptodata/1/pubpaa/US10_NEM_PUB pep: *
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep: *
13: /cgn2_6/ptodata/1/pubpaa/US60_NEM_PUB pep: *
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep: *
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1325	100.0	243	9	US-09-944-413-42
2	1325	100.0	243	9	US-09-944-403-42
3	1325	100.0	243	9	US-09-944-896-42
4	1325	100.0	243	9	US-09-944-944-42
5	1325	100.0	243	9	US-09-944-907-42
6	1325	100.0	243	9	US-09-944-929-42
7	1325	100.0	243	9	US-10-028-072-362
8	1325	100.0	243	9	US-10-121-049-362
9	1325	100.0	243	9	US-10-123-904-362
10	1325	100.0	243	9	US-10-140-470-362
11	1325	100.0	243	9	US-09-796-735-68
12	1325	100.0	243	9	US-10-175-746-362
13	1325	100.0	243	9	US-10-176-918-362
14	1325	100.0	243	9	US-10-176-921-362
15	1325	100.0	243	9	US-10-137-865-362
16	1325	100.0	243	9	US-10-140-474-362
17	1325	100.0	243	9	US-10-142-431-362
18	1325	100.0	243	9	US-10-143-114-362
19	1325	100.0	243	9	US-10-140-002-362

20	1325	100.0	243	9	US-10-142-419-362	Sequence 362, App
21	1325	100.0	243	9	US-10-123-262-362	Sequence 362, App
22	1325	100.0	243	9	US-10-142-423-362	Sequence 362, App
23	1325	100.0	243	9	US-10-121-050-362	Sequence 362, App
24	1325	100.0	243	9	US-10-141-755-362	Sequence 362, App
25	1325	100.0	243	9	US-10-143-033-362	Sequence 362, App
26	1325	100.0	243	9	US-10-123-108-362	Sequence 362, App
27	1325	100.0	243	9	US-10-123-236-362	Sequence 362, App
28	1325	100.0	243	9	US-10-123-261-362	Sequence 362, App
29	1325	100.0	243	9	US-10-140-921-362	Sequence 362, App
30	1325	100.0	243	9	US-10-140-928-362	Sequence 362, App
31	1325	100.0	243	9	US-10-121-045-362	Sequence 362, App
32	1325	100.0	243	9	US-10-123-292-362	Sequence 362, App
33	1325	100.0	243	9	US-10-123-903-362	Sequence 362, App
34	1325	100.0	243	9	US-10-124-819-362	Sequence 362, App
35	1325	100.0	243	9	US-10-124-822-362	Sequence 362, App
36	1325	100.0	243	9	US-10-140-925-362	Sequence 362, App
37	1325	100.0	243	9	US-10-160-498-362	Sequence 362, App
38	1325	100.0	243	9	US-09-944-884-42	Sequence 42, App1
39	1325	100.0	243	9	US-10-121-041-362	Sequence 362, App
40	1325	100.0	243	9	US-10-121-043-362	Sequence 362, App
41	1325	100.0	243	9	US-10-121-047-362	Sequence 362, App
42	1325	100.0	243	9	US-10-123-215-362	Sequence 362, App
43	1325	100.0	243	9	US-10-123-902-362	Sequence 362, App
44	1325	100.0	243	9	US-10-123-908-362	Sequence 362, App
45	1325	100.0	243	9	US-10-123-909-362	Sequence 362, App

## ALIGNMENTS

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RESULT 1
US-09-944-413-42
; Sequence 42, Application US/09944413
; Patent No. US20020156004A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,413
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 31, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
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1 MRPLVLLLLGLAAGSPPLDNDKIPSLCPGHHGLPCTGCHGHSQGLPGHGDGRDGAAG 60
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Query Match      100.0%; Score 1325; DB 9; Length 243;
Beat Local Similarity 100.0%; Pred. No. 2,36-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Db      1  MRPLLVLILLGLAAGSPPLDDNKIPSLCPGHPLPCTPCNHGSGQLPGRGRGRDGOAPG 60
QY      61  APGECEGEGRPCLPPRRGDDPGRCGEAGRPGLTGPAGCECVPPRSASAKRSESRVPPSD 120
Db      61  APGCEGEGGRPCLPPRRGDDPGRCGEAGRPGLTGPAGCECVPPRSASAKRSESRVPPSD 120
QY      121  APLPDRVLVNOGHHYDAVTGKFTCOVPGVYFAVAATYRASLQFDLVKNESISFFO 180
Db      121  APLPDRVLVNOGHHYDAVTGKFTCOVPGVYFAVAATYRASLQFDLVKNESISFFO 180
QY      181  FFGGPKPRKASISGGMVRLPEPDDQVWVQVGVSDYIGIYASIKTDSFFSGFLYSDMHS 240
Db      181  FFGGPKPRKASISGGMVRLPEPDDQVWVQVGVSDYIGIYASIKTDSFFSGFLYSDMHS 240
QY      241  VFA 243
Db      241  VFA 243

RESULT 2
US-09-944-403-42
; Sequence 42, Application US/09944403
; Patent No. US20020165143A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavir, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tomas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,403
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/067,411
; PRIOR FILING DATE: December 3, 1997
; PRIOR APPLICATION NUMBER: 60/069,334
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,335
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,278
; PRIOR FILING DATE: December 11, 1997
; PRIOR APPLICATION NUMBER: 60/069,425
; PRIOR FILING DATE: December 12, 1997
; PRIOR APPLICATION NUMBER: 60/069,696
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,694
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,702
; PRIOR FILING DATE: December 16, 1997
; PRIOR APPLICATION NUMBER: 60/069,870
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/069,873
; PRIOR FILING DATE: December 17, 1997
; PRIOR APPLICATION NUMBER: 60/068,017
; PRIOR FILING DATE: December 18, 1997
; PRIOR APPLICATION NUMBER: 60/070,440
; PRIOR FILING DATE: January 5, 1998
; PRIOR APPLICATION NUMBER: 60/074,086
; PRIOR FILING DATE: February 9, 1998

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PRIOR APPLICATION NUMBER: 60/074,092  
PRIOR FILING DATE: February 9, 1998  
PRIOR APPLICATION NUMBER: 60/075,945  
PRIOR FILING DATE: February 23, 1998  
PRIOR APPLICATION NUMBER: 60/112,850  
PRIOR FILING DATE: December 16, 1998  
PRIOR APPLICATION NUMBER: 60/113,296  
PRIOR FILING DATE: December 22, 1998  
PRIOR APPLICATION NUMBER: 60/146,222  
PRIOR FILING DATE: July 28, 1999  
PRIOR APPLICATION NUMBER: PCT/US98/19330  
PRIOR FILING DATE: September 16, 1998  
PRIOR APPLICATION NUMBER: PCT/US98/25108  
PRIOR FILING DATE: December 1, 1998  
PRIOR APPLICATION NUMBER: 09/216,021  
PRIOR FILING DATE: December 16, 1998  
PRIOR APPLICATION NUMBER: 09/218,517  
PRIOR FILING DATE: December 22, 1998  
PRIOR APPLICATION NUMBER: 09/254,311  
PRIOR FILING DATE: March 3, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/12252  
PRIOR FILING DATE: June 22, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: September 15, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28409  
PRIOR FILING DATE: No. US20020165143A1ember 30, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: No. US20020165143A1ember 30, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/28301  
PRIOR FILING DATE: December 1, 1999  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: December 16, 1999  
PRIOR APPLICATION NUMBER: PCT/US00/03565  
PRIOR FILING DATE: February 11, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: February 22, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/05841  
PRIOR FILING DATE: March 2, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/08439  
PRIOR FILING DATE: March 30, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/14042  
PRIOR FILING DATE: May 22, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/20710  
PRIOR FILING DATE: July 28, 2000  
PRIOR APPLICATION NUMBER: PCT/US00/32678  
PRIOR FILING DATE: December 1, 2000  
PRIOR APPLICATION NUMBER: PCT/US01/06520  
PRIOR FILING DATE: February 28, 2001  
NUMBER OF SEQ ID NOS: 120  
SEQ ID NO 42  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-944-403-42

Query Match 100.0% Score 1325; DB 9; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2,3e-89;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLGLAASPLDDNKKIPSLCPGHGLPCTPGHHSOGLPGRDGRDGRGAG 60  
DB 1 MRPLVLLGLAASPLDDNKKIPSLCPGHGLPCTPGHHSOGLPGRDGRDGRGAG 60  
QY 61 APGEKGGGREGLPGRGDPGPRGEGAPGPGAGGECVPPRSASFSAKRSRVPSPD 120  
DB 61 APGEKGGGREGLPGRGDPGPRGEGAPGPGAGGECVPPRSASFSAKRSRVPSPD 120  
QY 121 APLPDRVLYNCOGHVDAVTGKTCOVPEVYFAVHATYRSLSLQEDLVKNESIASFQ 180  
DB 121 APLPDRVLYNCOGHVDAVTGKTCOVPEVYFAVHATYRSLSLQEDLVKNESIASFQ 180  
QY 181 FFGMPKPASLSGGMVRLPEPDQVWVGVGDYIGIYASIKTDTSTFSGFLYSDMHSSP 240  
DB 181 FFGMPKPASLSGGMVRLPEPDQVWVGVGDYIGIYASIKTDTSTFSGFLYSDMHSSP 240

DB 181 FFGMPKPASLSGGMVRLPEPDQVWVGVGDYIGIYASIKTDTSTFSGFLYSDMHSSP 240  
QY 241 VFA 243  
DB 241 VFA 243  
RESULT 3  
US-09-944-896-42  
Sequence 42, Application US/09944896  
Patent No. US20020168715A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Botstein, David  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerlitsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gueney, Austin  
APPLICANT: Hillan, Kenneth  
APPLICANT: Kjaavin, Ivar  
APPLICANT: Napier, Mary  
APPLICANT: Roy, Margaret  
APPLICANT: Tumas, Daniel  
APPLICANT: Wood, William  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P2548P1C1  
CURRENT APPLICATION NUMBER: US/09/944,896  
PRIOR FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: 09/866,028  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/069,334  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069,335  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069,278  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069,425  
PRIOR FILING DATE: December 12, 1997  
PRIOR APPLICATION NUMBER: 60/069,696  
PRIOR FILING DATE: December 16, 1997  
PRIOR APPLICATION NUMBER: 60/069,694  
PRIOR FILING DATE: December 16, 1997  
PRIOR APPLICATION NUMBER: 60/069,702  
PRIOR FILING DATE: December 16, 1997  
PRIOR APPLICATION NUMBER: 60/069,870  
PRIOR FILING DATE: December 17, 1997  
PRIOR APPLICATION NUMBER: 60/069,873  
PRIOR FILING DATE: December 17, 1997  
PRIOR APPLICATION NUMBER: 60/068,017  
PRIOR FILING DATE: December 18, 1997  
PRIOR APPLICATION NUMBER: 60/070,440  
PRIOR FILING DATE: January 5, 1998  
PRIOR APPLICATION NUMBER: 60/074,086  
PRIOR FILING DATE: February 9, 1998  
PRIOR APPLICATION NUMBER: 60/074,092  
PRIOR FILING DATE: February 9, 1998  
PRIOR APPLICATION NUMBER: 60/075,945  
PRIOR FILING DATE: February 23, 1998  
PRIOR APPLICATION NUMBER: 60/112,850  
PRIOR FILING DATE: December 16, 1998  
PRIOR APPLICATION NUMBER: 60/113,296  
PRIOR FILING DATE: December 22, 1998  
PRIOR APPLICATION NUMBER: 60/146,222  
PRIOR FILING DATE: July 28, 1999  
PRIOR APPLICATION NUMBER: PCT/US98/19330  
PRIOR FILING DATE: September 16, 1998  
PRIOR APPLICATION NUMBER: PCT/US98/25108  
PRIOR FILING DATE: December 1, 1998

PRIOR APPLICATION NUMBER: 09/216,021  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: 09/218,517  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 09/254,311  
 PRIOR FILING DATE: March 3, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/12252  
 PRIOR FILING DATE: June 22, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: September 15, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28409  
 PRIOR FILING DATE: No. US20020168715A1ember 30, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28313  
 PRIOR FILING DATE: No. US20020168715A1ember 30, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28301  
 PRIOR FILING DATE: December 1, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/30095  
 PRIOR FILING DATE: December 16, 1999  
 PRIOR APPLICATION NUMBER: PCT/US00/03565  
 PRIOR FILING DATE: February 11, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/04414  
 PRIOR FILING DATE: February 22, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/05841  
 PRIOR FILING DATE: March 2, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/08439  
 PRIOR FILING DATE: March 30, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/14042  
 PRIOR FILING DATE: May 22, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/20710  
 PRIOR FILING DATE: July 28, 2000  
 PRIOR APPLICATION NUMBER: PCT/US00/32678  
 PRIOR FILING DATE: December 1, 2000  
 PRIOR APPLICATION NUMBER: PCT/US01/06520  
 PRIOR FILING DATE: February 28, 2001  
 NUMBER OF SEQ ID NOS: 120  
 SEQ ID NO 42  
 LENGTH: 243  
 TYPE: PRT  
 ORGANISM: Homo Sapien  
 US-09-944-944-42

Query Match 100.0%; Score 1325; DB 9; Length 243;  
 Best Local Similarity 100.0%; Pied. No. 2.3e-89;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHHGLPTPGHHSGGLPGRDGRDAPG 60  
 Db 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHHGLPTPGHHSGGLPGRDGRDAPG 60  
 QY 61 APGEKGGGRPLGPPGDEPPGEGAGPAGPTGPAAGCSVPPRSATSAKRSSESVPPSD 120  
 Db 61 APGEKGGGRPLGPPGDEPPGEGAGPAGPTGPAAGCSVPPRSATSAKRSSESVPPSD 120  
 QY 121 APLEFDVNLNEOGHYAVTGKFTQVPGYVYFAVHATVVRASIQFDLVNKGESIASFFQ 180  
 Db 121 APLEFDVNLNEOGHYAVTGKFTQVPGYVYFAVHATVVRASIQFDLVNKGESIASFFQ 180  
 QY 181 FFGGMPKASLSGGAMVRLPEEDQVWVQVGVGYIGIYASIKTDSFGFLVYSMDHSSP 240  
 Db 181 FFGGMPKASLSGGAMVRLPEEDQVWVQVGVGYIGIYASIKTDSFGFLVYSMDHSSP 240  
 QY 241 VFA 243  
 Db 241 VFA 243

RESULT 4  
 US-09-944-944-42  
 Sequence 42, Application US/0944944  
 Patent No. US20020173463A1  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin  
 APPLICANT: Botstein, David

APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gerritsen, Mary  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul  
 APPLICANT: Grimaldi, Christopher  
 APPLICANT: Gurney, Austin  
 APPLICANT: Hillan, Kenneth  
 APPLICANT: Kljavin, Ivar  
 APPLICANT: Napier, Mary  
 APPLICANT: Roy, Margaret  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Wood, William  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 FILE REFERENCE: P2548P1C1  
 CURRENT APPLICATION NUMBER: US/09/944,944  
 PRIOR FILING DATE: 2001-09-26  
 PRIOR APPLICATION NUMBER: 09/866,028  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: 60/067,411  
 PRIOR FILING DATE: December 3, 1997  
 PRIOR APPLICATION NUMBER: 60/069,334  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,335  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,278  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,425  
 PRIOR FILING DATE: December 12, 1997  
 PRIOR APPLICATION NUMBER: 60/069,696  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,694  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,702  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,870  
 PRIOR FILING DATE: December 17, 1997  
 PRIOR APPLICATION NUMBER: 60/069,873  
 PRIOR FILING DATE: December 17, 1997  
 PRIOR APPLICATION NUMBER: 60/068,017  
 PRIOR FILING DATE: December 18, 1997  
 PRIOR APPLICATION NUMBER: 60/070,440  
 PRIOR FILING DATE: January 5, 1998  
 PRIOR APPLICATION NUMBER: 60/074,086  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/074,092  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/075,945  
 PRIOR FILING DATE: February 25, 1998  
 PRIOR APPLICATION NUMBER: 60/112,850  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: 60/113,296  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 60/146,222  
 PRIOR FILING DATE: July 28, 1999  
 PRIOR APPLICATION NUMBER: PCT/US98/19330  
 PRIOR FILING DATE: September 16, 1998  
 PRIOR APPLICATION NUMBER: PCT/US98/25108  
 PRIOR FILING DATE: December 1, 1998  
 PRIOR APPLICATION NUMBER: 09/216,021  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: 09/218,517  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 09/254,311  
 PRIOR FILING DATE: March 3, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/12252  
 PRIOR FILING DATE: June 22, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: September 15, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28409  
 PRIOR FILING DATE: No. US20020173463A1ember 30, 1999

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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020173463A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 42
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-944-42

```

```

Query Match          100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRPLVLLLLGLIAGSPPLDNDKIPSLCPGHPGLPCTGHHGSGLPGRDGRDGAAG 60
   |||||
DB 1 MRPLVLLLLGLIAGSPPLDNDKIPSLCPGHPGLPCTGHHGSGLPGRDGRDGAAG 60
   |||||
QY 61 APGEKGGGREGLPGRDGPGRGEGAGPPTGPAEGCSVPPRSFSAKRSRVPSPSD 120
   |||||
DB 61 APGEKGGGREGLPGRDGPGRGEGAGPPTGPAEGCSVPPRSFSAKRSRVPSPSD 120
   |||||
QY 121 APPEPDRVLVNEQGHYDAVTGKFTCQVPGVYFFAVHATVYRASLQFDLVKNGESIASFEQ 180
   |||||
DB 121 APPEPDRVLVNEQGHYDAVTGKFTCQVPGVYFFAVHATVYRASLQFDLVKNGESIASFEQ 180
   |||||
QY 181 FFGGPKPASLSGGMVRLPEPDQVWVGVDYIGITASITDSTFSGFLVYSWMHSSP 240
   |||||
DB 181 FFGGPKPASLSGGMVRLPEPDQVWVGVDYIGITASITDSTFSGFLVYSWMHSSP 240
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QY 241 VFA 243
   |||
DB 241 VFA 243

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RESULT 5
US-09-944-907-42
; Sequence 42, Application US/09944907
; Publication No. US20020198147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret

```

```

; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,907
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 42
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-907-42

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```

Query Match          100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRPLVLLLLGLIAGSPPLDNDKIPSLCPGHPGLPCTGHHGSGLPGRDGRDGAAG 60
   |||||
DB 1 MRPLVLLLLGLIAGSPPLDNDKIPSLCPGHPGLPCTGHHGSGLPGRDGRDGAAG 60
   |||||
QY 61 APGEKGGGREGLPGRDGPGRGEGAGPPTGPAEGCSVPPRSFSAKRSRVPSPSD 120
   |||||
DB 61 APGEKGGGREGLPGRDGPGRGEGAGPPTGPAEGCSVPPRSFSAKRSRVPSPSD 120
   |||||
QY 121 APPEPDRVLVNEQGHYDAVTGKFTCQVPGVYFFAVHATVYRASLQFDLVKNGESIASFEQ 180
   |||||
DB 121 APPEPDRVLVNEQGHYDAVTGKFTCQVPGVYFFAVHATVYRASLQFDLVKNGESIASFEQ 180
   |||||
QY 181 FFGGPKPASLSGGMVRLPEPDQVWVGVDYIGITASITDSTFSGFLVYSWMHSSP 240
   |||||
DB 181 FFGGPKPASLSGGMVRLPEPDQVWVGVDYIGITASITDSTFSGFLVYSWMHSSP 240
   |||||
QY 241 VFA 243
   |||
DB 241 VFA 243

```

```

RESULT 6
US-09-944-929-42
; Sequence 42, Application US/09944929
; Publication No. US20020197612A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavlin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/944,929
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 42
; LENGTH: 243
; TYPE: PRT

```

ORGANISM: Homo Sapien  
US-09-944-929-42  
Query Match 100.0%; Score 1325; DB 9; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2,3e-89;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLVLLGLAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLRGDRDGRDAPG 60  
DB 1 MRPLVLLVLLGLAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLRGDRDGRDAPG 60  
QY 61 APGKGGGGRGRLGPPRGDGPGRGEAPAGTGTGAGSCSVPRRAFSAKRESRYPPSPD 120  
DB 61 APGKGGGGRGRLGPPRGDGPGRGEAPAGTGTGAGSCSVPRRAFSAKRESRYPPSPD 120  
QY 121 APLEPDLVNEQGHYAATGKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASPFQ 180  
DB 121 APLEPDLVNEQGHYAATGKFTQVPGVYFFAVHATVYRASLQFDLVKNGESIASPFQ 180  
QY 181 FFGGMPKPAISLGGAMVRLPEPDQVWVQVGVGDYIGIYASIKTDTSTFGFLVYSDWHSP 240  
DB 181 FFGGMPKPAISLGGAMVRLPEPDQVWVQVGVGDYIGIYASIKTDTSTFGFLVYSDWHSP 240  
QY 241 VFA 243  
DB 241 VFA 243

RESULT 7  
US-10-028-072-362  
Sequence 362, Application US/10028072  
Publication No. US20030004311A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang  
TITLE OR INVENTION:  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/028, 072  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059836  
PRIOR FILING DATE: 1997-09-24  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062285  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062814  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/062816  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063045  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063082  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/063127  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063327  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063329  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063550  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063561  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063704  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063733  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063735  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063738  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063755  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064248  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/064809  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065846  
PRIOR FILING DATE: 1997-11-17  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/066453  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066511  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/069212  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069278  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069334  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069694  
PRIOR FILING DATE: 1997-12-16  
PRIOR APPLICATION NUMBER: 60/072320  
PRIOR FILING DATE: 1998-01-23  
PRIOR APPLICATION NUMBER: 60/073612  
PRIOR FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: 60/074086  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/074092  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20



PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-02-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081695  
PRIOR FILING DATE: 1998-04-14  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081818  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082999  
PRIOR FILING DATE: 1998-04-24  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084627  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084637  
PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/085149  
PRIOR FILING DATE: 1998-05-12  
PRIOR APPLICATION NUMBER: 60/085323  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085338  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085339  
PRIOR FILING DATE: 1998-05-13  
PRIOR APPLICATION NUMBER: 60/085579  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/086414  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/086430  
PRIOR FILING DATE: 1998-05-22  
PRIOR APPLICATION NUMBER: 60/087106  
PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/088026  
PRIOR FILING DATE: 1998-06-04  
PRIOR APPLICATION NUMBER: 60/088730  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088741  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088810  
PRIOR FILING DATE: 1998-06-10  
PRIOR APPLICATION NUMBER: 60/088858  
PRIOR FILING DATE: 19/98-06-11  
PRIOR APPLICATION NUMBER: 60/089532  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089599  
PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089907  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089947  
PRIOR FILING DATE: 1998-06-19  
PRIOR APPLICATION NUMBER: 60/090349  
PRIOR FILING DATE: 1998-06-23  
PRIOR APPLICATION NUMBER: 60/090429  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090445

PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090538  
PRIOR FILING DATE: 1998-06-24  
PRIOR APPLICATION NUMBER: 60/090863  
PRIOR FILING DATE: 1998-06-26  
PRIOR APPLICATION NUMBER: 60/091360  
PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091519  
PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07

Query Match 100.0%; Score 1325; DB 9; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2.3e-89;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAASPPIDDKIPSLCPGHPGLPGRPHNGSGLPGNDGDXDGAAG 60  
DB 1 MRPLVLLLLGLAASPPIDDKIPSLCPGHPGLPGRPHNGSGLPGNDGDXDGAAG 60  
QY 61 APGEKGGGRPLDPRDPPGRGAGRPAGTGPAGECVSPRPSAFSAKRSESRVPPSD 120  
DB 61 APGEKGGGRPLDPRDPPGRGAGRPAGTGPAGECVSPRPSAFSAKRSESRVPPSD 120  
QY 121 APLPFDRLVYNEQHYDAVTGKFTQVPGVYFAVHATVYRASLPDLVKNESIASFEQ 180  
DB 121 APLPFDRLVYNEQHYDAVTGKFTQVPGVYFAVHATVYRASLPDLVKNESIASFEQ 180  
QY 181 FFGWPKPASLSGAMVRLPEPDQVVOGVGDYIGIYASIKTDSFSGFLVYSWHSPP 240  
DB 181 FFGWPKPASLSGAMVRLPEPDQVVOGVGDYIGIYASIKTDSFSGFLVYSWHSPP 240  
QY 241 VFA 243  
DB 241 VFA 243

## RESULT 8

US-10-121-049-362  
Sequence 362, Application US/10121049  
Publication No. US2003002239A1  
GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C17  
CURRENT APPLICATION NUMBER: US/10/121,049  
CURRENT FILING DATE: 2002-04-12  
Prior Application removed - See file Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 362  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-121-049-362

Query Match 100.0%; Score 1325; DB 9; Length 243;

Best Local Similarity 100.0%; Pred. No. 2.3e-89;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAPG 60  
DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAPG 60  
QY 61 APGEKGGGRGRLPGPRGDPGPRGEGAPGPTGAGCSVPPRSASFSAKRSSESVPPSPD 120  
DB 61 APGEKGGGRGRLPGPRGDPGPRGEGAPGPTGAGCSVPPRSASFSAKRSSESVPPSPD 120  
QY 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLOFDLVKNKESIASFFQ 180  
DB 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLOFDLVKNKESIASFFQ 180  
QY 181 FFGGMPKPAISGGAMRLEPEDQVWVOVGVDYIGIYASIKTSTSGFLVYSDWHSPP 240  
DB 181 FFGGMPKPAISGGAMRLEPEDQVWVOVGVDYIGIYASIKTSTSGFLVYSDWHSPP 240  
QY 241 VFA 243  
DB 241 VFA 243

RESULT 9  
US-10-123-904-362  
Sequence 362, Application US/10123904  
Publication No. US20030022328A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C54  
CURRENT FILING DATE: 2002-04-16  
Prior Application removed - See file wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 362  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-123-904-362

Query Match 100.0%; Score 1325; DB 9; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2.3e-89;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAPG 60  
DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAPG 60  
QY 61 APGEKGGGRGRLPGPRGDPGPRGEGAPGPTGAGCSVPPRSASFSAKRSSESVPPSPD 120  
DB 61 APGEKGGGRGRLPGPRGDPGPRGEGAPGPTGAGCSVPPRSASFSAKRSSESVPPSPD 120  
QY 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLOFDLVKNKESIASFFQ 180  
DB 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLOFDLVKNKESIASFFQ 180

DB 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLOFDLVKNKESIASFFQ 180  
QY 181 FFGGMPKPAISGGAMRLEPEDQVWVOVGVDYIGIYASIKTSTSGFLVYSDWHSPP 240  
DB 181 FFGGMPKPAISGGAMRLEPEDQVWVOVGVDYIGIYASIKTSTSGFLVYSDWHSPP 240  
QY 241 VFA 243  
DB 241 VFA 243

RESULT 10  
US-10-140-470-362  
Sequence 362, Application US/10140470  
Publication No. US20030022331A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Geritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C160  
CURRENT FILING DATE: 2002-05-06  
Prior Application removed - See file wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 362  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-470-362

Query Match 100.0%; Score 1325; DB 9; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2.3e-89;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAPG 60  
DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGDAPG 60  
QY 61 APGEKGGGRGRLPGPRGDPGPRGEGAPGPTGAGCSVPPRSASFSAKRSSESVPPSPD 120  
DB 61 APGEKGGGRGRLPGPRGDPGPRGEGAPGPTGAGCSVPPRSASFSAKRSSESVPPSPD 120  
QY 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLOFDLVKNKESIASFFQ 180  
DB 121 APLEPDRVLVNEOGHYDAVTKFTQVPGVYFFAVHATVYRASLOFDLVKNKESIASFFQ 180  
QY 181 FFGGMPKPAISGGAMRLEPEDQVWVOVGVDYIGIYASIKTSTSGFLVYSDWHSPP 240  
DB 181 FFGGMPKPAISGGAMRLEPEDQVWVOVGVDYIGIYASIKTSTSGFLVYSDWHSPP 240  
QY 241 VFA 243  
DB 241 VFA 243

RESULT 11  
US-09-796-753-68

```

; Sequence 68, Application US/09796753
; Publication No. US20030027998A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-227-999
; CURRENT APPLICATION NUMBER: US/09/796,753
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 68
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-753-68

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```

Query Match      100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MRPLVLLILGLAAGSPPLDNDKIPSLCPGHPGLPCTPGHNSGSLPGRDGRDGRGARG 60
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Db      1 MRPLVLLILGLAAGSPPLDNDKIPSLCPGHPGLPCTPGHNSGSLPGRDGRDGRGARG 60
QY      61 APGEKGGGRPGIPGRGDPGRGEGPAGPTGPRGECVPPRSASFARSRSRVPPSD 120
        |||||||
Db      61 APGEKGGGRPGIPGRGDPGRGEGPAGPTGPRGECVPPRSASFARSRSRVPPSD 120
QY      121 ADLPEDRVLVNBOGHDAVTGKFTQCVPEVYFAVAHATYRASLQFDLYKNESIASFFQ 180
        |||||||
Db      121 ADLPEDRVLVNBOGHDAVTGKFTQCVPEVYFAVAHATYRASLQFDLYKNESIASFFQ 180
QY      181 FFGWPKPASLSGAMVRLPEPDQVWVGVDYIGIYASIKTDSFTSGFLVYSDWHSPP 240
        |||||||
Db      181 FFGWPKPASLSGAMVRLPEPDQVWVGVDYIGIYASIKTDSFTSGFLVYSDWHSPP 240
QY      241 VFA 243
        |||
Db      241 VFA 243

```

RESULT 12

```

US-10-175-746-362
; Sequence 362, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: 09/597,993
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 362
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-746-362

```

```

Query Match      100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2.3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MRPLVLLILGLAAGSPPLDNDKIPSLCPGHPGLPCTPGHNSGSLPGRDGRDGRGARG 60
|||||
Db      1 MRPLVLLILGLAAGSPPLDNDKIPSLCPGHPGLPCTPGHNSGSLPGRDGRDGRGARG 60
QY      61 APGEKGGGRPGIPGRGDPGRGEGPAGPTGPRGECVPPRSASFARSRSRVPPSD 120
        |||||||
Db      61 APGEKGGGRPGIPGRGDPGRGEGPAGPTGPRGECVPPRSASFARSRSRVPPSD 120
QY      121 ADLPEDRVLVNBOGHDAVTGKFTQCVPEVYFAVAHATYRASLQFDLYKNESIASFFQ 180
        |||||||
Db      121 ADLPEDRVLVNBOGHDAVTGKFTQCVPEVYFAVAHATYRASLQFDLYKNESIASFFQ 180
QY      181 FFGWPKPASLSGAMVRLPEPDQVWVGVDYIGIYASIKTDSFTSGFLVYSDWHSPP 240
        |||||||
Db      181 FFGWPKPASLSGAMVRLPEPDQVWVGVDYIGIYASIKTDSFTSGFLVYSDWHSPP 240

```

QY 241 VFA 243  
Db 241 VFA 243

## RESULT 13

US-10-176-918-362  
; Sequence 362, Application US/10176918  
; Publication No. US20030027275A1  
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P330R1C382  
CURRENT FILING DATE: 2002-06-20  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 362  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-176-918-362

Query Match 100.0%; Score 1325; DB 9; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2.3e-89;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGPHHGSQGLPGRDGRDGRDAGP 60  
Db 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGPHHGSQGLPGRDGRDGRDAGP 60  
QY 61 APGEKGGGRGRLPGPRGDPGRGAGPAGTGPAGGECVPPRSASFSAKRSESRVPPSD 120  
Db 61 APGEKGGGRGRLPGPRGDPGRGAGPAGTGPAGGECVPPRSASFSAKRSESRVPPSD 120  
QY 121 APLEPDRVLVNEQGHYDAVTGKFTCOVGVYFFAVHATVYASLQFDLVKNGESTIASPFO 180  
Db 121 APLEPDRVLVNEQGHYDAVTGKFTCOVGVYFFAVHATVYASLQFDLVKNGESTIASPFO 180  
QY 181 FFGGMPKPRASLSGGAMVRLPEPDQVWVGVGDYIGIYASIKTSTFSGFLVYSDMHSSP 240  
Db 181 FFGGMPKPRASLSGGAMVRLPEPDQVWVGVGDYIGIYASIKTSTFSGFLVYSDMHSSP 240  
QY 241 VFA 243  
Db 241 VFA 243

## RESULT 14

US-10-176-921-362  
; Sequence 362, Application US/10176921  
; Publication No. US20030027276A1  
; GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen

APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P330R1C288  
CURRENT FILING DATE: 2002-06-20  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 362  
LENGTH: 243  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-176-921-362

Query Match 100.0%; Score 1325; DB 9; Length 243;  
Best Local Similarity 100.0%; Pred. No. 2.3e-89;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 APGEKGGGRGRLPGPRGDPGRGAGPAGTGPAGGECVPPRSASFSAKRSESRVPPSD 120  
QY 121 APLEPDRVLVNEQGHYDAVTGKFTCOVGVYFFAVHATVYASLQFDLVKNGESTIASPFO 180  
Db 121 APLEPDRVLVNEQGHYDAVTGKFTCOVGVYFFAVHATVYASLQFDLVKNGESTIASPFO 180  
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QY 241 VFA 243  
Db 241 VFA 243

## RESULT 15

US-10-137-865-362  
; Sequence 362, Application US/10137865  
; Publication No. US20030032155A1  
; GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Deforge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K

```

; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 362
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-865-362

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Query Match      100.0%; Score 1325; DB 9; Length 243;
Best Local Similarity 100.0%; Pred. No. 2,3e-89;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 APGEKGEGRPGPLPGRDPGPRGEGAGPAGTGPAGECSSVPPRSAFSAKRSESRVPPSD 120
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DB      121 APLPFDRLVNEQGHYDAVTGKFTQVPGVYFAVHATVYRASLQFDLVKNGESIASFFQ 180
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DB      181 FFGGWPKPASLSGGAMVRLEPEDQVQVGVGDYTGITASTKTSTFSGFLVYSDMHSSP 240
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DB      241 VFA 243

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Search completed: June 13, 2003, 16:11:09.  
Job time : 50 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 21, 2003, 16:09:26 ; Search time 2664 Seconds

(without alignments)  
2654.048 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325

Sequence: 1 MRPLVLLLLGLAAGSPPLD.....DSTFGSLVSDMHSPPVEA 243

Scoring table:

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Ygapop 10.0	Ygapext 0.5	
Fgapop 6.0	Fgapext 7.0	
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DOCALLIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
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-NO\_MMAR -LARGEQUERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOC  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1:	GenEmbl:
2:	gb_ba:
3:	gb_hg:
4:	gb_in:
5:	gb_ov:
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10:	gb_ro:
11:	gb_sts:
12:	gb_sy:
13:	gb_un:
14:	gb_vl:
15:	em_ba:
16:	em_fun:
17:	em_hum:
18:	em_in:
19:	em_mu:
20:	em_om:
21:	em_or:
22:	em_ov:
23:	em_pat:
24:	em_ph:
25:	em_pl:
26:	em_ro:
27:	em_sts:
28:	em_un:

29: em\_vl:  
30: em\_hg\_hum:  
31: em\_hg\_inv:  
32: em\_hg\_other:  
33: em\_hg\_mus:  
34: em\_hg\_pln:  
35: em\_hg\_rod:  
36: em\_hg\_mam:  
37: em\_hg\_vrt:  
38: em\_sy:  
39: em\_hggo\_hum:  
40: em\_hggo\_mus:  
41: em\_hggo\_other:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1325	100.0	1337	9	AF329841
2	1325	100.0	1347	6	AR138193
3	1325	100.0	1377	6	AX464228
4	1321	99.7	1370	9	BC029485
5	1258	94.9	4220	10	AF469650
6	1254	94.6	1234	10	BC025174
7	1254	94.6	1271	10	BC023068
8	1239.5	93.5	191362	9	AP003396
9	1239.5	93.5	219574	9	AP002956
10	1207	91.1	1068	9	HSMB00923
11	1183.5	89.3	173657	2	AC112557
12	1167.5	88.1	249283	2	AC112557
13	1072	80.9	729	6	AR138195
14	914.5	69.0	182429	2	AP001557
15	765	57.7	150653	2	AC107174
16	584	44.1	173038	2	AP001003
17	452	34.1	150653	2	AC107174
18	436	32.9	947	10	BC028770
19	436	32.9	1276	6	AR034252
20	436	32.9	1276	6	AX195209
21	436	32.9	1276	6	AX358519
22	436	32.9	1276	10	MMU37222
23	434	32.8	767	10	AY033885
24	432.5	32.6	1313	6	AR034253
25	432.5	32.6	4517	6	AR138194
26	432.5	32.6	4517	6	AX195211
27	432.5	32.6	4517	6	AX335029
28	432.5	32.6	4517	6	AX358521
29	432.5	32.6	4517	9	HUMPEST2
30	432.5	32.6	4545	6	AX134174
31	432	32.6	194674	2	AC124477
32	428.5	32.3	1886	5	AB067770
33	427	32.2	1134	4	AF269230
34	424.5	32.0	1152	6	AX195207
35	424.5	32.0	1152	6	AX358517
36	424.5	32.0	1152	10	MMU45915
37	422.5	31.9	1282	9	AX054815
38	422	31.8	734	9	AF404407
39	421.5	31.8	178850	9	AL359736
40	418.5	31.6	1973	9	HS10A1COL
41	418.5	31.6	3215	9	HS10A1COL
42	418.5	31.6	10058	9	HS10A1COL
43	418.5	31.6	107553	9	HS10A1COL
44	418.5	31.6	205594	2	AL355373
45	417.5	31.5	3226	6	AX333243

RESULT 1

#### ALIGNMENTS

LOCUS	AF329841	1337 bp	mRNA	linear	PRI 12-MAR-2001
DEFINITION	Homo sapiens complement-c1q tumor necrosis factor-related protein (CTRP5) mRNA, complete cds.				
ACCESSION	AF329841				
VERSION	AF329841.1 GI:13274527				
KEYWORDS	.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens.				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 1337)				
TITLE	Sheppard,P.O. and Humes,J.M.				
JOURNAL	Homo sapiens complement-c1q tumor necrosis factor-related protein Unpublished				
REFERENCE	2 (bases 1 to 1337)				
AUTHORS	Sheppard,P.O. and Humes,J.M.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-DEC-2000) Bioinformatics, ZymoGenetics, Inc., 1201 Eastlake Ave. East, Seattle, WA 98102, USA				
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ORIGIN					
Alignment Scores:					
Pred. No.:	2,83e-48	Length:	1337		
Score:	1325.00	Matches:	243		
Percent Similarity:	100.00%	Conservative:	0		
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Query Match:	100.00%	Indels:	0		
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DB	198	ATGAGGCGACATCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGAC	257		
QY	21	AspAsnLysIleProSerLeuCysProGlyHisProGlyLeuProGlyThrProGlyHis	40		
DB	258	GACACCAAGATCCACAGCTCTGCGCGGGGACACCCCGGCTTCCAGGACACCCCGGGCAC	317		
QY	41	HisGlySerGlnGlyLeuProGlyValArgAspGlyArgAspGlyArgAspGlyValAlaProGly	60		
DB	318	CATGGACACCGGCGCTTCCGGGGCGCGCATGGCGCGACGGCCCGCGACGGCGCGCGG	377		
QY	61	AlaProGlyIuLysGlyGlyGlyValArgProGlyLeuProGlyProAlaGlyLysPro	80		
DB	378	GCTCCGGGAGAAAGGGGAGGGGGGAGCGCGGAGACTGCCGGGAGCTCGAGGGGACCCC	437		
QY	81	GlyProAlaGlyGlyAlaGlyProAlaGlyProThrGlyProAlaGlyGlyLysSerVal	100		
DB	438	GGGCGCGGAGGAGGGGGGAGCCCGCGGGGCGCCACGGGCTGCGGGGGAGTCTCGGTG	497		

QY	101	ProProAsgSerAlaPheSerAlaLysArgSerGIuserArgValProProSerAsp	120
Db	498	CCTCCGGCATCCGCTTCAAGGACCAAGCGCTCCGAGACCGGAGTCCCGCGCTGCAC	557
QY	121	AlaProLeuProPheAspArgValLeuValAsnGIugInGIHISITyRAspAlaValThr	140
Db	558	GCACCTTGCCCTTGACCGGGGTGGTGTGAACGACGAGGACATTCAGCGCGTACC	617
QY	141	GIlytysPheThrCySGInValPProGIlyValIyTyRPhelaValHISAlaThValTyR	160
Db	618	GGCAAGTTCCACTGCAGGCTGGGGCTGCTACTACTTCCTGCCGTCACACCGCTCAC	677
QY	161	ArgAlaSerLeuGIInPheAspLeuValIlyAsnGIyGuserIleAlaSerPhePheGIIn	180
Db	678	CGGGCACCCTGCAGCTTTGATCTGGTGAAGATGGCGAATTCATTCCTTTCTTCAC	737
QY	181	PhePheGIyGIyTyRProLyPProAlaSerLeuSerGIyAlaMetValArgLeuGIIn	200
Db	738	TTTTTCGGGGGGTGGCCCAAGCAGCCTCGCTCGTGGGGGGGCGCATGTGAGCTGGAG	797
QY	201	ProGIuAspGIInValITrpValGIInValGIyAlaGIyAspTyRleGIyIleTyRAlaSer	220
Db	798	CCTGGAGCAACAAGTGGGTGCAGGTGGGTGGGTGACTACATTTGGCATCTATGCAAGC	857
QY	221	IleIyThrAspSerThrPheSerGIyPheLeuValTyRserAspITRPhISerSerPro	240
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QY	241	ValPheAla 243	
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LOCUS	Definition	Sequence 1 from patent US 6197930.	
ACCESSION	AR138193		
VERSION	AR138193.1	GI:14479702	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1347)		
TITLE	Sheppard, P.O. and Humes, J.M.		
JOURNAL	Adipocyte-specific protein homologs		
FEATURES	Patent: US 6197930-A 1 06-MAR-2001;		
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Db	198	ATGAGGCCACATCTCTGCTCTGCTCTCTCTGGGCTGGGGCGGCGGCTGCCGCCACATGGAC	257
QY	21	AspAsnIySIleProSerLeuCyAspProGIyHISProGIyLeuProGIyThProGIyHIS	40
Db	258	GACAACAAGATCCCAAGCTCTGCGCGGGGCAACCCCGGCTTCCAGGCACGCCGGGCAC	317
QY	41	HISGIySerGIInGIyLeuProGIyValArgAspIyArgAspGIyAlaArgAspGIyAlaProGIy	60



Db	318	CATGGACAGCAGGGGTTCCGGGGCCGCGATGGCCGACAGCGCCGAGCGGGCCCGGG	377
Oy	61	AlaProGlyIuIySgIyGluGlyIyAlaArgProGlyLeuProGlyProArgIyAsPro	80
Db	378	GCTCCGGGAGAAAGCGGAGGGCGGGAGCGCGGACTGCGGGAGCTCGAGGGGACCC	437
Oy	81	GlyProArgGlyGluAlaGlyProAlaGlyProThrGlyProAlaGlyGlyCysSerVal	100
Db	438	GGGGCGCAGAGAGGGCGGAGCCGGGGGCCACCGGGCCCTGGCGGGAAATGCTCGGTG	497
Oy	101	ProProArgSerAlaPheSerAlaLysArgSerGlySerArgValProProSerAsp	120
Db	498	CCTCCGCGATCCGCTTACGCGCCAGCGCTCCGAGACCGGGTCCCTCCGCGCTCAC	557
Oy	121	AlaProLeuProPheAspArgValLeuValAsnGluGlnGlyHisTyrAspAlaValThr	140
Db	558	GCACCCCTTGCCCTTCGACCGCGGTGGTGAAACGACGAGGACATATACAGCGCGTACC	617
Oy	141	GlyIysPheThrCysGlnValProGlyValIyTyrTyrPheAlaValHisAlaThrValTyr	160
Db	618	GGCAGATTCACCTCGACAGTGCCTGGGGCTACTACTTCGCCGCTCAACACACGTCAC	677
Oy	161	ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyCysSerIleAlaSerPheSerIle	180
Db	678	CGGGCCACCGCTGCAGTGTGATCTGGTGAAGAAATGGCGAATCATTCCTCTTCTTCAG	737
Oy	181	PhePheGlyGlyTyrProProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGlu	200
Db	738	TTTTTCGGGGGGTGGCCCAACCCAGCCCTCGCTCGGGGGGGCCATGGTGAAGCTGGAG	797
Oy	201	ProGluAspGlnValIyTyrValGlnValGlyAlaGlyAspTyrIleGlyIleTyrAlaSer	220
Db	798	CCTAGAGCACCAAGTGGGGTCCAGTGGGTGGGTGATCATTCATGGCATTCATGACGACG	857
Oy	221	IleIysThrAspSerThrPheSerGlyPheIleValTyrSerAspTyrHisSerSerPro	240
Db	858	ATCAAGACAGACAGACACCTCTCCGGAATTTGGTGTACTCCAGCTGGCAGACGTCGCCA	917
Oy	241	ValPheAla 243	
Db	918	GTCCTTGCT 926	
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LOCUS	AX464228	1377 bp	DNA
DEFINITION	Sequence 361 from Patent WO0140466.		linear
ACCESSION	AX464228		
VERSION	AX464228.1	GI:21899130	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Euthera; Primates; Carnaria; Homnidae; Homo.		
	1 Baker,K.P., Beresini,M., DeForge,L., Desnoyers,L., Filvaroff,E.,		
	Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,		
	Sherwood,S., Smith,V., Stewart,T.A., Tunas,D., Watanabe,C.K.,		
	Wood,W.L. and Zhang,Z.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding		
	same		
JOURNAL	Patent: WO 0140466-A 361 07-JUN-2001;		
FEATURES	Genentech Inc. (US)		
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[illegible]



[illegible]

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OY	201	ProgluspsglValItrPvalGlValglYValglYasPTyrIleagllyleryAlaser	220	
Db	3697	CCTGAGGACCAAGGTGGGTGGGTGACAGTGGCGGTGGGTGATTATACATTGGCATTATGCCAGC	3756	
OY	221	IlelystrhaspserrThrPheSerGlyPheleuVallyrSerAsPTTPHISerSerPro	240	
Db	3757	ATCAAGACAGACAGACTACTCTCTCGATATCTCGTATATCTGACATGGCACAGCTCCCA	3816	
OY	241	ValpheaLA 243		
Db	3817	GTCTTCGCT 3825		
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DEFINITION	Mus musculus, clone MGC:36714 IMAGE:3978387, mRNA, complete cds.			
ACCESSION	BC025174			
VERSION	BC025174.1			
KEYWORDS	MGC.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 1234)			
TITLE	Strausberg, R.			
JOURNAL	Direct Submission			
REMARK	Submitted (05-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINI) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: http://www.hgsc.bcm.tmc.edu/cdna/ Contact: amgbcn.tmc.edu			
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OY		21	AspaanlyIIEProSerLeuCysProGlyHisProGlyLeuProGlyThrProGlyHis	40					
Dd		213	GACAACAAGATCCCAGCGCTGTGTCCGGGCAAGCCGGCCCTCCAGCACACAGTCA	272					
OY		41	HISglYSerGIingLYLeuProGLyArGaspGLyArGaspGLyArGaspGLyAlaProGLy	60					
Dd		273	CATGGACACCAGAAGCGCTGCAGCGCGTGCAGCGCGTGTATGCGCCGACAGCGACCCGGA	332					
OY		61	AlaProGLyGIingLYSGLyGLyGLyArGProGLyLeuProGLyProArGLyAspPro	80					
Dd		333	GCTCCGGGAGAGAAAGGCGAGGGGCGGAGACCGGGACTCACTGGGGCCACGTGGGAGGCC	392					
OY		81	GLyProArGGLyGLyAlaGLyProAlaGLyProThrGLyProAlaGLyGLyCysSerVal	100					
Dd		393	GGCGCGGTGGAGAGCGAGGGCCCATGGGGGCTATCGGCGCTGGGGGGAGATTCTGGTA	452					
OY		101	ProProArGSerAlaPheSerAlaLysArgSerGIusArGValProProProSerAsp	120					
Dd		453	CCCCACAGCATGAGCTTCAGTCCAACGATCCAGAGCCGGGATACCTCCGACGACGAC	512					
OY		121	AlaProLeuProPheAspArgValLeuValasnGLyngInGLyHISTyArPaLaValThr	140					
Dd		513	ACACCCCTCACTTCCTGACCGGTGCTGTCTTAATAAGACGAGGCGCAATTCGACCCCACT	572					
OY		141	GLyLysPheThrCysGlnValProGLyValTYrTYrPheAlaValHisAlaThrValTYr	160					
Dd		573	GGCAAGTTCACTCGCAAGTCCGAGGCGTCACTACTTGGCTGTGACAGCCACATGTCAC	632					
OY		161	ArgAlaSerLeuGlnPheAspLeuValLysasnGLyIuserrIIeAlaSerPhePheGln	180					
Dd		633	CGGGCCACCTTGACAGTTTGATCTGTCAAACCGGCGATCCATCCGCTCTTCTTCAG	692					
OY		181	PhePheGLyGLYTTPProLYsPrOalASerLeuSerGLyGLyAlaMetValArgLeuGln	200					
Dd		693	TATTTGGGGGGTGGCCCAACGACGACCTCGCTTCAGAGGGGTGGGATGTAAAGCTAGAA	752					
OY		201	ProGLuasprGlnValTrpValGlnValGLyAspTYrIIeGLyIleTyAlaSer	220					
Dd		753	CCTAGAGCACAGGTGGGTGACAGTGGGCGTGGGTATTCATTGGCATTTATGCCAGC	812					
OY		221	IleLysTrpArSPserThrPheSerGLYPheLeuValTYrSerArPTPRhisSerSerPro	240					
Dd		813	ATCAAGACAGACATACCTTCCTGGAATTCCTGCTAATTCGTACGTGCACAGCTCCCA	872					
OY		241	ValPheala 243						
Dd		873							
			GTCTTCGCT 881						
<b>RESULT 8</b>									
AP003396/c									
LOCUS	AP003396	191362 bp	DNA	linear PRI 25-APR-2002					
DEFINITION	Homo sapiens genomic DNA, chromosome 11q clone:RP11-334E6, complete								
ACCESSION	AP003396								
VERSION	AP003396.1	GI:20302607							
KEYWORDS	HTG.								
SOURCE	Homo sapiens								
ORGANISM	Homo sapiens								
REFERENCE									
AUTHORS	1 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens genomic DNA Published Only in database (2002) 2 (bases 1 to 191362) Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.								
TITLE	REFERENCE								
AUTHORS									

[illegible]

Oy	89	AlaGlyProThrIleGlyProAlaGlyGluCysSerValProProAlaSerAlaPheSerAla	108
Db	6331	GGGGGGCCACACCGGGCCCTCCGGGGAGTGTCTCGCTGCTCCCGCATCCGCTTACAGGCC	6272
Oy	109	LysArgSerGluSerArgValProProProSerAspAlaProLeuProPheAspArgVal	128
Db	6271	AAGCGCTCCGAGACCGGGGCTCCCTCCGCGCTGTGACGACACCTTGCCCTTGACCGCGTG	6212
Oy	129	LeuValAsnGluGlnGlyHisTyrAspAlaValIleHrGlyLysPheIleCysGlnValPro	148
Db	6211	CTGGTGAACGACGACGGGACATTAGACGCCCTCACCGGCAAGTTCACCTGGCAGGTGCT	6152
Oy	149	GlyValTyrTyrPheAlaValHisAlaIleThrValTyrArgAlaSerLeuGlnPheAspLeu	168
Db	6151	GGGGCTCTACTCTTCGCGGTCCATGCCACCGCTCTACCGGGCCAGCTGTGACTTGAATCTG	6092
Oy	169	ValLysAsnGlyGluSerIleAlaSerPhePheGlnPhePheGlyGlyTyrProLysPro	188
Db	6091	GTGAAGAATAGCGCATCCATGCTCTTCTTCCAGTTTTCGGGGGGTGCCCAAGCA	6032
Oy	189	AlaSerLeuSerGlyGlyAlaMetValArgLeuGluProGluAspGlnValTyrValGln	208
Db	6031	GCCTCGCTCTCGGGGGGGCCATGTGGTGAGCTGTGAGCCCTGAGGACCAAGTGTGGGTCAAG	5972
Oy	209	ValGlyValGlyAspTyrIleGlyIleTyrAlaSerIleLysTyrAspSerThrPheSer	228
Db	5971	GTGGGTGTGGGTGACTACATTCGCAATTCGCAATCCAGCATCAAGACAGACGACCTTCTCC	5912
Oy	229	GlyPheLeuValTyrSerAspTyrPheIleSerSerProValPheAla	243
Db	5911	GGATTTCGTGGTGTACTCCGACTGCGACAGCTCCCAAGCTTGTGCT	5867
RESULT 9			
AP002956/c			
LOCUS	AP002956	219574 bp	DNA
DEFINITION	Homo sapiens genomic DNA, chromosome 11q clone:RI105H09, complete		
ACCESSION	AP002956		
VERSION	AP002956.1	GI:22525355	
KEYWORDS	HTG.		
SOURCE	Homo sapiens DNA, clone:RI105H09.		
ORGANISM	Homo sapiens		
	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
REFERENCE	1	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,	
AUTHORS		Tokochi,Y., Watanabe,H. and Sakaki,Y.	
		Homo sapiens 219,574 genomic DNA of 11q	
TITLE		Published Only in Database (2002)	
JOURNAL		2 (bases 1 to 219574)	
REFERENCE		Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,	
AUTHORS		Tokochi,Y., Watanabe,H. and Sakaki,Y.	
		Direct Submission	
TITLE		Submitted (24-NOV-2000) Masahira Hattori, The Institute of Physical	
JOURNAL		and Chemical Research (RIKEN), Genomic Sciences Center (GSC);	
REFERENCE		1-7-22 Suehiro-Chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan	
AUTHORS		(E-mail:hattori@gsr.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,	
		Tel:81-45-503-9111, Fax:81-45-503-9170)	
COMMENT		Overlapping Clones: pD11A, FQ3868	
		Cytogenetic Position: 21q22.1, region:D1S226-AML	
		STS Markers (ePCR): stsG53747, SHGC-16045, D1S2450, SHGC-7143,	
		WI-16056,	
		STS613054, sts-K57110, WI-8978, GDB:198117, stsG29284, SHGC-130657,	
		D1S1941E, WI-14589, stsG60191, stsS50535, A002048, stsG26546,	
		stsG41092,	
		TIGR-A005D38, BgaA7902, D1S869E, RH80030	
		Contamination: none detected	
		non-ACGT bases: none	
		Additional author information	
		Arai,Y., Kubo,T.,Ohki,M.	
		National Cancer Center Research Institute	
		Cancer Genomic Division	

[illegible]



Alsbrooks, S.L., Amaralunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbala, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnah, D., Bowck, J., Bowle, S., Brivea, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhury, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, R.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, R., Harris, C., Harris, R., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratoch, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Loulsged, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapa, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mel, G., Metzger, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okunolu, G., Orangun, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, X., Rivas, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherier, S., Scott, G., Shen, H., Shooshitari, N., Slisson, I., Sodergren, E., Sonalke, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Uman, K., Vasquez, L., Vera, Y., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczek, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y., Zhou, J., Zorrilla, S., Nelson, D., Weinstein, G., and Gibbs, R.

Unpublished  
2 (bases 1 to 173657)  
Direct Submission  
Morley, K.C.  
Submitted (22-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 173657)  
Morley, K.C.  
Direct Submission  
Submitted (14-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On Jul 12, 2002 this sequence version replaced g1:1860143.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GKAB  
Center clone name: CH230-904  
----- Summary Statistics  
Sequencing vector: Plasmid  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990329  
Consensus quality: 105614 bases at least Q40  
Consensus quality: 111210 bases at least Q30  
Consensus quality: 115587 bases at least Q20  
-----

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 72 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1137: contig of 1137 bp in length  
1138 1237: gap of unknown length  
1238 2720: contig of 1483 bp in length  
2721 2820: gap of unknown length  
2821 3984: contig of 1164 bp in length  
3985 4084: gap of unknown length  
4085 5158: contig of 1074 bp in length  
5159 5258: gap of unknown length  
5259 6306: contig of 1048 bp in length  
6307 6406: gap of unknown length  
6407 7523: contig of 1117 bp in length  
7524 7623: gap of unknown length  
7624 8631: contig of 1008 bp in length  
8632 8731: gap of unknown length  
8732 9806: contig of 1075 bp in length  
9807 9906: gap of unknown length  
9907 1115: contig of 1249 bp in length  
1116 1125: gap of unknown length  
1126 1256: contig of 1313 bp in length  
1257 1268: gap of unknown length  
1269 13704: contig of 1036 bp in length  
13705 13804: gap of unknown length  
13805 14931: contig of 1127 bp in length  
14932 15031: gap of unknown length  
15032 16084: contig of 1053 bp in length  
16085 16184: gap of unknown length  
16185 17858: contig of 1674 bp in length  
17859 17958: gap of unknown length  
17959 19035: contig of 1077 bp in length  
19036 19135: gap of unknown length  
19136 20291: contig of 1156 bp in length  
20292 20391: gap of unknown length  
20392 21643: contig of 1252 bp in length  
21644 21743: gap of unknown length  
21744 22846: contig of 1103 bp in length  
22847 22946: gap of unknown length  
22947 24684: contig of 1738 bp in length  
24685 24784: gap of unknown length  
24785 26405: contig of 1621 bp in length  
26406 26505: gap of unknown length  
26506 27716: contig of 1211 bp in length  
27717 27816: gap of unknown length  
27817 28876: contig of 1060 bp in length  
28877 28976: gap of unknown length  
28977 30019: contig of 1043 bp in length  
30020 30119: gap of unknown length  
30120 31550: contig of 1431 bp in length  
31551 31650: gap of unknown length  
31651 33128: contig of 1478 bp in length  
33129 33228: gap of unknown length  
33229 34763: contig of 1535 bp in length  
34764 34863: gap of unknown length  
34864 36404: contig of 1541 bp in length  
36405 36504: gap of unknown length  
36505 37957: contig of 1453 bp in length  
37958 38057: gap of unknown length  
38058 40293: contig of 2236 bp in length  
40294 40393: gap of unknown length  
40394 41696: contig of 1305 bp in length  
41697 41796: gap of unknown length  
41799 43155: contig of 1357 bp in length  
43156 43255: gap of unknown length  
43256 45193: contig of 1938 bp in length  
45194 45293: gap of unknown length  
45294 47217: contig of 1924 bp in length  
47218 47317: gap of unknown length



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* 47318 49331: contig of 1914 bp in length
* 49332 49331: gap of unknown length
* 49332 51305: contig of 1874 bp in length
* 51306 51305: gap of unknown length
* 51306 53117: contig of 1812 bp in length
* 53118 53217: gap of unknown length
* 53218 55542: contig of 2325 bp in length
* 55543 55642: gap of unknown length
* 55643 57451: contig of 1809 bp in length
* 57452 57551: gap of unknown length
* 57552 60851: contig of 3300 bp in length
* 60852 60951: gap of unknown length
* 60952 62718: contig of 1767 bp in length
* 62719 62818: gap of unknown length
* 62819 64976: contig of 2158 bp in length
* 64977 65076: gap of unknown length
* 65077 67855: contig of 2779 bp in length
* 67856 67955: gap of unknown length
* 67956 71313: contig of 3358 bp in length
* 71314 71413: gap of unknown length
* 71414 73659: contig of 2246 bp in length
* 73660 73759: gap of unknown length
* 73760 75549: contig of 1790 bp in length
* 75550 75649: gap of unknown length
* 75650 79106: contig of 3457 bp in length
* 79107 79206: gap of unknown length
* 79207 83551: contig of 4345 bp in length
* 83552 83651: gap of unknown length
* 83652 86053: contig of 2402 bp in length
* 86054 86153: gap of unknown length
* 86154 88659: contig of 2506 bp in length
* 88660 88759: gap of unknown length
* 88760 90078: contig of 1319 bp in length
* 90079 90178: gap of unknown length
* 90179 92201: contig of 2023 bp in length
* 92202 92301: gap of unknown length
* 92302 94877: contig of 2576 bp in length
* 94878 94977: gap of unknown length
* 94978 96946: contig of 1969 bp in length
* 96947 97046: gap of unknown length
* 97047 99897: contig of 2851 bp in length

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Alignment Scores:

Pred. No.:	1.05e-40	Length:	173657
Score:	1183.50	Matches:	225
Percent Similarity:	69.07%	Conservative:	5
Best Local Similarity:	67.57%	Mismatches:	6
Query Match:	89.32%	Indels:	97
DB:	2	Gaps:	1

US-09-944-944-42 (1-243) x AC112557 (1-173657)

```

QY 8 LeuLeuLeuGlyLeuAlaAlaGlySerProProLeuAspAspAsnLysIleProSerLeu 27
DB 43284 CTGCTTCGGGCTGTCGATCAGGCGCTCTCTCTGAGCAACAAATCCCGCCGCTG 43343
QY 28 CysProGlyHisProGlyLeuProGlyThrProGlyHisHisGlySerGlyLeuPro 47
DB 43344 TGTCCCGGACCGCCGCTCCACAGCACACCGACCCACACGACGACGACGCTGCTG 43403
QY 48 GlyArgAspGlyArgAspGlyArgAspGlyArgAspGlyArgAspGlyArgAspGly 67
DB 43404 GGGCGTGAAGCGCGCGATGCGCGGACGCGTGCACCGGAGCTCCGCGAGAGAAAGCG 43463
QY 68 GlyGlyArgPro----- 71
DB 43464 GGGCGGAGACCGCGGTGAAGACTATTTCGTTGACATGATGATGATGATGATGATG 43523
QY 71 ----- 71
DB 43524 CAGCCCTGCTCTGATGATGATCTTTGGGGGTCAGAGGTCGCCGAGGGGGCGCTACTCTC 43583
QY 71 ----- 71

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DB 43584 COTCATTCAGTACAGACGAGCGGGGAGGTGGGCTGCGGGTGGAGGGGTGATGAC 43643
QY 71 ----- 71
DB 43644 CCCCAGGAAATCAGAAACCTGATCCCTTACTACAGACTTCAGATCTGTCGCCGACAG 43703
QY 71 ----- 71
DB 43704 AGGTACAGCCTGGAGGCTGGAGGCTTGTGACTTTCCTCCCTTCCTCATCCCT 43763
QY 72 ---GlyLeuProGlyProArgGlyAspProGlyProArgGlyGlyAlaGlyProAlaGly 90
DB 43764 GCAGACATACCTGGGCGCACACGTGGGAGGCGCGCGCGCGCGGAGAGAGACCTGGGG 43823
QY 91 ProThrGlyProAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 110
DB 43824 GCTATCGGCGCGCGCGGAGGAGTGTGCGGTCGCCACATCAGCTTCAGTCCAAAGCGA 43883
QY 111 SerGlySerArgValProProProSerAspAlaProLeuProProAspArgValLeuVal 130
DB 43884 TCAGAGAGCGGGGTACCTCCGCGACGACACCCCTTACCTTGACCGGTGTGCTGCTC 43943
QY 131 AsnGlyGlyHisGlyAspAlaValThrGlyGlyPheThrCysGlyValProGlyVal 150
DB 43944 AATGACGAGGACATTAAGATGACATGACATGACGACGACGACGACGACGACGACGACG 44003
QY 151 TyrTyrPheAlaValHisAlaThrValThrValThrValThrValThrValThrValThr 170
DB 44004 TACTACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 44063
QY 171 AsnGlyGlySerIleAlaSerPhePheGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 190
DB 44064 AATGCGCAATCATAGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 44123
QY 191 LeuSerGlyGlyAlaMetValArgLeuGlyProGlyAspGlyValThrValGlyValGly 210
DB 44124 CTCCTGAGGGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 44183
QY 211 ValGlyAspTyrIleGlyIleTyrAlaSerIleTyrAlaSerIleTyrAlaSerIleTyr 230
DB 44184 GTGGGTGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 44243
QY 231 LeuValTyrSerAspThrHisSerSerProValPheAla 243
DB 44244 CTCGTATTCGATGACGACGCTCCCGAGCTTCGCT 44282

```

RESULT 12  
AC124577 249283 bp DNA linear HTG 11-AUG-2002  
LOCUS AC124577  
DEFINITION Mus musculus chromosome UNK clone R23-162p10, WORKING DRAFT  
SEQUENCE, 10 unordered pieces.  
AC124577.2 GI:22203905  
VERSION AC124577.2  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 249283)  
McPherson,J.D. and Waterston,R.H.  
The sequence of Mus musculus clone  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 249283)  
McPherson,J.D. and Waterston,R.H.  
Direct Submission  
TITLE Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park  
AUTHORS McPherson,J.D. and Waterston,R.H.  
JOURNAL 3 (bases 1 to 249283)  
Submitted (11-AUG-2002) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA



OY	173	GlsrserlIeaIaslerPhePhgclImphheglvlytRProLySProAlasSerleuSer	192
Dd	46810	CAGTCCATCGGCTCTTTCTTCACGATTATTTGGGGGGGTGCCCAACCACGCTCGCTGCA	46882
OY	193	GlYglYalameValarLargLeugluProGluaspGlnValatrpValGlnvalGlYalGlY	212
Dd	46870	GGGGGTGCAGTAGGTAAAGGCTAGAACCCTGAGACACGAGTGTTGGGTGCAGGTGGGCGTGGGT	46922
OY	213	AsprYrllegllYlleTyAlaSerlleYshraspserrThrhPheSerClYpheleuVal	232
Dd	46930	GATTCACATGGCATCTATGATCCAGCAYTCAAGACAGACAGTACCTCTCGATTTCTCGTC	46982
OY	233	TySerAsprThrasSerSerProValPheala	243
Dd	46990	TATTCGTACTGGCACAGCTCCCAAGTCTTCGCT	47022
RESULT 13			
LOCUS	AR138195	729 bp	DNA linear PAT 16-JUN-2001
DEFINITION	Sequence 10 from patent US 6197930.		
ACCESSION	AR138195		
VERSION	AR138195.1 GI:14479704		
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 729)		
AUTHORS	Sheppard,P.O. and Humes,J.M.		
TITLE	Adipocyte-specific protein homologs		
JOURNAL	Patent: US 6197930-A 10 06-Mar-2001;		
FEATURES	Location/Qualifiers		
source	1..729		
BASE COUNT	77 a 101 c 160 g 81 t 310 others		
ORIGIN	/organism="unknown"		
Alignment Scores:			
Pred. No.:	7.96e-38	Length:	729
Score:	1072.00	Matches:	191
Percent Similarity:	78.60%	Conservative:	0
Best Local Similarity:	78.60%	Mismatches:	52
Query Match:	80.91%	Indels:	0
DB:	6 Gaps:		0
US-09-944-944-42 (1-243) x AR138195 (1-729)			
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Dd	1	ATGAGNCNCNTNYNTNGTYNTYTNTNTNTNGNTNCGNGCMSCCNCTYNAY	60
OY	21	AspasnlyslleProSerleucysProglyHtsProglyleuProglyThProglyHis	40
Dd	61	GAYAAYARAARHCNCMSNYTMTGYCCMGNCAVCCNGCNTNYTCCNGMAACMCNCGNCAY	120
OY	41	HlsGlSerGlnglyleuProglYArGraspGlyArGraspGlyArGraspGlyAlAProgly	60
Dd	121	CAYGGMNSNCRGRGNYTTCCKGCMNGMNCAYGCMNGMGAYGGMNGATGGMNCNCGN	180
OY	61	AlAbProglyluYsglyGlyglYlarGrProglyleuProglyProatrglyYasPro	80
Dd	181	GCNCCNCGNGARRAARGGANGRGNGMNCNCGNNTNCCNCGMCMGNGMGAYCCN	240
OY	81	GLYProarGglYgluaIaglyProalaglyProthrGlyProalaglyGlcusserval	100
Dd	241	GGNCCNMNGNGGARCGNGCMNGCMNCGMNCNCGNCCNCGNGCGARTGYWSNCTN	300
OY	101	ProProarGserAlaPheSerAlalyArGserGjuseArGvalProProPaserasp	120
Dd	301	CCNCCNMNGMSNGCNTTYWMSGCNAABRMGSNAGRWMSNMONGNTNCCNCCNCSNAY	360
OY	121	AlAProleuProPheaspArgValleuValasnGluGnglyHstYrAspalayaThr	140
Dd	361	GCNCCNCTNCTTYGAAMGNGTYNTNTNAAYGARCRGNCNCAYTAAGAAGCMGTNACN	420

Y	141	GI:141594164	182429 bp	DNA	linear	HTG 03-NOV-2000
LOCUS	AP001557	182429 bp	DNA	linear	HTG 03-NOV-2000	
DEFINITION	Homo sapiens chromosome 11 clone RP11-680A7 map 11q23, WORKING DRAFT SEQUENCE, 21 unordered pieces.					
ACCESSION	AP001557	GI:11094164				
VERSION	AP001557.3					
KEYWORDS	HTG; HTGS-PHASE1; HTGS-DRAFT					
SOURCE	Homo sapiens DNA, clone:RP11-680A7.					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.					
AUTHORS	1 (bases 1 to 182429)					
TITLE	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.					
JOURNAL	Homo sapiens 182,429 genomic DNA of 11q23					
REFERENCE	Published only in Database (2000)					
AUTHORS	2 (bases 1 to 182429)					
TITLE	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.					
JOURNAL	Direct Submission					
COMMENT	Submitted (29-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), genomic Sciences Center (GSC); 1-7-2 Tetsuhiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)					
	On Nov 3, 2000 this sequence version replaced gi:8117391.					
	----- Genome Center					
	Center: RIKEN Genomic Sciences Center (GSC)					
	Center code: RIKEN					
	Web site: http://hgp.gsc.riken.go.jp/					
	Contact: hattori@gsc.riken.go.jp					
	----- Project Information					
	Center project name: Humdrat11					
	Center clone name: RP11-680A7					
	----- Summary Statistics					
	Sequencing vector: PCR products; 100% of reads					
	Chemistry: Dye-terminator ET-amersham; 100% of reads					
	Assembly program: Phrap; version 0.990329					
	Consensus quality: 175597 bases at least Q40					
	Consensus quality: 178555 bases at least Q30					
	Consensus quality: 179768 bases at least Q20					
	Insert size: 180429; sum-of-contigs					
	Quality coverage: 9.01x in Q20 bases; sum-of-contigs					
	-----					
	NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and the order in this sequence record is arbitrary. Gaps between the					

NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the

contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```

1 30107 contig of 30107 bp in length
30208 54357 contig of 24150 bp in length
54458 69839 contig of 15382 bp in length
69940 84048 contig of 14109 bp in length
84149 95177 contig of 11029 bp in length
95278 10763 contig of 12486 bp in length
107864 119057 contig of 11194 bp in length
119158 128134 contig of 8977 bp in length
128235 136903 contig of 8659 bp in length
137004 145887 contig of 8884 bp in length
145988 153199 contig of 7212 bp in length
153300 159565 contig of 6266 bp in length
159666 163580 contig of 3915 bp in length
163681 165152 contig of 1472 bp in length
165153 165252 contig of 100 bp in length
165253 166901 contig of 1649 bp in length
166902 167001 contig of 100 bp in length
167002 170460 contig of 3459 bp in length
170461 170560 contig of 100 bp in length
170561 172761 contig of 2201 bp in length
172762 172861 contig of 100 bp in length
172862 173605 contig of 2744 bp in length
173606 175705 contig of 100 bp in length
175706 178308 contig of 2603 bp in length
178309 178408 contig of 100 bp in length
178409 180918 contig of 2510 bp in length
180919 181018 gap of 100 bp

```

\* NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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1 30107: contig of 30107 bp in length
30108 30207: gap of 100 bp
30208 54357: contig of 24150 bp in length
54358 54457: gap of 100 bp
54458 69839: contig of 15382 bp in length
69840 69939: gap of 100 bp
69940 84048: contig of 14109 bp in length
84049 84148: gap of 100 bp
84149 95177: contig of 11029 bp in length
95178 95277: gap of 100 bp
95278 107763: contig of 12486 bp in length
107764 107863: gap of 100 bp
107864 119057: contig of 11194 bp in length
119058 119157: gap of 100 bp
119158 128134: contig of 8977 bp in length
128135 128234: gap of 100 bp
128235 136903: contig of 8659 bp in length
136904 137003: gap of 100 bp
137004 145887: contig of 8884 bp in length
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145988 153199: contig of 7212 bp in length
153200 153289: gap of 100 bp
153300 159565: contig of 6266 bp in length
159566 159665: gap of 100 bp
159666 163580: contig of 3915 bp in length
163581 163680: gap of 100 bp
163681 165152: contig of 1472 bp in length
165153 165252: gap of 100 bp
165253 166901: contig of 1649 bp in length
166902 167001: gap of 100 bp
167002 170460: contig of 3459 bp in length
170461 170560: gap of 100 bp
170561 172761: contig of 2201 bp in length
172762 172861: gap of 100 bp
172862 173605: contig of 2744 bp in length
173606 175705: gap of 100 bp
175706 178308: contig of 2603 bp in length
178309 178408: gap of 100 bp
178409 180918: contig of 2510 bp in length
180919 181018: gap of 100 bp

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FEATURES \* 181019 182429: contig of 1411 bp in length.  
source 1..182429

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/map="11q23"
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181019..182429
/note="assembly-fragment"
BASE COUNT 45724 a 42083 c 43875 g 48747 t 2000 others
ORIGIN

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Alignment Scores: 2.29e-29 Length: 182429  
Pred. No.: 914.50 Matches: 183  
Score: 82.43% Conservative: 0  
Percent Similarity: 82.43% Mismatches: 12  
Best Local Similarity: 69.02% Indels: 28  
Query Match: 2 Gaps: 3

US-09-944-944-42 (1-243) x AP001557 (1-182429)

QY 48 G1YARGASPG1YARGASPG1YALAPROGLYALAPROGLYGLYGLY 67  
||||| ||| ||| ||| |||

Db 107866 GGAAGGGGTGAGAGAGTACCGTGGCGGAGGA---GGCGTGGCCAGACTCAGGCAGG 107922  
||||| ||| ||| ||| |||

QY 68 GLYGLY----- 69  
|||||

Db 107923 GCGCGGAGGGGTGACCTAGAGTCCGCGCGCGGTGAGCGCGCGCTA 107982  
|||||

QY 70 -----ATGPT-----G1YLEUPROGLYPROAG1YASPPROGLY 81  
|||||

[illegible]

TITLE	JOURNAL	REFERENCE	AUTHORS	REFERENCE	TITLE	JOURNAL		
Unpublished	2 (bases 1 to 150653)	Worley,K.C.	Submitted (16-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA	3 (bases 1 to 150653)	Worley,K.C.	Direct Submission Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA		
On Jul 12, 2002 this sequence version replaced gi.18702083.	-----	Genome Center	Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Project Information Center project name: GPFP Center clone name: CH230-21501	-----	Summary Statistics	Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 86559 bases at least Q40 Consensus quality: 95630 bases at least Q30 Consensus quality: 102140 bases at least Q20		
* NOTE: Estimated insert size may differ from sequence length ( see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html) * NOMP: This is a 'working draft' sequence. It currently * consists of 78 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.	*	1	1221: contig of 1221 bp in length	*	1	1221: contig of 1221 bp in length		
*	1222	1321: gap of unknown length	*	1222	1321: gap of unknown length	*	1222	1321: gap of unknown length
*	1322	2837: contig of 1516 bp in length	*	1322	2837: contig of 1516 bp in length	*	1322	2837: contig of 1516 bp in length
*	2838	2937: gap of unknown length	*	2838	2937: gap of unknown length	*	2838	2937: gap of unknown length
*	2938	4040: contig of 1103 bp in length	*	2938	4040: contig of 1103 bp in length	*	2938	4040: contig of 1103 bp in length
*	4041	4140: gap of unknown length	*	4041	4140: gap of unknown length	*	4041	4140: gap of unknown length
*	4141	5496: contig of 1356 bp in length	*	4141	5496: contig of 1356 bp in length	*	4141	5496: contig of 1356 bp in length
*	5497	5596: gap of unknown length	*	5497	5596: gap of unknown length	*	5497	5596: gap of unknown length
*	5597	7002: contig of 1406 bp in length	*	5597	7002: contig of 1406 bp in length	*	5597	7002: contig of 1406 bp in length
*	7003	7102: gap of unknown length	*	7003	7102: gap of unknown length	*	7003	7102: gap of unknown length
*	7103	8482: contig of 1380 bp in length	*	7103	8482: contig of 1380 bp in length	*	7103	8482: contig of 1380 bp in length
*	8483	8582: gap of unknown length	*	8483	8582: gap of unknown length	*	8483	8582: gap of unknown length
*	8583	9994: contig of 1412 bp in length	*	8583	9994: contig of 1412 bp in length	*	8583	9994: contig of 1412 bp in length

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11536 11635: gap of unknown length  
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14621 16066: contig of 1446 bp in length  
16067 17258: contig of 1092 bp in length  
17259 17358: gap of unknown length  
17359 18699: contig of 1341 bp in length  
18700 18799: gap of unknown length  
18800 20300: contig of 1501 bp in length  
20301 20400: gap of unknown length  
22507 22607: contig of 2107 bp in length  
22608 24037: gap of unknown length  
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33141 33240: gap of unknown length  
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37460 37559: gap of unknown length  
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38853 38952: gap of unknown length  
38953 40667: contig of 1715 bp in length  
40668 42359: gap of unknown length  
42359 42459: contig of 1592 bp in length  
42460 43493: gap of unknown length  
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43594 44854: contig of 1261 bp in length  
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44955 46196: contig of 1242 bp in length  
46197 46296: gap of unknown length  
46297 47678: contig of 1382 bp in length  
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60721 61925: contig of 1205 bp in length  
61926 62025: gap of unknown length  
62026 63066: contig of 1041 bp in length  
63067 63166: gap of unknown length  
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69577 70984: contig of 1408 bp in length  
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71085 73266: contig of 2182 bp in length  
73267 73366: gap of unknown length  
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## Alignment Scores:

Score: 3.89e-23 Length: 150653  
Percent Similarity: 765.00 Matches: 174  
Best Local Similarity: 51.14% Conservative: 6  
Query Match: 57.74% Mismatches: 45  
DB: Gaps: 128

US-09-944-944-42 (1-243) x AC107174 (1-150653)

QY 11 G1YLeuAlaIaG1SerProLeuAspAspAnylsIleProSerLeuCySProGly 30  
Db 34683 GCGCGGGCCCGGGGGGGAACCA-----CCGCGAAGGGCA 34648  
QY 31 HisProGlyLeuProGlyThrPro----- 38  
Db 34647 GAGCGAGGGCGGGAGGACCGCGGAGGAGGAGCGGCGGGGGGGAG 34588  
QY 39 -----G1YHisG1SerG1ng1LeuProGly----- 48  
Db 34587 GGAAGGGGGGAAGGAGGAGCGGGCGGAGGAGGAGGAGGAGGAGGAGG 34528  
QY 49 -----ArgAspG1YArgAspG1YArgAsp 56  
Db 34527 AGAGGGGGGGCGCCAGGAGTAAAGAGAGGGGGGAGGAGGAGGAGGAGG 34468  
QY 57 G1YAlaProGlyAlaProGlyG1YLeuG1YLeuG1YArg----- 70  
Db 34467 GGGCGGGAAGAGAGCGGAGTATCGCGGGGGGGCGAGAGGAGGGGGAGA 34408  
QY 70 ----- 70  
Db 34407 GGGNN 34348  
QY 70 ----- 70  
Db 34347 NNACTACAATACGCCN 34288  
QY 70 ----- 70  
Db 34287 TCGCGCGAGTATACCGGTACGGGGAACGATCCNCCCGTTCANTCTGGGTGCA 34228  
QY 71 -----ProGlyLeu--- 73  
Db 34227 TCACCCCGGCCAGGGGAGGAGGAGNNNGGNNNTTCTCTCTTCACTCCCATAGG 34168  
QY 74 ---ProG1YProArg1YAspProG1YProArg-G1YAlaG1YProAlaG1YProTh 92  
Db 34167 ACTGCTGGGCGCGGAGAGACCCCGCGCGGTGAGAGACCAACCTGGGGGTCTAT 34108  
QY 92 rG1YProAlaG1YLeuCySserValProProArgSerAlaPheSerAlaYsArgSerG1 112



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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 21, 2003, 16:07:46 ; Search time 266 Seconds

(without alignments)  
2057.277 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325  
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Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
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Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1325	100.0	1347	20	AAK24684	Human adipocyte-sp
2	1325	100.0	1377	20	AAK87258	CDNA clone encodin
3	1325	100.0	1377	20	AAK80052	Human PRO344 nucle
4	1325	100.0	1377	21	AAK58626	Human PRO344 prote
5	1325	100.0	1377	21	AAK01241	Human PRO344 prote
6	1325	100.0	1377	21	AAK46907	CDNA encoding nove
7	1325	100.0	1377	21	AAK49560	Human PRO344 CDNA
8	1325	100.0	1377	22	AAK21424	Human CDNA sequenc
9	1295	97.7	728	22	AAK44971	Human TANGO 253 OR
10	1295	97.7	728	22	AAK44995	Human secreted pro
11	1295	97.7	728	22	AAK44997	Human secreted pro
12	1295	97.7	1338	22	AAK44970	Human TANGO 253 co
13	1295	97.7	1338	22	AAK44998	Human secreted pro
14	1293	97.6	728	22	AAK44994	Human secreted pro
15	1293	97.6	1338	22	AAK45001	Human secreted pro
16	1291	97.4	728	22	AAK44996	Human secreted pro
17	1291	97.4	1338	22	AAK44999	Human secreted pro
18	1291	97.4	1338	22	AAK45000	Human secreted pro
19	1271	95.9	1001	21	AAK61745	CDNA encoding rat
20	1271	95.9	1001	22	AAK99678	SKN cell CDNA, SE
21	1271	95.9	1001	24	ABL34830	Rat CDNA isolated
22	1271	95.9	1015	21	AAK61635	CDNA encoding rat
23	1271	95.9	1015	22	AAK99568	SKN cell CDNA, SE
24	1271	95.9	1015	22	ABL34720	Rat CDNA isolated
25	1258	94.9	729	22	AAK44973	Murine TANGO 253 O
26	1258	94.9	1263	22	AAK44972	Murine secreted pr
27	1256	94.8	729	22	AAK45001	Murine secreted pr
28	1256	94.8	1263	22	AAK45009	Murine secreted pr
29	1254	94.6	729	22	AAK45038	Murine secreted pr
30	1254	94.6	729	22	AAK45039	Murine secreted pr
31	1254	94.6	729	22	AAK45040	Murine secreted pr
32	1254	94.6	1263	22	AAK45006	Murine secreted pr
33	1254	94.6	1263	22	AAK45007	Murine secreted pr
34	1254	89.6	1263	22	AAK45008	Murine secreted pr
35	1183	89.3	1082	23	AAK76911	DNA encoding novel
36	1072	80.9	729	20	AAK24685	Degenerate DNA enc
37	1048	79.1	3248	24	AAK39624	Human secreted pro
38	659	49.7	764	24	AAK62228	CDNA sequence #15
39	535.5	40.4	601	22	AAK44991	Rat TANGO 253 codi
40	478	36.1	536	23	AAK76910	DNA encoding novel
41	449.5	33.9	678	24	ABL57719	Human sbg103026C1
42	442.5	33.4	1002	24	ABL57718	Human sbg103026C1
43	436	32.9	1276	18	AAK51048	Murine adipocyte c
44	436	32.9	1276	22	AAK10372	Mouse ACRP30 CDNA
45	436	32.9	1276	24	ABA96119	Mouse acrp30 prote

## ALIGNMENTS

RESULT 1  
AAK24684

ID AAK24684 standard: CDNA: 1347 BP.

AC AAK24684;

DT 21-JUN-1999 (first entry)

DE Human adipocyte-specific protein zsig39 CDNA.

KW Adipocyte-specific protein; zsig39; human; fatty acid metabolism;

KW energy balance; nutrition; antimicrobial; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 198..929

/\*tag= a

FT sig\_peptide 198..251  
 FT /\*tag= b  
 FT /note= "alternatively nucleotides 198-242"  
 FT mat\_peptide 252..926  
 FT /\*tag= c  
 FT /note= "alternatively nucleotides 243-926"  
 PN W09910492-A1.  
 PD 04-MAR-1999.  
 PE 26-AUG-1998; 98WO-US17724.  
 PF 26-AUG-1997; 97US-0056983.  
 PR 26-AUG-1997; 97US-0056983.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Humes JM, Shepard PO;  
 DR WPI: 1999-204665/17.  
 DR P-PSDB; AAW97984.  
 XX zsig39 protein - used to modulate fatty acid metabolism  
 PS Claim 16; 109-111; 132pp; English.  
 XX This isolated polynucleotide encodes human adipocyte-specific  
 CC protein zsig39 (AAW97984). Claimed polynucleotides comprise  
 CC nucleotides 243-962, 285-482, 285-485, 285-485, 285-488,  
 CC 285-491, 285-491, 491-926 of this isolated polynucleotide.  
 CC Novel zsig39 polypeptides were initially identified by querying an  
 CC EST database for secretory signal sequences characterised by an  
 CC upstream methionine start site, a hydrophobic region of approximately  
 CC 13 amino acids and a cleavage site. A single EST sequence was  
 CC discovered, and the novel polypeptide encoded by the full-length  
 CC cDNA allowed the identification of a homologue relationship with  
 CC adipocyte complement related protein Acrp30 and adipocyte secreted  
 CC protein apM1. A full-length clone was obtained from a lung tissue  
 CC library. The zsig39 gene maps to the 11q23.3 region. Expression  
 CC vectors, cultured cells and a method of producing zsig39 polypeptide  
 CC are claimed, as well as probes and primers (useful in diagnostic  
 CC applications), and a method for modulating free fatty acid  
 CC metabolism by administering a zsig39 polypeptide. The zsig39  
 CC polypeptide may also be used in organ preservation, for  
 CC cryopreservation, for surgical pretreatment to prevent injury due  
 CC to ischaemia and/or inflammation, and as an antimicrobial agent,  
 CC promoting lysis or phagocytosis of infectious agents.  
 XX  
 SO Sequence 1347 BP; 235 A; 421 C; 465 G; 226 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 7.57e-54 Length: 1347  
 Score: 1325.00 Matches: 243  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 20 Gaps: 0  
 US-09-944-944-42 (1-243) x AAX24684 (1-1347)  
 QY 1 MetArgProLeuLeuValLeuLeuLeuLeuLeuAlaAlaGlySerProProLeuAsp 20  
 DB 198 ATGAGGCGACCTCTGCTGCTCTCTGCGGCTGCGGCGCGCTGCCCTCCACTGAC 257  
 QY 21 AspAsnLysIleProSerLeuCySProGlyHisProGlyLeuProGlyThProGlyHis 40  
 DB 258 GACAACAAGATCCCAAGCTCTGCTCCGCGGCAACCCGCTTCCAGGCAACGCGGCGCAC 317  
 QY 41 HisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyAlaProGly 60  
 DB 318 CATGGCAGCAGGCGCTGCGCGGCGCGATGCGCGACGCGCGCGACGCGCGCGCGCGG 377  
 QY 61 AlaProGlyIleuLysGlyGlnGlyArgProGlyLeuProGlyProAlaGlyAspPro 80

DB 378 GCTCCGGAGAGAAAGGAGGCGCGGAGCGCGGAGCTCCGCGGAGCTCGAGGAGCC 437  
 QY 81 GlyProArgGlyGlnAlaGlyProAlaGlyProHnGlyProAlaGlyGlnCysSerVal 100  
 DB 438 GGGCGCGCAGAGAGGCGGAGACCCCGGGGCGCCACCGGGCTCGCGGGAGTGTGGTG 497  
 QY 101 ProProArgSerAlaPheSerAlaLysArgSerGlnSerArgValProProSerAsp 120  
 DB 498 CCGCGGATCGCGCTTCAGCGCGCAAGCGCTCCGAGACCGGGTCCCTCCGCGCTGAC 557  
 QY 121 AlaProLeuProPheAspArgValLeuValAsnGlnGlnGlyHisTyrAspAlaValThr 140  
 DB 558 GCACCCCTGGCCCTTCGACGCGCGGTGTGTGAACGAGCGGAGCATTTACAGCCCTCAC 617  
 QY 141 GlyLysPheThrCysGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyr 160  
 DB 618 GGCAGATTACCTGCGCAGGTGCTGGGTCTACTACTCTCCGCTCAGTCCAGCGCTCAC 677  
 QY 161 ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyLysSerIleAlaSerPhePheGln 180  
 DB 678 CGGGCAGACCTGCAAGTTGATCTGTGAAGATGCGAATTCATTGCTTCTTCAG 737  
 QY 181 PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGlu 200  
 DB 738 TTTTTCGGGGGTGGCCACACCTCTGCTGCGGGGGCCATGAGGTGAG 797  
 QY 201 ProGluAspGlnValAlaTyrValGlnValGlyAlaGlyAspTyrIleGlyIleTyrAlaSer 220  
 DB 798 CCGGAGGCAAGTGTGGGTGTGAGGTGTGGGTGTGCTACTATTCATTCATTCATTCAGC 857  
 QY 221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspTrpHisSerSerPro 240  
 DB 858 ATCAAGACAGACAGACACTTCTCGGATTTCTGTGTGACTCGACTGACAGCTCCCA 917  
 QY 241 ValPheAla 243  
 DB 918 GTCTTGTCT 926  
 RESULT 2  
 AAX87258 standard; cDNA: 1377 BP.  
 AC AAX87258;  
 XX 27-SEP-1999 (first entry)  
 DE cDNA clone encoding human PRO344, amplified in tumour cells.  
 XX PRO344; UNQ303; cancer; tumour; diagnosis; therapy; human; ss.  
 XX Homo sapiens.  
 OS  
 XX Key 227..958 Location/Qualifiers  
 FT CDS 227..958  
 FT sig\_peptide 227..271  
 FT /\*tag= a  
 FT mat\_peptide 272..955  
 FT /\*tag= b  
 FT /\*tag= c  
 PN W09935170-A2.  
 PD 15-JUL-1999.  
 PE 05-JAN-1999; 99WO-US00106.  
 PF 20-NOV-1998; 98US-0109304.  
 PR 05-JAN-1998; 98US-0070440.  
 PR 29-APR-1998; 98US-0083500.  
 PR 22-MAY-1998; 98US-0086414.  
 PR 10-JUN-1998; 98US-0088742.  
 PR 10-NOV-1998; 98US-0107783.





[illegible]

QY	16	ArgylaserleuGlnPheaspheValuILysasnglyIuserIleAlaSerPhephGln	180
Db	707	CGGGCAGCCTGCAAGTTTGATCTGGTGAAGAAAGCGAATCCATTGCTTCTCCAG	766
QY	181	PhephGlyIYtPRPolysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGlu	200
Db	767	TTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGCCATGTGAGGCTGAG	826
QY	201	ProGluAspGlnValITrPValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSer	220
Db	827	CCCTGAGCAGCCAACTGGGGGCGAGGGGTGTGGGTGACTCATTTGGCATCTAAGCCAGC	886
QY	221	IleYThrAspSerThrPheSerGlyPheLeuValIYrSerAspTyrPHisSerSerPro	240
Db	887	ATCAAGACACACAGCAGCATTCTCCGATTTCTGTGTGTTACTCCGACTGGACAGCTCCCA	946
QY	241	ValPheAla 243	
Db	947	GTCCTTCTCT 955	
RESULT 5			
ID	AAD01241	standard; cDNA; 1377 BP.	
XX	AAD01241		
AC	AAD01241		
XX			
DT	08-NOV-2000	(first entry)	
XX			
DE	Human PRO344	protein encoding cDNA clone, DNA0592-1242.	
XX			
KW	PRO344: DNA0592-1242; human: ATCC No: 209492; antiproliferative;		
KW	neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;		
KW	breast; prostate; colon; lung; renal; ovarian; central nervous system;		
KW	CNS; leukemia; melanoma; Expressed Sequence Tag; EST; secreted protein;		
KW	extracellular domain; ECD; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	227..958	
FT		/*tag= a	
FT		/product= "Human PRO344 protein"	
FT		/note= "Derived from clone DNA0592-1242"	
FT	sig_peptide	227..271	
FT		/*tag= b	
FT	mat_peptide	272..955	
FT		/*tag= c	
FT		/product= "Mature human PRO344 protein"	
XX			
XX	WO200032778-A2.		
XX			
PD	08-JUN-2000.		
XX			
PF	30-NOV-1999;	99WO-US28409.	
XX			
PR	01-DEC-1998;	98WO-US25108.	
PR	16-DEC-1998;	98US-0112850.	
PR	22-DEC-1998;	98US-0113296.	
PR	20-JUL-1999;	99US-0144758.	
PR	26-JUL-1999;	99US-0145698.	
PA	(GETH ) GENENTECH INC.		
XX			
PI	Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;		
XX			
XX	WPI: 2000-412325/35.		
DR	P-PSDB; AAY71468.		
XX			
PT	New composition useful for inhibiting neoplastic cell growth and for		
PT	treating cancers, comprises PRO635, PRO344 or PRO364 polypeptide or		
PT	their antagonists		
XX			









QY 81 GlyProArgGlyGluAlaGlyProAlaGlyProThrGlyProAlaGlyGluCysSerVal 100  
DB 467 GGGCCGCGAGAGAGAGCGGAGCCCGGGGCGCCGCGGAGTGTCTGGAG 526  
QY 101 ProProArgSerAlaPheSerAlaLysArgSerGlySerValProProSerasp 120  
DB 537 CCTCGCGATCGCTTCAGCGCCAAAGCGCTCCGAGAGCGGGGCTCCCGCGCTCTGAC 586  
QY 121 AlaProLeuProPheAspArgValLeuValAsnGluGlnGlyHisTyrAspAlaValThr 140  
DB 587 GCACCTTGCCCTTGACCGCGCTGCTGTGAACGACGAGGACATTACGACCGCTCAC 646  
QY 141 GlyLysPheThrCysGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyr 160  
DB 647 GGCAGATTACCTGCGCAGGTGCTGGGTCTACTACTCTCCGCTCATGCGCCGCTTAC 706  
QY 161 ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyGlySerIleAlaSerPheGln 180  
DB 707 CGGGCCACCTGCATTTGATCTGGTGAAGATGCGGAATCCATTCCTCTTCTCCAG 766  
QY 181 PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGlu 200  
DB 767 TTTTTCGGGGGGTGGCCCAAGCCAGCTGCTCTCGGGGGGGCCATGCGTGAAG 826  
QY 201 ProGluAspGlnValTyrValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSer 220  
DB 827 CCTGAGACCAAGTGTGGGTGAGGTGGGTGGGTGACTACTGATGGCATCTATCCAC 886  
QY 221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspTyrHisSerSerPro 240  
DB 887 ATCAGACAGACAGCACCTTCTCCGATTTCTGCTACTCTCGACTGCGACAGCTCCCA 946  
QY 241 ValPheAla 243  
DB 947 GTCTTTGCT 955

RESULT 9  
AAFA4971  
ID AAFA4971 standard; cDNA; 728 BP.

NC AAF44971;

DT 28-MAR-2001 (first entry)

DE Human TANGO 253 ORF SEQ ID NO: 2.

KW Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;

KW INTERCEPT 258; coronary disorder; olfactory disorder;

KW neurological disorder; pulmonary disorder; immunological disorder;

KW developmental disorder; kidney disorder; ss.

OS Homo sapiens.

FN WO200078808-A1.

PD 28-DEC-2000.

PF 19-JUN-2000; 2000WO-US16883.

PR 18-JUN-1999; 99US-0336536.

PA (MILL-) MILLENNIUM PHARM INC.

PI Leiby KR, McKay C, Bossone S.

WP1: 2001-050109/06.

PT New nucleic acids for treating diseases and disorders, e.g.  
PT atherosclerosis, infection, autoimmune diseases, obesity, ear  
PT disorders, brain disorders, tumors, diabetes, arthritis, multiple  
PT sclerosis and asthma

PS Claim 1; Page 210-211; 332pp; English.

XX The present invention provides the protein and coding sequences of the  
CC human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,  
CC TANGO 281 and INTERCEPT 258. These are useful in the treatment of  
CC coronary, pulmonary, olfactory, immunological, neurological,  
CC developmental and kidney disorders.

Sequence 728 BP; 108 A; 249 C; 250 G; 121 T; 0 other;

Alignment Scores:

Pred. No.:	1,13e-52	Length:	728
Score:	1295.00	Matches:	242
Percent Similarity:	99.59%	Conservative:	0
Best Local Similarity:	99.59%	Mismatches:	1
Query Match:	97.74%	Indels:	1
DB:	22	Gaps:	0

US-09-944-944-42 (1-243) x AAF44971 (1-728)

QY 1 MetArgProLeuLeuValLeuLeuLeuGlyLeuAlaGlySerProProLeuAsp 20  
DB 1 ATGAGGCCACTCTCTGCTCTGCTCTCTGAGGCTGGGCGGCGGCTGCGCCACTGGAC 60  
QY 21 AspAsnLysIleProSerLeuCysProGlyHisProGlyLeuProGlyThrProGlyHis 40  
DB 61 GACACCAAGATCCAGGCTGTGCGCGGGGACCCCGGCGCTTCCAGGACGCGCGGCAC 120  
QY 41 HisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyAlaProGly 60  
DB 121 CATGCGCACCCAGGCGCTTCCGCGCGCGCATGAGCCCGCGAGCGCGCGCGCGCGGG 180  
QY 61 AlaProGlyLysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 80  
DB 181 GCTCCGGGAGAGAAAGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAG 239  
QY 81 GlyProArgGlyGluAlaGlyProAlaGlyProThrGlyProAlaGlyGluCysSerVal 100  
DB 240 GGGCCGCGAGAGAGAGCGGAGCCCGCGGGCCACCGGGGCGTGGGGGAGTGTCTGGAG 299  
QY 101 ProProArgSerAlaPheSerAlaLysArgSerGlySerValProProSerasp 120  
DB 300 CCTCGCGATCGCTTCAGCGCCAAAGCGCTCCGAGAGCCGGGTCCCTCCGCGCTTAC 359  
QY 121 AlaProLeuProPheAspArgValLeuValAsnGluGlnGlyHisTyrAspAlaValThr 140  
DB 360 GCACCTTGCCCTTGACCGCGCTGCTGTGAACGACGAGGACATTACGACCGCTCAC 419  
QY 141 GlyLysPheThrCysGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyr 160  
DB 420 GGCAGATTACCTGCGCAGGTGCTGGGTCTACTACTCTCCGCTCATGCGCACGCTTAC 479  
QY 161 ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyGlySerIleAlaSerPheGln 180  
DB 480 CGGGCCACCTGCATTTGATCTGGTGAAGATGCGGAATCCATTCCTTCTTCTCCAG 539  
QY 181 PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGlu 200  
DB 540 TTTTTCGGGGGGTGGCCCAAGCCAGCTTCTCTCGGGGGGGCCATGCTGAGCTGAG 599  
QY 201 ProGluAspGlnValTyrValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSer 220  
DB 600 COTGAGACCAAGTGTGGGTGAGGTGGGTGGGTGACTACTGATGGCATCTATGCCAGC 659  
QY 221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspTyrHisSerSerPro 240  
DB 660 ATCAGACAGACAGCACCTTCTCCGATTTCTGCTACTCTCGACTGCGACAGCTCCCA 719  
QY 241 ValPheAla 243  
DB 720 GTCTTTGCT 728

RESULT 10  
AAFA4995







DE	Human secreted protein related coding sequence SEQ ID NO: 80.
XX	
KW	Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;
KM	INTERCEPT 258; coronary disorder; olfactory disorder;
KV	neurological disorder; pulmonary disorder; immunological disorder;
KW	developmental disorder; kidney disorder; ss.
XX	
OS	Homo sapiens.
PN	
PD	WO20007808-A1.
XX	
PD	28-DEC-2000.
XX	
PP	19-JUN-2000; 2000MO-USI6883.
XX	
PR	18-JUN-1999; 99US-0336536.
XX	
PA	(MILL-) MILLENNIUM PHARM INC.
XX	
PI	Lelby KR, McKay C, Bossone S;
XX	
DR	WPI; 2001-050109/06.
XX	
PT	New nucleic acids for treating diseases and disorders, e.g.
PT	atherosclerosis, infection, autoimmune diseases, obesity, ear
PT	disorders, brain disorders, tumors, diabetes, arthritis, multiple
PT	scleriosis and asthma -
PS	
PS	Disclosure: Page 260; 332pp; English.
XX	
CC	The present invention provides the protein and coding sequences of the
CC	human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,
CC	TANGO 281 and INTERCEPT 258. These are useful in the treatment of
CC	coronary, pulmonary, olfactory, immunological, neurological,
CC	developmental and kidney disorders.
XX	
SQ	Sequence 728 BP; 107 A; 250 C; 250 G; 121 T; 0 other;
Alignment Scores:	
Pred. No.:	1,4e-52 Length: 728
Score:	1293.00 Matches: 241
Percent Similarity:	99.59% Conservative: 1
Best Local Similarity:	99.18 Mismatches: 1
Query Match:	97.58 Indels: 1
DB:	22 Gaps: 0
US-09-944-944-42 (1-243) x AAF44994 (1-728)	
OY	1 MetArgProLeuValLeuLeuLeuGlyLeuAlaAlaGlySerProProLeuAsp 20
Dd	1 ATGAAGCCACATCTCTGTCTGTCTCGGGCCTTGCGCGGCCGCACATGGAC 60
OY	21 AspAnLysIleProSerLeucCysProGlyHisProGlyLeuProGlyThrProGlyHis 40
Dd	61 GACACAGAATGCCACAGCTCTGCCCCGGGGCACCCGGCCTTCAGGACACGGGGCAC 120
OY	41 HisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyAlaProGly 60
Dd	121 CATGGACACCAGGGCTTGGCGGGCGCGCATGGCGCGCGCGCGCGCGCGCGGG 180
OY	61 AlaProGlyGluGlyGlyGlnGlyGlyArgProGlyLeuProGlyProArgGlyAspPro 80
Dd	181 GCTCCGGAGAAAGAACGGCGAGGGCGAGGCG-GGACTCCGGGACCTCGAGGGGACCCC 239
OY	81 GlyProArgGlyGluAlaGlyProAlaGlyProThrGlyProAlaGlyGluCysSerVal 100
Dd	240 GGCGCGGAGAGAGCGCGGACCCGGGGGCCACCGGGGCTCGCGGGAGATGCTCGGTG 299
OY	101 ProProArgSerAlaPheSerAlaLysAAsSerGluSerArgValPropProProSerAsp 120
Dd	300 CCTCGCGCATCGCCTTCAGGCGCAAGCGCTCGAGAGCGGGGTGCTCGCGCGTCTGAC 359
OY	121 AlaProLeuProPheAspArgValLeuValAsnGlnGlnGlyHisTyrAspAlaValThr 140

Db	360	GCACCCCTTCCTTCGACCCGCGCTGCTGTAACGACAGGACATTACGACGCCGTAC	419
Qy	141	GIlySPheThrCysGlnValProGIlyValTYrTYrPheAlaValHsAlaThrValTYr	160
Db	420	GGCAAGTTACCTGCCAGGTGGCTGGGCTCTACTTGGCCCTCCATGCCACGCTAC	479
Qy	161	ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyLuserIleAlaSerPhePheGln	180
Db	480	CGGGCAGCCCTCAGATTGATCTGGTGAAGAAATGGCGAAATCCCTTCCTTCTTCAG	539
Qy	181	PhePheGlyTYrTyrProLysProAlaSerIleSerGlyAlaMetValArgLeuGln	200
Db	540	TTTTTCGGGGGTGGGCCCAAGCAGCTCTCTCGGGGGGGGCCATGGGAGGCTGAG	599
Qy	201	ProGIuAspGlnValTYrPValGlnValGIlyValGIlyAspTYrIleGlyIleTYrAlaSer	220
Db	600	CCTGAGACCAAGTGTGGGTGCAGGTGGGTGGGTGAGTACTACTTGGCATCTATGCCAGC	659
Qy	221	IleLYrTHrAspSerThrPheSerGlyPheLeuValTYrSerAspThrPheSerPro	240
Db	660	ATCAAGACAGACAGCACCCTTCTCCGGATTCTGTGTACTCCACACTGGCACACCTCCCA	719
Qy	241	ValPheAla 243	
Db	720	GTCTTTGCT 728	
RESULT 15			
AAAF5001			
ID	AAAF5001	standard; cDNA; 1338 BP.	
XX	AAAF5001;		
AC			
XX			
DT			
XX	28-MAR-2001 (first entry)		
DE			
XX	Human secreted protein related coding sequence SEQ ID NO: 109.		
KW	Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;		
KW	INTERCEPT 258; coronary disorder; olfactory disorder;		
KW	neurological disorder; pulmonary disorder; immunological disorder;		
KW	developmental disorder; kidney disorder; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200078808-A1.		
XX			
PD			
XX	28-DEC-2000.		
PF	19-JUN-2000; 2000WO-US16883.		
XX			
PR	18-JUN-1999; 99US-0336536.		
XX			
PA	(MILL-) MILLENNIUM PHARM INC.		
XX			
PI	Leiby KR, McKay C, Bossone S;		
DR	WPI; 2001-050109/06.		
XX			
PT	New nucleic acids for treating diseases and disorders, e.g.		
PT	atherosclerosis, infection, autoimmune diseases, obesity, ear		
PT	disorders, brain disorders, tumors, diabetes, arthritis, multiple		
XX	sclerosis and asthma -		
PS			
XX	Disclosure; Page 274-275; 332pp; English.		
CC	The present invention provides the protein and coding sequences of the		
CC	human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,		
CC	TANGO 281 and INTERCEPT 258. These are useful in the treatment of		
CC	coronary, pulmonary, olfactory, immunological, neurological,		
CC	developmental and kidney disorders.		
XX			
Sequence	1338 BP; 228 A; 424 C; 460 G; 226 T; 0 other;		





[illegible]

```

RESULT 2
US-09-336-536-2
; Sequence 2, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leidy, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossonne, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-336-536-2

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Percent Similarity:	99.59%	Conservative:	0
Best Local Similarity:	99.59%	Mismatches:	1
Query Match:	97.74%	Indels:	1
DB:	4	Gaps:	0

[illegible]

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: RESULT 3
: US-09-336-536-1
: Sequence 1, Application US/09336536
: Patent No. 6406884
: GENERAL INFORMATION:
: APPLICANT: Leiby, K.
: APPLICANT: McKay, C.
: APPLICANT: Bossone, S.
: TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
: FILE REFERENCE: 7853-144
: CURRENT APPLICATION NUMBER: US/09/336, 536
: CURRENT FILING DATE: 1999-06-18
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: PatentIn Ver. 2.0

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Db      301 CCCCCAGCATGCGCTTACGTGCCAAGGATCCGAGAGCGGGGTACCTCCGACCGCAGC 360
QY      121 ALAProLeuProPhaSPaRgYAlleuValaNSgluNGlyHisTYrASpAlaValThr 140
Db      361 ACACCCCTACCTTTTGACCGGTGTGCTGCTAAATGAGCAGGGCCATTACACCCCACTACT 420
QY      141 GlySPheThrCysGlnValProGlyValTYrTYrPheAlaValHisAlaThrValTYr 160
Db      421 GGCAAGTTCACCTGCCAAGTGGCTGGCTTACTTCTTGCTGTGACGCGCCTGTCTAC 480
QY      161 ArgAlaSerLeuGlnPheASPleuValLysASnglyGluSerIleAlaSerPhePheGln 180
Db      481 CGGGCAGCTTCACATTTGATCTGTCAAAAAGGGGACGTCCATCGCCCTTCTTCCAG 540
QY      181 PhePheGlyGlyTYrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGlu 200
Db      541 TATTTTGGGGGTGGCCCAAGCCAGCTCGCTCTCAGGGGGGTGCATGTGTAAGGCTAGAA 600
QY      201 ProGluASPglNValTYrPValGlnValGlyValGlyASPTrIleGlyTleTYrAlaSer 220
Db      601 CCTGAGGACCAAGTGTGGGTGCAAGTGGGCGTGGGTATTCATTGCGCATTCATGCCAGC 660
QY      221 IleLysThrASPserThrPheSerGlyPheLeuValTYrSerASPTrPHisSerSerPro 240
Db      661 ATCAAGACAGACAGTACCTCTCTGATTTCTCGTATTCGTACTGGCAGACGCTCCCA 720
QY      241 ValPheAla 243
Db      721 GTCTTCGCT 729

```

## RESULT 7

```

US-09-336-536-8
; Sequence 8, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leiby, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336,536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1263
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-336-536-8

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## Alignment Scores:

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Pred. No.: 6,51e-83 Length: 1263
Score: 1258.00 Matches: 228
Percent Similarity: 96.30% Conservative: 6
Best Local Similarity: 93.83% Mismatches: 9
Query Match: 94.94% Indels: 0
DB: 4 Gaps: 0

```

US-09-944-944-42 (1-243) x US-09-336-536-8 (1-1263)

```

QY      1 MetaGProLeuLeuValleuLeuLeuGlyLeuAlaGlySerProProLeuASP 20
Db      135 ATGAGGCCACTTCTGCGCTCTGCTTGGGTCTGAGGTCTCTCTCTCTCTGAGC 194
QY      21 AspAsnLysIleProSerLeuCysProGlyHisProGlyLeuProGlyThrProGlyHis 40
Db      195 GACAACAAGATCCCAAGCTGTGTCGCGGCGAGCCGCGCTTCAGGACACACAGGTAC 254
QY      41 HisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyAlaProGly 60
Db      255 CATGGACCAAGGCTCTGCGCTGCGGTAGAGCCCGGTATGCGCGGACGTGACACCGGA 314

```

```

QY      61 ALAProGlyLutLysGlyGluGlyArgProGlyLeuProGlyProArgLysPro 80
Db      315 GCTCCGGAGAGAAAGGCGAGGCGGAGACCGGACTTCTGCGCCAGCTGGGAGGCC 374
QY      81 GlyProArgGlyLutAlaGlyProAlaGlyProThrGlyProAlaGlyLutCysSerVal 100
Db      375 GGGCGCGGTGAGAGAGCAGAGGGCCCANRGGGGCTATTCGGGGCTGCGGGGAGTGTGCGTA 434
QY      101 ProProArgSerAlaPheSerAlaLysArgSerGluSerAlaValProProSerASP 120
Db      435 CCCCCACATCAGCTTCAGTCCAGGATCCGAGAGCCGGGTACTCTCCGACCCGAGC 494
QY      121 ALAProLeuProPhaSPaRgYAlleuValaNSgluNGlyHisTYrASpAlaValThr 140
Db      495 ACACCCCTACCTTTTGACCGGTGTGCTGCTAAATGAGCAGGGCCATTACACCCCACTACT 554
QY      141 GlySPheThrCysGlnValProGlyValTYrTYrPheAlaValHisAlaThrValTYr 160
Db      555 GGCAAGTTCACCTGCCAAGTGGCTGGCTGCTACTTGTGCTGACGCGCAGCTGTCTAC 614
QY      161 ArgAlaSerLeuGlnPheASPleuValLysASnglyGluSerIleAlaSerPhePheGln 180
Db      615 CGGGCAGCTTCACATTTGATCTGTCAAAAAGGGGACGTCCATCGCCCTTCTTCCAG 674
QY      181 PhePheGlyGlyTYrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGlu 200
Db      675 TATTTTGGGGGTGGCCCAAGCCAGCTTCGCTCTCAGGGGGTGCATGTGTAAGGCTAGAA 734
QY      201 ProGluASPglNValTYrPValGlnValGlyValGlyASPTrIleGlyTleTYrAlaSer 220
Db      735 CCTGAGGACCAAGTGTGGGTGCAAGTGGGCGTGGGTATTCATTGCGCATTCATGCCAGC 794
QY      221 IleLysThrASPserThrPheSerGlyPheLeuValTYrSerASPTrPHisSerSerPro 240
Db      795 ATCAAGACAGACAGTACCTCTCTGATTTCTCGTATTCGTACTGGCAGACGCTCCCA 854
QY      241 ValPheAla 243
Db      855 GTCTTCGCT 863

```

## RESULT 8

```

US-09-140-804-10
; Sequence 10, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Degenerate nucleotide sequence encoding the zs1g39
US-09-140-804-10

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## Alignment Scores:

```

Pred. No.: 9.98e-70 Length: 729
Score: 1072.00 Matches: 191
Percent Similarity: 78.60% Conservative: 0
Best Local Similarity: 78.60% Mismatches: 52
Query Match: 80.91% Indels: 0
DB: 4 Gaps: 0

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US-09-944-944-42 (1-243) x US-09-140-804-10 (1-729)





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Qy 57 gylalaproglialaproglylulysglylgluylglarprogllyleuprogllypro 76
    ||| ||||| ||||| ||| ||||| |||||
Db 250 -----GGCACCCCTGGTGAGAGAGGTGAGAAAGAGATCCAGGCTTATTGGTCT 300
Qy 77 Argglyasp-----ProglyProatrglylualagly 87
    ::||| ||||| ||||| ||||| |||||
Db 301 AAGGAGACATCGGTGAACCGAGTACCCGGGGCTGAGAGTCCCGAGCTTCCGGGA 360
Qy 88 ProalaglyProthrglyProalaglylucyseryalProProatrgserAlapheser 107
    ||| ||||| ||||| ||||| |||||
Db 361 ATCCAGGACGAGAAAGAGAACCTGGAGAGGTGCTATGATACCGCTGAGCTTACGT 420
Qy 108 AlalysargsergluserArgvalProProProseraspAlaProleuProPhaspary 127
    ||||| ||||| ||||| ||||| |||||
Db 421 GTG---GGATTGGAGACTTACGTACTATCCCC---AACATGCCATTCGCTTACCAAG 474
Qy 128 ValleuValasnglnglyhlystyrAspAlaValThrelyllysphehCysglVal 147
    ||||| ||||| ||||| ||||| |||||
Db 475 ATCTTACATCAATCGCAAAACCACTATGATGCTCCACTGTAATTCACACTGCAACATT 534
Qy 148 ProglyValtyrtyrPheAlaValAlaThraValtyrArgAlaSerleuGlnPheasp 167
    ||||| ||||| ||||| ||||| |||||
Db 535 CCTGGGCTGATCTTCTTGTCTTACCATCATCATCTATGAGAGATGTAAGGTACAGC 594
Qy 168 LeuVallysasnlygluser---IleAlaSerPhepheGlnPhepheglylytyrPro 186
    ||| ||||| ||||| ||||| |||||
Db 595 CTCTTCAAGAAGAGCAAGAGGTATGCTCTTCACTATGATGACAGCAAGAAATATATGTG 654
Qy 187 LysProAlaSerleuSerArglyAlaMetValArgleuGluProGluAspGlnValTyr 206
    ||| ||||| ||||| ||||| |||||
Db 655 GACCAGGCC-----TCCGGCTCTGTCTCTCATCTGAGGGGCGACCAAGTCTGG 708
Qy 207 ValGlnVal---glyValGlyAspTyrIleGlyIleTyrAlaSerIleLysThrAspser 225
    ::||| ||| ||||| ||||| |||||
Db 709 CTCAGGTGATGGGAGAGAGAGAGAGCTATGACTGATGCTATGATGACAAATGACTCC 768
Qy 226 ThrseserGlyPheleuValTyrSerAspTyrHisSerProval 241
    ||||| ||||| ||||| ||||| |||||
Db 769 ACCTTACAGGCTTCTTCTTACCATGACACCAATGATCACACCA 816

RESULT 12
US-09-140-804-9
: Sequence 9, Application US/09140804
: Patent No. 6197930
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Humes, Jacqueline M.
: TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
: FILE REFERENCE: 97-49
: CURRENT APPLICATION NUMBER: US/09/140, 804
: CURRENT FILING DATE: 1998-08-26
: EARLIER APPLICATION NUMBER: 60/056, 983
: EARLIER FILING DATE: 1997-08-26
: NUMBER OF SEQ ID NOS: 47
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 9
: LENGTH: 4517
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-140-804-9

Alignment Scores:
Pred. No.: 1.62e-22 Length: 4517
Score: 432.50 Matches: 111
Percent Similarity: 50.72% Conservative: 29
Best Local Similarity: 40.22% Mismatches: 75
Query Match: 32.64% Indels: 61
DB: 4 Gaps: 11

US-09-944-42 (1-243) x US-09-140-804-9 (1-4517)
Qy 1 MetArgProleuLeu-----ValleuLeuLeuLeuGlyLeuAlaAlaGlySerPro 17

```

```

Db 21 CTCAGAGTGTCTGTCTGGAGAGTGTCTTACTGCTATATAGCTTG----- 65
Qy 18 ProteusaspAspAnlysIleProSerleuEusProglyhly----- 31
Db 66 -----CCCGGGCATGACCAAGAAACCAAGACT 92
Qy 32 -----Progly-----LeuProgly 36
    |||||
Db 93 CAAGGGCCCGGAGTCTGTCTTCCCTGCCCAAGGGGGCTGCACAGGTGGATGGCGGGC 152
Qy 37 ThrsProglyhlyhlysglyserGlnlyleuProglyltyrArgAspGlyArgAsp 56
    ||||| ||||| ||||| ||||| |||||
Db 153 ATCCAGGACATCCGGCCATATAGGGCCCCAGCCGCTGTATGGCAGAGAT----- 203
Qy 57 gylalaproglialaproglylulysglylgluylglarprogllyleuprogllypro 76
    ||| ||||| ||||| ||||| |||||
Db 204 -----GGCACCCCTGGTGAGAGAGGTGAGAAAGAGATCCAGGCTTATTGGTCT 254
Qy 77 Argglyasp-----ProglyProatrglylualagly 87
    ::||| ||||| ||||| ||||| |||||
Db 255 AAGGAGACATCGGTGAACCGAGTACCCGGGGCTGAGAGTCCCGAGGCTTCCGGGA 314
Qy 88 ProalaglyProthrglyProalaglylucyseryalProProatrgserAlapheser 107
    ||||| ||||| ||||| ||||| |||||
Db 315 ATCCAGGACGAGAAAGAGAACCTGGAGAGGTGCTATGATACCTGCACTTACGT 374
Qy 108 AlalysargsergluserArgvalProProProseraspAlaProleuProPhaspary 127
    ||||| ||||| ||||| ||||| |||||
Db 375 GTG---GGATTGGAGACTTACGTACTATCCCC---AACATGCCATTCGCTTACCAAG 428
Qy 128 ValleuValasnglnglyhlystyrAspAlaValThrelyllysphehCysglVal 147
    ||| ||||| ||||| ||||| |||||
Db 429 ATCTTACATCAATCGCAAAACCACTATGATGCTCCACTGTAATTCACACTGCAACATT 488
Qy 148 ProglyValtyrtyrPheAlaValAlaThraValtyrArgAlaSerleuGlnPheasp 167
    ||||| ||||| ||||| ||||| |||||
Db 489 CCTGGGCTGATCTTGTCTTACCATCATCATCTATGATGAGAGTGAAGGTACAGC 548
Qy 168 LeuVallysasnlygluser---IleAlaSerPhepheGlnPhepheglylytyrPro 186
    ||| ||||| ||||| ||||| |||||
Db 549 CTCTTCAAGAAGAGCAAGAGGTATGCTCTTCACTATGATGACAGCAAGAAATATATGTG 608
Qy 187 LysProAlaSerleuSerArglyAlaMetValArgleuGluProGluAspGlnValTyr 206
    ||| ||||| ||||| ||||| |||||
Db 609 GACCAGGCC-----TCCGGCTCTGTCTCTCATCTGAGGGGCGACCAAGTCTGG 662
Qy 207 ValGlnVal---glyValGlyAspTyrIleGlyIleTyrAlaSerIleLysThrAspser 225
    ::||| ||| ||||| ||||| |||||
Db 663 CTCAGGTGATGGGAGAGAGAGAGAGCTATGACTGATGCTATGATGACAAATGACTCC 722
Qy 226 ThrseserGlyPheleuValTyrSerAspTyrHisSerProval 241
    ||||| ||||| ||||| ||||| |||||
Db 723 ACCTTACAGGCTTCTTCTTACCATGACACCAATGATCACACCA 770

RESULT 13
US-09-188-930-217
: Sequence 217, Application US/09188930A
: Patent No. 6150502
: GENERAL INFORMATION:
: APPLICANT: Watson, James D.
: APPLICANT: Strechan, Lorna
: APPLICANT: Sleeman, Matthew
: APPLICANT: Murison, James Greg
: TITLE OF INVENTION: Compositions Isolated From Skin Cells
: FILE REFERENCE: 11000, 1011c1
: CURRENT APPLICATION NUMBER: US/09/188, 930A
: CURRENT FILING DATE: 1998-11-09
: NUMBER OF SEQ ID NOS: 348
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 217

```



: EARLIER FILING DATE: 1997-09-12  
 : NUMBER OF SEQ ID NOS: 672  
 : SOFTWARE: Patent In Ver. 2.0  
 : SEQ ID NO 51  
 : LENGTH: 1333  
 : TYPE: DNA  
 : ORGANISM: Homo sapiens  
 : FEATURE:  
 : NAME/KEY: SITE  
 : LOCATION: (485)  
 : OTHER INFORMATION: n equals a,t,g, or c  
 : FEATURE:  
 : NAME/KEY: SITE  
 : LOCATION: (486)  
 : OTHER INFORMATION: n equals a,t,g, or c  
 : FEATURE:  
 : NAME/KEY: SITE  
 : LOCATION: (493)  
 : OTHER INFORMATION: n equals a,t,g, or c  
 : FEATURE:  
 : NAME/KEY: SITE  
 : LOCATION: (496)  
 : OTHER INFORMATION: n equals a,t,g, or c  
 : FEATURE:  
 : NAME/KEY: SITE  
 : LOCATION: (587)  
 : OTHER INFORMATION: n equals a,t,g, or c  
 : FEATURE:  
 : NAME/KEY: SITE  
 : LOCATION: (633)  
 : OTHER INFORMATION: n equals a,t,g, or c  
 : FEATURE:  
 : NAME/KEY: SITE  
 : LOCATION: (1330)  
 : OTHER INFORMATION: n equals a,t,g, or c  
 : US-09-227-357-51

Alignment Scores:  
 Pred. No.: 1,43e-18 Length: 1333  
 Score: 369.50 Matches: 97  
 Percent Similarity: 50.40% Conservative: 28  
 Best Local Similarity: 39.11% Mismatches: 83  
 Query Match: 27.89% Indels: 40  
 Gaps: 7

US-09-944-42 (1-243) x US-09-227-357-51 (1-1333)

QY 24 IleProSerLeu-----CysProGlyHisProGlyLeuProGlyHisHis 41  
 Db 212 ATTCTGCTGCTGCTGCACTCCAGGCCCCCTGACCAATGCTGCCCTGGCCCAT 271  
 QY 42 GlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyArgAsp 59  
 Db 272 GGTGCGATCGGCTTCAGAGAGATGTAAGAGAGAGAGAGAGAGAGAGAGAGAG 331  
 QY 60 -----GlyAlaProGlyGluGly 66  
 Db 332 AAGGAGACTGCAAGTTGAGAGTAAGTAAGTCAAGTCAAGTCAAGTCAAGTCAAG 391  
 QY 67 GlnGlyArgProGlyLeuProGlyProArgGlyAspProGlyProArgGlyAla 86  
 Db 392 GACCAAGAGAGACTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 451  
 QY 87 GlyProAlaGlyProThrGlyProAlaGlyGlu----- 97  
 Db 452 GGTCAATGCTGCTCTCTGACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 511  
 QY 98 -----Cys-----SerValProProArgSerAlaPheSerAlaValArgSer 111  
 Db 512 CTTGAGATTGACATGTGAGAGATGCTGCTCAATCCGCTTTCTGTTGGCATACA 571  
 QY 112 GluSerArgValProProProSerAspAlaProLeuProPheAspArgValLeuVal-As 131

Db 572 ACCAGTAC-----CCAGANMAAAGACTACCTATTATTATTAAAGAGTCCCTCCA 625  
 QY 131 nGlnGlnGlyHisTyrAspAlaValThr-GlyLysPheThrCysGlnValPro-GlyVal 150  
 Db 626 CGAGGAGNAGCAGTACACACCTGCCACAGGAGAGAGAGAGAGAGAGAGAGAGAG 685  
 QY 151 TyrTyrPheAlaValHisAlaThrValTyrArgAlaSerLeuGlnPheAspLeuVallys 170  
 Db 686 TATTACTTTCTTGTATGATATACATATGCTTAATAGCATCTGCATCGCATCGTACAC 745  
 QY 171 AsnGlyGluSerIleAlaSerPhePheGlnPheGlyGlyTyrProLysProAlaSer 190  
 Db 746 AATGGCAATACCGCATTAACCTTCGAGCCCAACAGAGAAACATGATGGCT--- 802  
 QY 191 LeuSerGlyGlyAlaMetValArgLeuGluProGlyLysAspGlnValTyrValGlnValGly 210  
 Db 803 ---TCGGGCTCCAGATCATCTATCTGACAGCCAGAGATGAGCTGGTGGAGATTTC 859  
 QY 211 ValGlyAspTyrIleGlyIleTyrAlaSerIleLys---ThrAspSerThrPheSerGly 229  
 Db 860 TTCACAGACCAAGATGCGCTCTCTCAGACCCAGGTGGCAGACACTTATCTCCGGG 919  
 QY 230 PheLeuValTyrSerAsp 235  
 Db 920 TTCTCTTATACGTTGAC 937

RESULT 15

US-08-383-744-1  
 : Sequence 1, Application US/08383744  
 : Patent No. 5702948

: GENERAL INFORMATION:  
 : APPLICANT: Greene, Mark I.  
 : TITLE OF INVENTION: Saccular collagen and Compositions  
 : TITLE OF INVENTION: and  
 : NUMBER OF SEQUENCES: 2  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
 : ADDRESSEE: No. 5702948rls  
 : STREET: One Liberty Place, 46th floor  
 : CITY: Philadelphia  
 : STATE: PA  
 : COUNTRY: USA  
 : ZIP: 19103

: COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Wordperfect 5.1  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/383,744  
 : FILING DATE:

: CLASSIFICATION: 435  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Deluca, Mark  
 : REGISTRATION NUMBER: 33,229  
 : REFERENCE/DOCKET NUMBER: UPN-2039  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: 215-568-3100  
 : TELEFAX: 215-568-3439

: INFORMATION FOR SEQ ID NO: 1:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1839 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: both  
 : MOLECULE TYPE: cDNA  
 : FEATURE:  
 : NAME/KEY: CDS  
 : LOCATION: 331..1602

US-08-383-744-1



Alignment Scores:	
Pred. No.:	4,53e-17
Score:	351.00
Percent Similarity:	46.488
Best Local Similarity:	37.508
Query Match:	26.498
DB:	1
Length:	1839
Matches:	96
Conservative:	23
Mismatches:	99
Indels:	39
Gaps:	6

US-09-944-944-42 (1-243) x US-08-383-744-1 (1-1839)

QY	15	glyserProPLeuaspPasnlys-----lleProSerLeuCsProGlylYhiPro	32
Db	799	GGAAAGCCCTGGCCCTAAATGAACCTAAAGAAAGCAATCCGGCGAGAGGGGCCCATGGCTCT	858
QY	33	GlyLeuPProGlylYthrProGlylYhiShiGlySerGlnGlyLeuPProGlylYarg-----Asp	50
Db	859	GGGTAGACTGGGACAAAGGGCTGTAAAGGTGAACAGGGGGCTTAAAGGGAGATGTTTACAA	918
QY	51	GlylYrGAspGlylYargAspGlylYAlaPProGlylYAlaPProGlylYulYsGlylYglYlYarg	70
Db	919	GGCAGAAAGAGGTGAGCGGGGCCCTGGCTTTGAGAGGTGAGATGGATTCGAATGGAACCT	978
QY	71	ProGlyLeuPProGlylYProArgGlylYAspProGlylYPro-----	82
Db	979	GATGGTGTAAAGGAGAGAGAGGGAGCCCAAGGCCCTTGGAGGAAAGGGGCACTGGCT	1038
QY	82	-----	82
Db	1039	GCCAGAGGGCCCCCAGGTCCTCCAGAGAGGAGGGGCGATGGCAGGGGTGGAGGGGAGAGAG	1098
QY	83	-----ArgGlylYulAlaGlylYProAlaGlylYProThrGlylYProAlaGlylYlYcysSerVal	100
Db	1099	GGCGTTAAAGGTGTGCGTGGGGCCAAAGGGGCCCTTAAAGGCCCAACAGGTGAAGATGTGGAG	1158
QY	101	ProProArgSerAlaPheSerAlaLylYargSerGluSerArgValPProProProSerAsp	120
Db	1159	CAGATTGGCTCTGCTTTCAGTGTGGCGCTGTTCGCCAGCAAGATCTTCCTCCGCCCCAGC	1218
QY	121	AlaProLeuPProPheAspArgValLeuValasnGlnGlylYhiStyArgSpAlaValAlaThr	140
Db	1219	CTGCTGTGAAGTTGATTAAGTGTTTTACAAAGGGGAGGGGCGACTGGAGCCAAACCTC	1278
QY	141	GlylYsPheThrCysGlnValPProGlylYAlYlYrYrPheAlaValAlHisAlaThrValYlr	160
Db	1279	AACAAATTCAAATGTCACCTTACCACGGGGGTCTACATTAAGTTCACATCACCCTGGCGC	1338
QY	161	ArgAlaSerLeuGlnPheAspLeuValLysasnGlylY-----GluSerlYleAlaSerPhehe	179
Db	1339	AACAGGCGCTGGCTGCTGCCCTTAAGTGGTTAATGGGTGAGCGAAGCTGAGGACCCGGCAT	1398
QY	180	GlnPhePheGlylYlYrYrProLysProAlaSerLeuSerGlylYAlaMetValArgLeu	199
Db	1399	TCCTGTGACGCCAGACATGATCAGAGC-----TCCAACTCCGACCTCTGTGATCT	1452
QY	200	GluPProGluAspGlnValAlaTrpValAlaGlnValGlylYAlaGlylYAspYlrIleGlylYleTala	219
Db	1453	ACTGACGGTGCACCGTGTGGCTGTGAGACACA---CTGAGAGACTGGAAATGGAGT-TACTCC	1508
QY	220	SerlYlYsThrAspSerThrPheSerGlylYheLeuValYlYrSerAsp	235
Db	1509	AGCGATGAGATGACACACTTCTCTGGCTTCTCTGTCTTCTTACCTCGTAC	1556

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Job time : 68 secs

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 21, 2003, 17:37:33 ; Search time 192 Seconds

(without alignments)  
1857.213 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325  
Sequence: 1 MRPLVLLGLAGSPPLD.....DSTRSGRLVSDMHSPPVFA 243

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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Bl0sum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=ext -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09944944 -CGN\_1\_1\_156 -runat\_13062003\_150050\_24368  
-NCPU=6 -ICPU=3 -NO\_MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEROUT=120 -WARN\_TIMEROUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published.Applications\_NA:\*

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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEM\_PUB.seq:\*  
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8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_NEM\_PUB.seq:\*  
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12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US60\_NEM\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1325	100.0	1377	9	US-09-944-403-41
3	1325	100.0	1377	9	US-09-944-896-41
4	1325	100.0	1377	9	US-09-944-944-41

#### ALIGNMENTS

RESULT 1  
US-09-944-413-41  
; Sequence 41, Application US/09944413  
; Patent No. US20020156004A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerlitsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kijavini, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548p1c1  
; CURRENT APPLICATION NUMBER: US/09/944,413  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25

5	1325	100.0	1377	9	US-09-944-907-41	Sequence 41, Appl
6	1325	100.0	1377	9	US-09-944-929-41	Sequence 41, Appl
7	1325	100.0	1377	9	US-10-028-072-361	Sequence 361, App
8	1325	100.0	1377	9	US-10-121-049-361	Sequence 361, App
9	1325	100.0	1377	9	US-10-123-904-361	Sequence 361, App
10	1325	100.0	1377	9	US-10-140-470-361	Sequence 361, App
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12	1325	100.0	1377	9	US-10-176-918-361	Sequence 361, App
13	1325	100.0	1377	9	US-10-176-921-361	Sequence 361, App
14	1325	100.0	1377	9	US-10-137-865-361	Sequence 361, App
15	1325	100.0	1377	9	US-10-140-474-361	Sequence 361, App
16	1325	100.0	1377	9	US-10-142-431-361	Sequence 361, App
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18	1325	100.0	1377	9	US-10-140-002-361	Sequence 361, App
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36	1325	100.0	1377	9	US-10-160-498-361	Sequence 361, App
37	1325	100.0	1377	9	US-09-944-884-41	Sequence 41, Appl
38	1325	100.0	1377	9	US-10-121-041-361	Sequence 361, App
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40	1325	100.0	1377	9	US-10-121-047-361	Sequence 361, App
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1	PRIOR APPLICATION NUMBER: 60/067,411	
2	PRIOR FILING DATE: December 3, 1997	
3	PRIOR APPLICATION NUMBER: 60/069,334	
4	PRIOR FILING DATE: December 11, 1997	
5	PRIOR APPLICATION NUMBER: 60/069,335	
6	PRIOR FILING DATE: December 11, 1997	
7	PRIOR APPLICATION NUMBER: 60/069,278	
8	PRIOR FILING DATE: December 11, 1997	
9	PRIOR APPLICATION NUMBER: 60/069,425	
10	PRIOR FILING DATE: December 12, 1997	
11	PRIOR APPLICATION NUMBER: 60/069,696	
12	PRIOR FILING DATE: December 16, 1997	
13	PRIOR APPLICATION NUMBER: 60/069,694	
14	PRIOR FILING DATE: December 16, 1997	
15	PRIOR APPLICATION NUMBER: 60/069,702	
16	PRIOR FILING DATE: December 16, 1997	
17	PRIOR APPLICATION NUMBER: 60/069,870	
18	PRIOR FILING DATE: December 17, 1997	
19	PRIOR APPLICATION NUMBER: 60/069,873	
20	PRIOR FILING DATE: December 17, 1997	
21	PRIOR APPLICATION NUMBER: 60/068,017	
22	PRIOR FILING DATE: December 18, 1997	
23	PRIOR APPLICATION NUMBER: 60/070,440	
24	PRIOR FILING DATE: January 5, 1998	
25	PRIOR APPLICATION NUMBER: 60/074,086	
26	PRIOR FILING DATE: February 9, 1998	
27	PRIOR APPLICATION NUMBER: 60/074,092	
28	PRIOR FILING DATE: February 9, 1998	
29	PRIOR APPLICATION NUMBER: 60/075,945	
30	PRIOR FILING DATE: February 25, 1998	
31	PRIOR APPLICATION NUMBER: 60/112,850	
32	PRIOR FILING DATE: December 16, 1998	
33	PRIOR APPLICATION NUMBER: 60/113,296	
34	PRIOR FILING DATE: December 22, 1998	
35	PRIOR APPLICATION NUMBER: 60/146,222	
36	PRIOR FILING DATE: July 28, 1999	
37	PRIOR APPLICATION NUMBER: PCT/US98/19330	
38	PRIOR FILING DATE: September 16, 1998	
39	PRIOR APPLICATION NUMBER: PCT/US98/25108	
40	PRIOR FILING DATE: December 1, 1998	
41	PRIOR APPLICATION NUMBER: 09/216,021	
42	PRIOR FILING DATE: December 16, 1998	
43	PRIOR APPLICATION NUMBER: 09/218,517	
44	PRIOR FILING DATE: December 22, 1998	
45	PRIOR APPLICATION NUMBER: 09/254,311	
46	PRIOR FILING DATE: March 3, 1999	
47	PRIOR APPLICATION NUMBER: PCT/US99/12252	
48	PRIOR FILING DATE: June 22, 1999	
49	PRIOR APPLICATION NUMBER: PCT/US99/21090	
50	PRIOR FILING DATE: September 15, 1999	
51	PRIOR APPLICATION NUMBER: PCT/US99/28409	
52	PRIOR FILING DATE: No. US20020156004Alamber 30, 1999	
53	PRIOR APPLICATION NUMBER: PCT/US99/28313	
54	PRIOR FILING DATE: No. US20020156004Alamber 30, 1999	
55	PRIOR APPLICATION NUMBER: PCT/US99/28301	
56	PRIOR FILING DATE: December 1, 1999	
57	PRIOR APPLICATION NUMBER: PCT/US99, 130095	
58	PRIOR FILING DATE: December 16, 1999	
59	PRIOR APPLICATION NUMBER: PCT/US00/03565	
60	PRIOR FILING DATE: February 11, 2000	
61	PRIOR APPLICATION NUMBER: PCT/US00/04414	
62	PRIOR FILING DATE: February 22, 2000	
63	PRIOR APPLICATION NUMBER: PCT/US00/05841	
64	PRIOR FILING DATE: March 2, 2000	
65	PRIOR APPLICATION NUMBER: PCT/US00/08439	
66	PRIOR FILING DATE: March 30, 2000	
67	PRIOR APPLICATION NUMBER: PCT/US00/14042	
68	PRIOR FILING DATE: May 22, 2000	
69	PRIOR APPLICATION NUMBER: PCT/US00/20710	
70	PRIOR FILING DATE: July 28, 2000	
71	PRIOR APPLICATION NUMBER: PCT/US00/32678	
72	PRIOR FILING DATE: December 1, 2000	
73	PRIOR APPLICATION NUMBER: PCT/US01/06520	

[illegible]

Patent No. US20020165143A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

APPLICANT: Bolstein, David

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Gerlitsen, Mary

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul

APPLICANT: Grimaldi, Christopher

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APPLICANT: Kijavian, Ivar

APPLICANT: Napier, Mary

APPLICANT: Roy, Margaret

APPLICANT: Tumas, Daniel

APPLICANT: Wood, William

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P2548P1C1

CURRENT APPLICATION NUMBER: US/09/944,403

CURRENT FILING DATE: 2001-09-26

PRIOR APPLICATION NUMBER: 09/866,028

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/067,411

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Prior FILING DATE:	No. US20020165143A1ember 30, 1999
Prior APPLICATION NUMBER:	PCT/US99/28301
Prior FILING DATE:	December 1, 1999
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Prior APPLICATION NUMBER:	PCT/US00/03565
Prior FILING DATE:	February 11, 2000
Prior APPLICATION NUMBER:	PCT/US00/04414
Prior FILING DATE:	February 22, 2000
Prior APPLICATION NUMBER:	PCT/US00/05841
Prior FILING DATE:	March 2, 2000
Prior APPLICATION NUMBER:	PCT/US00/08439
Prior FILING DATE:	March 30, 2000
Prior APPLICATION NUMBER:	PCT/US00/14042
Prior FILING DATE:	May 22, 2000
Prior APPLICATION NUMBER:	PCT/US00/20710
Prior FILING DATE:	July 28, 2000
Prior APPLICATION NUMBER:	PCT/US00/32678
Prior FILING DATE:	December 1, 2000
Prior APPLICATION NUMBER:	PCT/US01/06520
Prior FILING DATE:	February 28, 2001
NUMBER OF SEQ ID NOS:	120
SEQ ID NO 41	
LENGTH: 1377	
TYPE: DNA	
ORGANISM: Homo Sapien	
US-09-944-403-41	

  

Alignment Scores:			
Pred. No.:	1, 67e-107	Length:	1377
Score:	1325.00	Matches:	243
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

  

US-09-944-944-42 (1-243) x US-09-944-403-41 (1-1377)

QY	1	MetatgProleuDeuValLeuleuDeuLenglyLeuaAlaaglySerProProleuAsp	20
Dd	227	ATGAGCGCACTCCTGTCTGGTCCCTGGGCGTGCGGCCTGCCACCTGACC	288
QY	21	ASpaSuNylIeProSeRteucysProglYnHSProglYLeuProglYThnProglYHis	40
Dd	287	GACAAACAATCCCCAGCCTTCGCCGGGCGCACCCGCCCTTCAGAGCACCCGGGCCAC	346
QY	41	HISGLySerglNglyLeuProglYnrgaspGlYArgraspGlYArgraspGlYALAProgly	60
Dd	347	CATGGAGCGCAGGCGTTGCGGGGCGCGCATGGCGCGAGGCGCGGAGCGCGCCGGG	406
QY	61	ALAProglYgluNygSlngluNlglyLArgrProglYLeuProglYProarGlYASPPro	80
Dd	407	GCTCGGGAGAGAAGCGCAGGCGCGGAGCGCGGACTCGCGGAGACTCGAGGGGACCCC	466
QY	81	GLYPtoARGLYgluNAaglYProAlaglYProthngLYProAlaglYluCyseSerVal	100
Dd	467	GGGCGCGAGAGAGCGCGGACCCCGGGGCCACCGGGCGCTGGCGGGAGTGTCTGGTG	526
QY	101	PROProrISerAlapheserAlaySarngsergiuseArayvalPropoProSerAsp	120
Dd	527	CCPCCGCGATCGCCTTAGCGCCAAGCGCTCCGAGAGCGGGGTGCTCGCGCTCGAC	586
QY	121	ALAProLeuProPhesprAYalLeuValasnIngInglYHisTYrASPAlaValThr	140
Dd	587	GCACCTTGCCCTTCGACCGCGCTGCTGGTAACGACGAGGACATTACAGACCGGTACCC	646
QY	141	GLYSphethnCysglnValaProglYalValtyTyrrhealaValahSalatrHValtyTr	160



QY 41 HisGlySerGlnGlyLeuProGlyIleArgAspGlyArgAspGlyValAlaProGly 60  
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Db 347 CATGCGACGACGAGGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 406  
QY 61 AlaProGlyGlyLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 80  
407 GCTCCGGGAGAGAAAGCGAGGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCG 466  
QY 81 GlyProArgGlyGlyLeuGlyProAlaGlyProThrGlyProAlaGlyGlyGlySerVal 100  
467 GGGCGCGCAGAGAGAGCGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 526  
QY 101 ProProArgSerAlaPheSerAlaIleArgSerGlySerArgValProProProSerAsp 120  
527 CCG 586  
QY 121 AlaProLeuProPheAspArgValLeuValAsnGlnGlnGlnGlnGlnGlnGlnGlnGln 140  
587 GCACCGCTTGCCCTTCGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 646  
QY 141 GlyIlePheThrCysGlnIleValProGlyValIleTyrPheAlaValHisAlaThrValTyr 160  
647 GCGCAGTTCACCG 706  
QY 161 ArgAlaSerLeuGlnPheAspLeuValIleValAsnGlnGlnGlnGlnGlnGlnGlnGln 180  
707 CG 766  
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767 TTTTTCGGGGGGTGGCG 826  
QY 201 ProGluAspGlnValTyrValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSer 220  
827 CCGGAGGACCAAGTGGCG 886  
QY 221 IleTyrThrAspSerThrPheSerGlyPheLeuValIleTyrSerAspTyrPheSerPro 240  
887 ATCAAGACAGACGACCGCTTCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 946  
Db 241 ValPheAla 243  
QY 241 ValPheAla 243  
Db 947 GCTTTTGGT 955

RESULF 4  
US-09-944-944-41  
; Sequence 41, Application US/09944944  
; Patent No. US20020173463A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kijavich, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,944  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25

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;; PRIOR FILING DATE: July 28, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/32678  
;; PRIOR FILING DATE: December 1, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US01/06520







1	PRIOR APPLICATION NUMBER: 60/056977
2	PRIOR FILING DATE: 1997-08-26
3	PRIOR APPLICATION NUMBER: 60/051113
4	PRIOR FILING DATE: 1997-09-17
5	PRIOR APPLICATION NUMBER: 60/059115
6	PRIOR FILING DATE: 1997-09-17
7	PRIOR APPLICATION NUMBER: 60/058117
8	PRIOR FILING DATE: 1997-09-17
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21	PRIOR APPLICATION NUMBER: 60/062255
22	PRIOR FILING DATE: 1997-10-24
23	PRIOR APPLICATION NUMBER: 60/062814
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25	PRIOR APPLICATION NUMBER: 60/062816
26	PRIOR FILING DATE: 1997-10-24
27	PRIOR APPLICATION NUMBER: 60/063045
28	PRIOR FILING DATE: 1997-10-24
29	PRIOR APPLICATION NUMBER: 60/063082
30	PRIOR FILING DATE: 1997-10-31
31	PRIOR APPLICATION NUMBER: 60/063127
32	PRIOR FILING DATE: 1997-10-24
33	PRIOR APPLICATION NUMBER: 60/063327
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36	PRIOR FILING DATE: 1997-10-27
37	PRIOR APPLICATION NUMBER: 60/063550
38	PRIOR FILING DATE: 1997-10-28
39	PRIOR APPLICATION NUMBER: 60/063561
40	PRIOR FILING DATE: 1997-10-28
41	PRIOR APPLICATION NUMBER: 60/063704
42	PRIOR FILING DATE: 1997-10-29
43	PRIOR APPLICATION NUMBER: 60/063733
44	PRIOR FILING DATE: 1997-10-29
45	PRIOR APPLICATION NUMBER: 60/063755
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47	PRIOR APPLICATION NUMBER: 60/063788
48	PRIOR FILING DATE: 1997-10-29
49	PRIOR APPLICATION NUMBER: 60/063755
50	PRIOR FILING DATE: 1997-10-17
51	PRIOR APPLICATION NUMBER: 60/064248
52	PRIOR FILING DATE: 1997-11-03
53	PRIOR APPLICATION NUMBER: 60/064809
54	PRIOR FILING DATE: 1997-11-07
55	PRIOR APPLICATION NUMBER: 60/065186
56	PRIOR FILING DATE: 1997-11-12
57	PRIOR APPLICATION NUMBER: 60/065846
58	PRIOR FILING DATE: 1997-11-17
59	PRIOR APPLICATION NUMBER: 60/066364
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61	PRIOR APPLICATION NUMBER: 60/066433
62	PRIOR FILING DATE: 1997-11-24
63	PRIOR APPLICATION NUMBER: 60/066511
64	PRIOR FILING DATE: 1997-11-24
65	PRIOR APPLICATION NUMBER: 60/066770
66	PRIOR FILING DATE: 1997-11-24
67	PRIOR APPLICATION NUMBER: 60/069212
68	PRIOR FILING DATE: 1997-12-11
69	PRIOR APPLICATION NUMBER: 60/069278

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PRIOR FILING DATE:	1997-12-16
PRIOR APPLICATION NUMBER:	60/072322
PRIOR FILING DATE:	1998-01-23
PRIOR APPLICATION NUMBER:	60/073612
PRIOR FILING DATE:	1998-02-04
PRIOR APPLICATION NUMBER:	60/074086
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PRIOR APPLICATION NUMBER:	60/074092
PRIOR FILING DATE:	1998-02-09
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PRIOR APPLICATION NUMBER:	60/081225
PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081699
PRIOR FILING DATE:	1998-04-16
PRIOR APPLICATION NUMBER:	60/081817
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081818
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/082999
PRIOR FILING DATE:	1998-04-24
PRIOR APPLICATION NUMBER:	60/083322
PRIOR FILING DATE:	1998-04-28
PRIOR APPLICATION NUMBER:	60/083545
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/084600
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084622
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084637
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/085149
PRIOR FILING DATE:	1998-05-12
PRIOR APPLICATION NUMBER:	60/085323
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085338
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085399
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085579
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085697
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085704
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/086414
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/086430
PRIOR FILING DATE:	1998-05-22
PRIOR APPLICATION NUMBER:	60/087106
PRIOR FILING DATE:	1998-05-28
PRIOR APPLICATION NUMBER:	60/088026
PRIOR FILING DATE:	1998-06-04
PRIOR APPLICATION NUMBER:	60/088730
PRIOR FILING DATE:	1998-06-10
PRIOR APPLICATION NUMBER:	60/088741
PRIOR FILING DATE:	1998-06-10

US-09-944-944-42 (1-243) x US-10-028-072-361 (1-1377)





QY	61	AlAPrGGLVGLuysGSLyGLuGLyGLyAqPrGGLyLysPPrGGLyPPrOArGLyASPro	80
Db	407	GCTCCGGAGAGAAAGGCGAGGGCCGGAGGCGGGAGCTGCCGGACTTCGAGGGAGCC	466
QY	81	GLyPrOArGGLyGLuGLaGLyPrOALaGLyPrOArhGLyPrOALaGLyGLuCySeSerVal	100
Db	467	GGCGCCGAGAGAGAGGCGGGAGCCCGGGGGCCACCGGGGCTGCCGGGAGTGCCTGGTG	528
QY	101	PrOPrArGSeSLaPhSeSerLALysArGSeSerGusSerArGyALPrOPrOPrOSerAsp	120
Db	527	CTCTCCGAGATCCGCTTCAGCCCAAGCCCTCCAGAGCCGGGTCCCTCCGCGCTGAC	588
QY	121	ALAPrOArPrOPheASpArGyALLeUVALsnGLInGLInHISLyASpALaValThr	140
Db	587	GCACCTTGCCCTTCAGACCGCGCTGCGTGAAGACAGAGGACATTAGACGCCGTAC	648
QY	141	GLyLysPheThrCySGInVALPrOGLyVALyTyTyThrEALaVALHISALaThrVALyTr	160
Db	647	GGCAATTCACCTCGCCAGGCTGCCGGGTCTACTCTAGCCGTCACATGCACCGCTTAC	706
QY	161	ArGALSeSerLeuGLInPhASpLeUVALySAsnGLyGusSerLLeALaSerPhPheGLIn	180
Db	707	CGGGCCAGCCTGCAGATTGATCTGGGAAGATGGCGAATCATTCATTCCTTTCTTCAG	766
QY	181	PhASpHeGLyGLyTrPrOLysPrOALaSerLeuSerGLyGLyALaMetVALaArgLeuGLu	200
Db	767	TTTTTGGGGGGGGGGCCAGGCACGCTCGCTCGGGGGGGCCATGTAAGCTGGAG	828
QY	201	PrOGLyASpGLInVALTrPrVALInVALyGLyGLyASpTyTLeGLyLLeTyTrALaSer	220
Db	827	CTCGAGAGACCAAGTGGGGTGCAGGTGGGTGGGTGACTCATATGGCATCTATAGCCAGC	886
QY	221	ILeLyThrASpSerThrPhSeSerGLyPheLeUVALTySArASpTrPHISerSerPro	240
Db	887	ATCAAGACAGACAGCACCTTCTCCGGATTCTGTGTACTCGACTGGACAGCTCCCA	948
QY	241	VALPheALa 243	
Db	947	GTCCTTGCT 955	
RESULT 12			
US-10-176-918-361			
/ Sequence 361, Application US/10176918			
/ Publication No. US20030027275A1			
/ GENERAL INFORMATION:			
/ APPLICANT: Baker, Kevin P.			
/ APPLICANT: Beresini, Maureen			
/ APPLICANT: DeForge, Laura			
/ APPLICANT: Desnoyers, Luc			
/ APPLICANT: Filvaroff, Ellen			
/ APPLICANT: Gao, Wei-Qiang			
/ APPLICANT: Gerltsen, Mary E.			
/ APPLICANT: Goddard, Audrey			
/ APPLICANT: Godowski, Paul J.			
/ APPLICANT: Gurney, Austin L.			
/ APPLICANT: Sherwood, Steven			
/ APPLICANT: Smith, Victoria			
/ APPLICANT: Stewart, Timothy A.			
/ APPLICANT: Tumas, Daniel			
/ APPLICANT: Watanabe, Colin K			
/ APPLICANT: Wood, William			
/ APPLICANT: Zhang, Zemin			
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME			
/ FILE REFERENCE: P3330R1C382			
/ CURRENT APPLICATION NUMBER: US/10/176,918			
/ CURRENT FILING DATE: 2002-06-20			
/ Prior Application removed - See File Wrapper or Palm			
/ NUMBER OF SEQ ID NOS: 550			
/ SEQ ID NO 361			
/ LENGTH: 1377			
/ TYPE: DNA			

[illegible]



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QY 61 AlaProglyIuLysGlyGlyValArgProGlyLeuProGlyProAlaGlyAspPro 80
DB 407 GCTCGGGAGAGAAAGGCGAGGCGGAGCGGAGCTCGGGAGCTCGAGGGGAGCC 466
QY 81 GlyProArgGlyIuAlaGlyProAlaGlyProThrGlyProAlaGlyGlyCysSerVal 100
DB 467 GGGCGGCGAGAGAGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGAGTGTCTCGGTG 526
QY 101 ProProArgSerAlaPheSerAlaLysArgSerGlySerArgValProProProSerAsp 120
DB 527 CCTCGCGGATCGGCTTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 586
QY 121 AlaProLeuProPheAspArgValLeuValAsnGlyGlyIleAlaSerPhePheGln 140
DB 587 GCACCTTGCCCTTCGACCGCGGTGCTGTAACGAGCGAGGACATTAGACGCGCTCAC 646
QY 141 GlyLysPheThrCysGlnValProGlyValTyrTyrPheAlaValAlaThrValTyr 160
DB 647 GGCAGGTTCACCTCGACGAGTCTGGGGTCTACTACTCTGCGCTCCATGCGCACCGCTAC 706
QY 161 ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyGlySerIleAlaSerPhePheGln 180
DB 707 CGGGCAGCCGCGAGTTGATCTGTGAAGAATGCGAATCCATTGCTCTTCTTCAG 766
QY 181 PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGln 200
DB 767 TTTTTCGGGGGGTGGCCCAAGCCGCTCTCGGGGGGGCGCATGTAGAGCTGAG 826
QY 201 ProGluAspGlnValITTPValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSer 220
DB 827 CCTAGAGACCAAGTGTGGTCCAGGTGGGTGGGTGCTCATTTGGCATTTAGGCCAGC 886
QY 221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspTyrPheLysSerSerPro 240
DB 887 ATCAAGACAGACACACCTTCTCCGATTCTCGGTACTCGTACTCGACTGGCACAGCTCCCA 946
QY 241 ValPheAla 243
DB 947 GTCCTTGCT 955

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## RESULT 15

US-10-140-474-361

Sequence 361, Application US/10140474

Publication No. US20030032136A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P330R1C162

CURRENT APPLICATION NUMBER: US/10/140,474

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 361

LENGTH: 1377

TYPE: DNA

ORGANISM: Homo Sapien

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US-10-140-474-361
Alignment Scores:
Pred. No.: 1,67e-107 Length: 1377
Score: 1325.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-944-944-42 (1-243) x US-10-140-474-361 (1-1377)

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QY 1 MetArgProLeuLeuValLeuLeuLeuGlyLeuAlaAlaGlySerProProLeuAsp 20
DB 227 ATGAGGCACTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTG 286
QY 21 AspAsnLysIleProSerLeuCysProGlyIleHisProGlyLeuProGlyThrProGlyHis 40
DB 287 GACAAACAGATCCCAAGCTCTGCGCGGAGCCCGGCGGCGGCGGCGGCGGCGGCGGCG 346
QY 41 HisGlySerGlnGlyLeuProGlyValArgAspGlyValArgAspGlyValArgAspGly 60
DB 347 CATGGCAGCCAGGCGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 406
QY 61 AlaProGlyIuLysGlyGlyValArgProGlyLeuProGlyProAlaGlyAspPro 80
DB 407 GCTCGGGAGAGAAAGGCGAGGCGGAGCGGCGGAGCTGCGGGAGCTCGAGGGGAGCC 466
QY 81 GlyProArgGlyIuAlaGlyProAlaGlyProThrGlyProAlaGlyGlyCysSerVal 100
DB 467 GGGCGGCGAGAGAGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 526
QY 101 ProProArgSerAlaPheSerAlaLysArgSerGlySerArgValProProProSerAsp 120
DB 527 CCTCGGAGATCGGCTTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 586
QY 121 AlaProLeuProPheAspArgValLeuValAsnGlyGlyIleAlaSerPhePheGln 140
DB 587 GCACCTTGCCCTTCGACCGCGGTGCTGTAACGAGCGAGGACATTAGACGCGCTCAC 646
QY 141 GlyLysPheThrCysGlnValProGlyValTyrTyrPheAlaValAlaThrValTyr 160
DB 647 GGCAGGTTCACCTCGACGAGTCTGGGGTCTACTACTCTGCGCTCCATGCGCACCGCTAC 706
QY 161 ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyGlySerIleAlaSerPhePheGln 180
DB 707 CGGGCAGCCGCGAGTTGATCTGTGAAGAATGCGAATCCATTGCTCTTCTTCAG 766
QY 181 PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGln 200
DB 767 TTTTTCGGGGGGTGGCCCAAGCCGCTCTCGGGGGGGCGCATGTAGAGCTGAG 826
QY 201 ProGluAspGlnValITTPValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSer 220
DB 827 CCTAGAGACCAAGTGTGGTCCAGGTGGGTGGGTGCTCATTTGGCATTTAGGCCAGC 886
QY 221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspTyrPheLysSerSerPro 240
DB 887 ATCAAGACAGACACACCTTCTCCGATTCTCGGTACTCGTACTCGACTGGCACAGCTCCCA 946
QY 241 ValPheAla 243
DB 947 GTCCTTGCT 955

```

Search completed: June 21, 2003, 19:02:47  
 Job time : 205 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 13, 2003, 15:55:46 ; Search time 22 seconds

(without alignments)  
458.125 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325  
Sequence: 1 MRPLVLLGLAAGSPPLD.....DSFGFLVSDMHSPIYFA 243

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1325	100.0	243	1	COT5_HUMAN
2	433.5	32.7	247	1	Q60994_0 homo sapien
3	424	32.0	244	1	APM1_MOUSE
4	418.5	31.6	680	1	APM1_HUMAN
5	417	31.5	674	1	CA1A_HUMAN
6	412	31.1	246	1	CA1A_CHICK
7	411.5	31.0	674	1	CA1A_BOVIN
8	410.5	30.8	289	1	COT7_HUMAN
9	408	30.4	680	1	CA1A_MOUSE
10	403	30.0	285	1	COT2_HUMAN
11	397	28.2	744	1	CA18_HUMAN
12	374	28.2	744	1	CA18_RABIT
13	373	28.2	419	1	COLE_MOUSE
14	368	27.8	744	1	CA18_HUMAN
15	366.5	27.7	743	1	CA18_MOUSE
16	363	27.4	635	1	CA28_HUMAN
17	362	27.3	251	1	C10B_HUMAN
18	360.5	27.2	253	1	C10B_RAT
19	350	26.4	253	1	C10B_MOUSE
20	314	23.7	245	1	C10A_HUMAN
21	314	23.7	245	1	C10A_MOUSE
22	298.5	22.5	255	1	GLIC_MOUSE
23	285.5	21.5	258	1	C1RF_HUMAN
24	282	21.3	258	1	C1RF_MOUSE
25	280.5	21.2	215	1	HP25_TAMSI
26	277.5	20.9	215	1	HP25_TAMSI
27	264.5	20.0	246	1	COT3_HUMAN
28	261.5	19.7	196	1	HP20_TAMSI
29	230.5	17.4	1049	1	CA13_BOVIN
30	228.5	17.3	281	1	COT1_HUMAN
31	228	17.2	684	1	CA39_HUMAN
32	224	16.9	636	1	CA13_RAT
33	223	16.8	1464	1	CA13_MOUSE

34	222.5	16.8	1758	1	CA24_CAEEL	P17140 caenorhabd
35	221.5	16.7	170	1	CA28_MOUSE	P25318 mus musculu
36	221	16.7	1019	1	CA16_CHICK	P20785 gallus galli
37	221	16.7	1262	1	CA13_CHICK	P12105 gallus galli
38	220	16.6	248	1	PSPA_CANFA	P06908 canis fam11
39	220	16.6	360	1	CCD2_CAEEL	P35799 caenorhabd1
40	219.5	16.6	247	1	PSPA_RABIT	P12842 oryctolagu
41	219.5	16.6	1466	1	CA13_HUMAN	P02461 homo sapien
42	219	16.5	671	1	CA11_RAT	P02454 rattus norv
43	218.5	16.5	1453	1	CA11_MOUSE	P11087 mus musculu
44	217.5	16.4	1516	1	CA1H_HUMAN	P39060 homo sapien
45	217	16.4	747	1	CA12_BOVIN	P02459 bos taurus

## ALIGNMENTS

RESULT 1  
COT5\_HUMAN STANDARD; PRT; 243 AA.  
ID COT5\_HUMAN Q90FX4;  
AC Q90FX4; 15-JUN-2002 (Rel. 41, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DE 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Complement-clq tumor necrosis factor-related protein 5 precursor.  
GN C1QTNF5 OR CTRP5.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RA Sheppard P.O., Humes J.M.;  
RT "Homo sapiens complement-clq tumor necrosis factor-related protein.";  
RT Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.  
RP [2]  
RP SEQUENCE OF 25-243 FROM N.A.  
RC TISSUE=uterus;  
RA Ottenweider B., Obermaier B., Mewes H.-W., Gassenhuber J.,  
RA Wiemann S.;  
RA Submitted (AUG-1999) to the EMBL/Genbank/DBJ databases.  
RL -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC  
CC EMBL; AF329841; AAK17965.1; -  
CC EMBL; AL110261; CAB53702.1; -  
CC Gene; HGNC:14344; C1QTNF5.  
DR InterPro; IPR001073; C1q.  
DR InterPro; IPR000087; Collagen.  
DR Pfam; PF00386; C1q; 1.  
DR Pfam; PF01391; Collagen; 1.  
DR PRINTS; PR00007; COMPLEMENTC1Q.  
DR SMART; SM00110; C1Q; 1.  
DR PROSITE; PS01113; C1Q; FALSE\_NEG.  
DR Collagen; Signal.  
FT SIGNAL 1 15 POTENTIAL.  
FT CHAIN 16 243 COMPLEMENT-C1Q TUMOR NECROSIS FACTOR-  
FT DOMAIN 30 95 RELATED PROTEIN 5.  
FT FT 97 243 COLLAGEN-LIKE.  
SQ SEQUENCE 243 AA: 25298 MW: 70CDAA65CD87EB784 CRC64;  
Query Match 100.0%; Score 1325; DB 1; Length 243;  
Best Local Similarity 100.0%; Pred. No. 1,7e-85;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAGSPPLDNDKIPSLCPGHHGSGGLPCRDGRDGDGAPG 60  
 DB 1 MRPLVLLLLGLAGSPPLDNDKIPSLCPGHHGSGGLPCRDGRDGDGAPG 60  
 QY 61 APGKGGGGRGLGPRDPPGPRGAGAGTGAECGVPRRASFSAKRSRYPSPD 120  
 DB 61 APGKGGGGRGLGPRDPPGPRGAGAGTGAECGVPRRASFSAKRSRYPSPD 120  
 QY 121 APLEFDRLVNEOGHYAVTGTGKCOVPGVYFFAVHATVYRASLOFDLVKNGESTIASPFQ 180  
 DB 121 APLEFDRLVNEOGHYAVTGTGKCOVPGVYFFAVHATVYRASLOFDLVKNGESTIASPFQ 180  
 QY 181 FFGGMPKPRASLGGAMVRLPEDDOVWVGVGDYIGIYASIKTSTSGFLVYSDWHSPP 240  
 DB 181 FFGGMPKPRASLGGAMVRLPEDDOVWVGVGDYIGIYASIKTSTSGFLVYSDWHSPP 240  
 QY 241 VFA 243  
 DB 241 VFA 243

## RESULT 2

APML\_MOUSE STANDARD; PRT: 247 AA.

AC Q6094; Q62400; Q9DC68;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Adiponectin precursor (30 kDa adipocyte complement-related protein)  
 DE (ACRP30) (Adipocyte specific protein AdipoQ).  
 GN APML OR ACRP30 OR ADIPOQ.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID:10090;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE-Adipocyte;  
 RX MEDLINE=96070757; PubMed=7592907;  
 RA Scherer P.E., Williams S., Fogliano M., Baldini G., Lodish H.F.;  
 RT "A novel serum protein similar to C1q, produced exclusively in  
 RT adipocytes".  
 RL J. Biol. Chem. 270:26746-26749(1995).  
 RN [2]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE-Fibroblast;  
 RX MEDLINE=96209999; PubMed=8631877;  
 RA Hu E., Liang P., Spiegelman B.M.;  
 RT "AdipoQ is a novel adipose-specific gene dysregulated in obesity".  
 RL J. Biol. Chem. 271:10697-10703(1996).  
 RN [3]  
 RC SEQUENCE FROM N.A.  
 RC PubMed=11162643;  
 RA Das K., Lin Y., Widen E., Zhang Y., Scherer P.E.;  
 RT "Chromosomal localization, expression pattern, and promoter analysis  
 RT of the mouse gene encoding adipocyte-specific secretory protein  
 RT Acrp30".  
 RL Biochem. Biophys. Res. Commun. 280:1120-1129(2001).  
 RN [4]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Heart;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleishmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilmink L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection".  
 RL Nature 409:685-690(2001).  
 RN [5]  
 RC FUNCTION.  
 RX MEDLINE=21372498; PubMed=11479627;  
 RA Yamauchi T., Kamon J., Maki H., Terauchi Y., Kubota N., Hara K.,  
 RA Mori Y., Ide T., Murakami K., Tsuboyama-Kasaoka N., Ezaki O.,  
 RA Akiyama Y., Gavrilova O., Vinson C., Reitman M.L., Kagechika H.,  
 RA Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,  
 RA Froguel P., Kadowaki T.;  
 RT "The fat-derived hormone adiponectin reverses insulin resistance  
 RT associated with both lipodystrophy and obesity".  
 RL Nat. Med. 7:941-946(2001).  
 RN [6]  
 RC FUNCTION.  
 RX MEDLINE=21372499; PubMed=11479628;  
 RA Berg A.H., Combs T.P., Du X., Brownlee M., Scherer P.E.;  
 RT "The adipocyte-secreted protein Acrp30 enhances hepatic insulin  
 RT action".  
 RL Nat. Med. 7:947-953(2001).  
 RN [7]  
 CC -1- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIESIS AND IMMUNE  
 CC SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH  
 CC ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPA-B SIGNALING  
 CC THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED  
 CC EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE  
 CC CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.  
 CC -1- SUBUNIT: HOMODIGOMER.  
 CC -1- SUBCELLULAR LOCATION: SECRETED IN PLASMA.  
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED EXCLUSIVELY BY ADIPOCYTES AND  
 CC SECRETED INTO SERUM.  
 CC -1- INDUCTION: DURING HORMONE-INDUCED ADIPOSE DIFFERENTIATION AND  
 CC ACTIVATED BY INSULIN.  
 CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 C10 DOMAIN.  
 CC  
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 CC  
 CC EMBL: U37222; AAA80543.1; -;  
 CC EMBL: U49915; AAB06706.1; -;  
 CC EMBL: AF304466; AAK13417.1; -;  
 CC EMBL: AK003138; BAB2357.1; -;  
 CC MGD: MGI:106675; Acrp30.  
 CC InterPro: IPR001073; C1q.  
 CC InterPro: IPR000087; Collagen.  
 CC Pfam: PF00336; C1q; 1.  
 CC Pfam: PF01391; collagen; 1.  
 CC PRINTS: PR00007; COMPLEMENTC1Q.  
 CC SMART: SM00110; C1Q; 1.  
 CC PROSITE: PS01113; C1Q; 1.  
 CC Hormone; Collagen; Signal; Repeat; Hydroxylation; Plasma;  
 CC Polymorphism.  
 CC SIGNAL 1 17  
 CC CHAIN 18 247  
 CC DOMAIN 45 110  
 CC DOMAIN 111 247  
 CC DISULFID 39 39  
 CC MOD\_RES 47 47  
 CC MOD\_RES 50 50  
 CC MOD\_RES 56 56  
 CC POTENTIAL.  
 CC ADIPONECTIN.  
 CC COLLAGEN-LIKE.  
 CC C1Q.  
 CC INTERCHAIN (BY SIMILARITY).  
 CC HYDROXYLATION (BY SIMILARITY).  
 CC HYDROXYLATION (BY SIMILARITY).  
 CC HYDROXYLATION (BY SIMILARITY).

FT	MOD_RES	65	HYDROXYLATION (BY SIMILARITY).
FT <th>MOD_RES</th> <td>79 <td>HYDROXYLATION (BY SIMILARITY). </td></td>	MOD_RES	79 <td>HYDROXYLATION (BY SIMILARITY). </td>	HYDROXYLATION (BY SIMILARITY).
FT <th>MOD_RES</th> <td>98 <td>HYDROXYLATION (BY SIMILARITY). </td></td>	MOD_RES	98 <td>HYDROXYLATION (BY SIMILARITY). </td>	HYDROXYLATION (BY SIMILARITY).
FT <th>MOD_RES</th> <td>107 <td>HYDROXYLATION (BY SIMILARITY). </td></td>	MOD_RES	107 <td>HYDROXYLATION (BY SIMILARITY). </td>	HYDROXYLATION (BY SIMILARITY).
FT <th>VARIANT</th> <td>113 <td>M -&gt; V. </td></td>	VARIANT	113 <td>M -&gt; V. </td>	M -> V.
FT <th>CONFLICT</th> <td>50 <td>P -&gt; S (IN REF. 2). </td></td>	CONFLICT	50 <td>P -&gt; S (IN REF. 2). </td>	P -> S (IN REF. 2).
FT <th>CONFLICT</th> <td>74 <td>A -&gt; S (IN REF. 2). </td></td>	CONFLICT	74 <td>A -&gt; S (IN REF. 2). </td>	A -> S (IN REF. 2).
FT <th>CONFLICT</th> <td>117 <td>A -&gt; G (IN REF. 2). </td></td>	CONFLICT	117 <td>A -&gt; G (IN REF. 2). </td>	A -> G (IN REF. 2).
FT <th>CONFLICT</th> <td>148 <td>G -&gt; N (IN REF. 2). </td></td>	CONFLICT	148 <td>G -&gt; N (IN REF. 2). </td>	G -> N (IN REF. 2).
FT <th>CONFLICT</th> <td>243 <td>Y -&gt; F (IN REF. 2). </td></td>	CONFLICT	243 <td>Y -&gt; F (IN REF. 2). </td>	Y -> F (IN REF. 2).
Q9 <th>SEQUENCE</th> <td>247 AA; 26841 MW; 137B6B7DB73588C4 CRC64; <td></td> </td>	SEQUENCE	247 AA; 26841 MW; 137B6B7DB73588C4 CRC64; <td></td>	

Query Match	32.7%;	Score 433.5;	DB 1;	Length 247;
Best Local Similarity	40.6%;	Pred. No. 1.2e-23;		
Matches 102;	Conservative 32;	Mismatches 92;	Indels 25;	Gaps 8

[illegible]

RESULT 3	
APM1_HUMAN	
ID	APM1_HUMAN
STANDARD:	PRT; 244 AA

AC	Q15848;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Adiponectin precursor (30 kDa adipocyte complement-related protein)
DE	(ACRP30) (Adipose most abundant gene transcript 1) (apm-1) (Gelatin-
DE	binding protein).
GN	APM1 OR ACRP30 OR GBP28.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	TISSUE=Adipose tissue;
RC	MEDLINE=96224171; PubMed=8619847;
RA	Maeda K., Okubo K., Shimomura I., Funahashi T., Matsuzawa Y.,
RA	Matsubara K.;
RT	cDNA cloning and expression of a novel adipose specific collagen-like
RT	factor, apm1 (Adipose Most abundant Gene transcript 1).";
RL	Biochem. Biophys. Res. Commun. 221:286-289(1996).
RN	[2]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=99196984; PubMed=10095105;
RA	Saito K., Tobe T., Minoshima S., Asakawa S., Sumiya J., Yoda M.,
RA	Nakano Y., Shimizu N., Tomita M.;
RT	Organisation of the gene for gelatin-binding protein (GBP28).";
RT	Gene 229:67-73(1999).
RN	[3]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=99333693; PubMed=10403784;
RA	Schaeffler A., Orso E., Palitzsch K.D., Buechler C., Drobnik W.,
RA	Fuerst A., Schoelmerich J., Schmitz G.;

RT "The human apy-1, an adipocyte-specific gene linked to the family of  
RT TNF's and to genes expressed in activated T cells, is mapped to  
RT chromosome 1q11.3-q23, a susceptibility locus identified for familial  
RT combined hyperlipidemia (FCH).";  
RL Biochem. Biophys. Res. Commun. 260:416-425(1999).  
nu

RN [4]  
 RP CHARACTERIZATION.  
 RX MEDLINE=20417747; PubMed=10961870;  
 RA Yokota T., Oritani K., Takahashi I., Ishikawa J., Matsuyama A.,  
 RA Ouchi N., Kihara S., Funahashi T., Tenner A.J., Tomiyama Y.,  
 RA Matsuzawa Y.,  
 RT "Adiporectin, a new member of the family of soluble defense collagens,  
 RT negatively regulates the growth of myelomonocytic progenitors and the  
 RT functions of macrophages."  
 RL Blood 96:1723-1732(2000).

RN CHARACTERIZATION: PubMed-10962546;  
 RN MEDLINE-20440368;  
 RA Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyama H.,  
 RA Nakata K., Nishida M., Takahashi M., Muraguchi M., Omoto Y.,  
 RA Nakamura T., Yamashita S., Funahashi T., Matsuzawa Y.,  
 RT Adiponectin, an adipocyte-derived plasma protein, inhibits  
 RL endothelial NF-kappaB signaling through a cAMP-dependent pathway. "  
 [6] Circulation 102:1296-1301(2000).  
 RN

RP FUNCTION.  
RX MEDLINE=21372498; PubMed=11479627;  
RA Yamauchi T., Kamon J., Maki H., Terauchi Y., Kubota N., Hara K.,  
RA Mori Y., Ide T., Murakami K., Tsuboyama-Kasao K., Ezaki O.,  
RA Akamune Y., Gavrilova O., Vlasov C., Reitman M.D., Kagechika H.,  
RA Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,  
RA Froguet P., Kadwaki T.;  
RT "The fat-derived hormone adiponectin reverses insulin resistance  
RT associated with both lipodystrophy and obesity.";  
RL Nat. Med. 7:941-946(2001).

RN [7]  
RP VARIANT ADIPOLECTIN DEFICIENCY CYS-112.  
RX MEDLINE=20378830; PubMed=10918532;  
RA Takahashi M., Aita Y., Yamagata K., Matsukawa Y., Okamoto K.,  
RA Horie M., Shimomura I., Hotta K., Kuriyama H., Kihara S., Nakamura T.,  
RA Nasahita S., Punashashi T., Matsuzawa Y.,  
RT "Genomic structure and mutations in adipose-specific gene,  
RT adiponectin";  
RL Int. J. Obes. Relat. Metab. Disord. 24:861-868(2000).

RN [8]  
RP VARIANTS ARG-84; MET-117; THR-184; SER-221 AND PRO-241.  
RX MEDLINE=21671103; PubMed=11812766;  
RA Hara K., Boutin P., Mori Y., Tobe K., Dina C., Yasuda K., Yamauchi T.,  
RA Otaka S., Okada T., Eto K., Kadowaki H., Hagura R., Ahanuma Y.,  
RA Yuzaki Y., Nagai R., Taniyama M., Matubara K., Yoda M., Nakano Y.,  
RA Kimura S., Tomita M., Kimura S., Ito C., Froguet P., Kadowaki T.,  
RT "Genetic variation in the gene encoding adiponectin is associated with  
RT an increased risk of type 2 diabetes in the Japanese population.",  
RL Diabetes 51:536-540(2002).

CC -1- FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIETIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHELIAL NF-KAPPAB SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED EXPRESSION OF ENDOTHELIAL ADHESION MOLECULES. INVOLVED IN THE CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.

CC -1- SUBUNIT: HOMOLIGOMER (POTENTIAL).

CC -1- SUBCELLULAR LOCATION: SECRETED IN PLASMA.

CC -1- TISSUE SPECIFICITY: EXPRESSED ONLY IN THE ADIPOSE TISSUE.

CC -1- DISEASE: Defects in APM1 are the cause of adiponectin deficiency,

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CC -----  
CC -1 SIMILARITY: CONTAINS 1 CLO DOMAIN.  
CC -1 PHARMACEUTICAL: Adiponectin might be used in the treatment of  
CC diabetes type 2 and insulin resistance.  
CC -1 SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
CC -----  
CC

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DR EMBL; D45371; BAA08227.1; -  
 DR EMBL; AB012165; BAA86716.1; -  
 DR EMBL; AB012164; BAA86716.1; JOINED.  
 DR EMBL; AJ131460; CAB52413.1; -  
 DR EMBL; AJ131461; CAB52413.1; JOINED.  
 DR MIM; 605441; -  
 DR InterPro; IPR001073; C1q.  
 DR InterPro; IPR000087; collagen.  
 DR Pfam; PF00386; C1q; 1.  
 DR Pfam; PF01391; collagen; 1.  
 DR PRINTS; PR00007; COMPLEMENTC1Q.  
 DR SMART; SM00110; C1Q; 1.  
 DR PROSITE; PS01113; C1Q; 1.  
 KW Hormone; Collagen; Signal; Repeat; Hydroxylation; Plasma;  
 KW Polymorphism; Disease mutation; Obesity; Diabetes mellitus.  
 FT SIGNAL 1 14  
 FT CHAIN 15 244  
 FT DOMAIN 42 107  
 FT DUF 108 244  
 FT DISULFID 36 36  
 FT MOD\_RES 44 44  
 FT MOD\_RES 47 47  
 FT MOD\_RES 53 53  
 FT MOD\_RES 62 62  
 FT MOD\_RES 71 71  
 FT MOD\_RES 76 76  
 FT MOD\_RES 86 86  
 FT MOD\_RES 95 95  
 FT MOD\_RES 104 104  
 FT VARIANT 84 84  
 FT VARIANT 112 112  
 FT VARIANT 117 117  
 FT VARIANT 164 164  
 FT VARIANT 221 221  
 FT VARIANT 241 241  
 SQ SEQUENCE 244 AA; 26414 MW; 64D8C6C1204B1018 CRC64;  
 Query Match 32.0%; Score 424; DB 1; Length 244;  
 Best Local Similarity 40.5%; Pred. No. 5.3e-23;  
 Matches 106; Conservative 26; Mismatches 72; Indels 58; Gaps 10;

RESULT 4  
 C1QA\_HUMAN STANDARD; PRT; 680 AA.  
 ID C03692;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Collagen alpha 1(X) chain precursor.  
 GN COL10A1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92109659; PubMed-1764025;  
 RA Thomas J.T., Cresswell C.J., Rash B., Nicolai H., Jones T.,  
 RA Solomon E., Grant M.E., Boot-Handford R.P.;  
 RT "Type human collagen X gene. Complete primary translated sequence and  
 RT chromosomal localization.";  
 RL Biochem. J. 280:617-623(1991).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-93012005; PubMed-1397333;  
 RA Reichenberger E., Belter F., Luvall P., Olsen B.R., von der Mark K.,  
 RA Bertling W.M.;  
 RT "Genomic organization and full-length cDNA sequence of human collagen  
 RT X.";  
 RL FEBS Lett. 311:305-310(1992).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RA Belter F., Lammli M.B., von der Mark K.;  
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.  
 [4]  
 RP SEQUENCE FROM N.A.  
 RA Williams S.;  
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.  
 [5]  
 RP SEQUENCE OF 52-680 FROM N.A.  
 RX MEDLINE-92267014; PubMed-1587271;  
 RA Apte S.S., Seidlin M.F., Hayashi M., Olsen B.R.;  
 RT "Cloning of the human and mouse type X collagen genes and mapping of  
 RT the mouse type X collagen gene to chromosome 10.";  
 RL Eur. J. Biochem. 206:217-224(1992).  
 [6]  
 RP SEQUENCE OF 561-666 FROM N.A.  
 RX MEDLINE-91243838; PubMed-2037056;  
 RA Apte S., Mattei M.-G., Olsen B.R.;  
 RT "Cloning of human alpha 1(X) collagen DNA and localization of the  
 RT COL10A1 gene to the q21-q22 region of human chromosome 6.";  
 RL FEBS Lett. 282:393-396(1991).  
 [7]  
 RP SEQUENCE OF 547-655 FROM N.A.  
 RX MEDLINE-92077285; PubMed-1743401;  
 RA Reichenberger E., Aigner T., von der Mark K., Stoeck H., Bertling W.;  
 RT "In situ hybridization studies on the expression of type X collagen  
 RT in fetal human cartilage.";  
 RL Dev. Biol. 148:562-572(1991).  
 [8]  
 RP REVIEW ON VARIANTS.  
 RX MEDLINE-97255959; PubMed-9101290;  
 RA Kuivaniemi H., Tromp G., Prockop D.J.;  
 RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-  
 RT associated collagen (type IX), and network-forming collagen (type X)  
 RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";  
 RL Hum. Mutat. 9:300-315(1997).  
 [9]  
 RP VARIANTS SMCD ASP-598 AND PRO-614.  
 RX MEDLINE-94136476; PubMed-8304336;  
 RA Wallis G.A., Rash B., Sweetman W.A., Thomas J.T., Super M., Evans G.,  
 RA Grant M.E., Boot-Handford R.P.;



DB 521 MPEGFIRAGORPISLSTGPIVLSANGVTGMPVSAFTVILSKAY--PAIGTPIPFKILYNR 578  
 QY 133 QGHAYATGKFTCCVPEYFAVATYRASLOFDLVKNGESIA-SFFQFGGMPKPSL 191  
 DB 579 QGHDPRTGFTGTCIPGITYFSYVHVKGFVWGLKNGSPVATYDEYKGLDQA-- 636  
 QY 192 SGGAMVRLPEDDVWVGVDYIGIYASIKTSTSGFLV 232  
 DB 637 SGAHIDLTENDQVWLPLPNAESNGLYSSEYVHSSFGFLV 677  
 RESULT 5  
 CALA\_CHICK STANDARD; PRT; 674 AA.  
 ID CALA\_CHICK  
 AC P08125;  
 DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Collagen alpha 1(x) chain precursor.  
 GN COL10A1.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE OF 48-674 FROM N.A., AND SEQUENCE OF 103-117 AND 453-466.  
 RX MEDLINE=6616827; PubMed=3082876;  
 RA Nishimura Y., Gordon M., van der Rest M., Schmid T., Linsemayer T.,  
 RA Olsen B.R.;  
 RT "The developmentally regulated type X collagen gene contains a long  
 RT open reading frame without introns."  
 RL J. Biol. Chem. 261:5041-5050(1986).  
 RN [2]  
 RP SEQUENCE OF 1-75 FROM N.A.  
 RX MEDLINE=89054019; PubMed=2461368;  
 RA Luvalle P., Nishimura Y., Rosenblum N.D., Olsen B.R.;  
 RT "The type X collagen gene. Intron sequences split the 5'-untranslated  
 RT region and separate the coding regions for the non-collagenous amino-  
 RT terminal and triple-helical domains."  
 RL J. Biol. Chem. 263:18378-18385(1988).  
 RN [3]  
 RP REVISIONS TO C-TERMINUS.  
 RX MEDLINE=89380199; PubMed=2476437;  
 RA Yamaguchi N., Benay P.D., van der Rest M., Nishimura Y.;  
 RT "The cloning and sequencing of alpha 1(VIII) collagen cDNAs  
 RT demonstrate that type VIII collagen is a short chain collagen and  
 RT contains triple-helical and carboxyl-terminal non-triple-helical  
 RT domains similar to those of type X collagen."  
 RL J. Biol. Chem. 264:16022-16029(1989).  
 CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC  
 CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE  
 CC MINERALIZATION ZONES OF HYALINE CARTILAGE.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- PM: PROLINS AT THE THIRD POSITION OF THE TRIPLET REPEATING  
 CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.  
 CC -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.  
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.  
 CC  
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 CC  
 CC EMBL; M13496; AAA48736.1; ALT\_SEQ.  
 CC EMBL; J04194; AAA48634.1; -  
 CC PIR; A31896; A31896.  
 CC InterPro: IPR001073; C1q.  
 CC InterPro: IPR000087; Collagen.  
 CC Pfam; PF00386; C1q; 1.

DR Pfam; PF01391; Collagen; 8.  
 DR PRINTS; PRO0007; COMPLEMENTC1Q.  
 DR SMART; SM00110; C1Q; 1.  
 DR PROSITE; PS01113; C1Q; 1.  
 KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;  
 KW Cartilage; Collagen; Signal.  
 FT SIGNAL  
 FT CHAIN 1 18  
 FT CHAIN 19 674  
 FT DOMAIN 19 52  
 FT DOMAIN 53 512  
 FT DOMAIN 513 674  
 FT DOMAIN 539 674  
 FT MOD\_RES 453 453  
 FT MOD\_RES 456 456  
 FT SEQUENCE 674 AA; 66434 MW; EAB4B1EF174B145 CRC64;  
 Query Match 31.5%; Score 417; DB 1; Length 674;  
 Best Local Similarity 36.0%; Pred. No. 4,4e-22;  
 Matches 96; Conservative 34; Mismatches 84; Indels 53; Gaps 6;  
 QY 14 AGSPPLDNRKIPSLCPGHPGLPGTGHHSGLPGRDRDGRDAPGAPGEGGGRPL 73  
 DB 408 AGHPGLGPGVPGQVKGVPNGEPGRGPGSGITGVGPGTGPMPGAPKAGAPGL 467  
 QY 74 GPRP-----GDPGRGEA-----GPAGPTGAGGCSVP----- 101  
 DB 468 GPGAGIYTKGLRGPMGLPGPKGNSEPEGLPGPPGPPGPGSTIPEGYKGSRELS 527  
 QY 102 -----PRSAFSARSRSRVPPDPALPPPRVLYNCGHDAVTKFTC 145  
 DB 528 GMSFMKAGANALTGMPVSAFTVILSKAY--PGATVPKPEKILYNRQAHDPRTGLFTC 585  
 QY 146 QVPEYFAVATYRASLOFDLVKNGESIA-SFFQFGGMPKPSLSSGAMVRLPEDD 204  
 DB 586 RLPGLYFSYVHAKGNVWALYKNGSPVATYDEYKGLDQA--SGSAVIDLMENDQ 643  
 QY 205 VWVQVGVGDYIGIYASIKTSTSGFL 231  
 DB 644 VWLQPLPNSSENGLYSSEYVHSSFGFL 670  
 RESULT 6  
 C1QC\_MOUSE STANDARD; PRT; 246 AA.  
 ID C1QC\_MOUSE  
 AC Q02105;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Complement C1q subcomponent, C chain precursor.  
 GN Complement C1q.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BAB/c; TISSUE-Liver;  
 RX MEDLINE=96186528; PubMed=8606057;  
 RA Petry F., Reid K.B.M., Loos M.;  
 RT "Isolation, sequence analysis and characterization of cDNA clones  
 RT coding for the C chain of mouse C1q. Sequence similarity of  
 RT complement subcomponent C1q, collagen type VIII and type X and  
 RT precerebellin."  
 RL Eur. J. Biochem. 209:129-134(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BAB/c; TISSUE-Liver;  
 RX MEDLINE=96186528; PubMed=8606057;  
 RA Petry F., McClive P.J., Botto M., Morley B.J., Morahan G., Loos M.;  
 RT "The mouse C1q genes are clustered on chromosome 4 and show  
 RT conservation of gene organization."  
 RL Immunogenetics 43:370-376(1996).  
 CC -1- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1S TO YIELD

```
CC C1 THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE
CC COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT
CC CLR(2)CIS(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1
CC TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE
CC FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.
CC -1 SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R
CC AND S IN THE MOLAR RATIO OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED
CC OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE
CC A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF
CC THE C CHAIN.
CC -1 SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
CC -1 SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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CC -----
DR EMBL; X66295; CAA4693.1; -.
DR EMBL; X92960; CAA63535.1; -.
DR PIR; S29328; S29328.
DR MGI; MGI:88225; ClqC-.
DR InterPro; IPRO01073; Clq.
DR InterPro; IPRO00087; Collagen.
DR Pfam; PF00386; Clq; 1.
DR Pfam; PF01391; Collagen; 1.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR SMART; SM0110; C1Q; 1.
DR PROSITE; PS0113; C1Q; 1.
KW Complement pathway; Plasma; Hydroxylation; Glycoprotein; Collagen;
KW Repeat; Signal.
FT SIGNAL 1 29
FT CHAIN 30 246
FT DOMAIN 32 113
FT DOMAIN 114 246
FT DISULFD 33 33
FT MOD_RES 37 37 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 40 40 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 43 43 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 61 61 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 64 64 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 73 73 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 76 76 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 79 79 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 82 82 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 97 97 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 100 100 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 106 106 HYDROXYLATION (BY SIMILARITY).
FT MOD_RES 109 109 HYDROXYLATION (BY SIMILARITY).
SQ SEQUENCE 246 AA; 25966 MW; 2879EA1274BCB8E0 CRC64;
Query Match 31.1%; Score 412; DB 1; Length 246;
Best Local Similarity 42.2%; Pred. No. 3.7e-22;
Matches 103; Conservative 33; Mismatches 84; Indels 24; Gaps 10;
```

Db	187	LARASCDHMFN-SKQVS-SGGLALLQKGDFTW--LSVNDYNGMGIIBSNSVFSGFL	242
QY	232	VYSD 235	
Db	243	LFPPD 246	
RESULT 7			
ID	CALA_BOVIN	STANDARD:	PRT: 674 AA.
AC	P23206;		
DT	01-NOV-1991 (Rel. 20, Created)		
DT	01-NOV-1991 (Rel. 20, Last sequence update)		
DT	15-JUL-1999 (Rel. 38, Last annotation update)		
DE	Collagen alpha 1(X) chain precursor.		
GN	COL10A1.		
OS	Bos taurus (Bovine).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;		
OC	Bovidae; Bovinae; Bos.		
OX	NCBI_TaxID=9913;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE:Collage:		
RX	MEDLINE=9111313; PubMed=1703407;		
RA	Thomas J.T., Kwan A.P.U., Grant M.E., Boot-Handford R.P.;		
RT	"Isolation of cDNAs encoding the complete sequence of bovine type X		
RT	collagen. Evidence for the condensed nature of mammalian type X		
RL	Biochem. J. 273:141-148(1991).		
CC	-1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC		
CC	CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE		
CC	MINERALIZATION ZONES OF HYALINE CARTILAGE.		
CC	-1- SUBUNIT: HOMOTRIMER.		
CC	-1- PPM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING		
CC	UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.		
CC	-1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.		
CC	-1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.		
CC	-----		
CC	CC This SWISS-PROT entry is copyright. It is produced through a collaboration		
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CC	CC entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>		
CC	CC or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).		
CC	-----		
DR	EMBL: X53556; CA37624.1; -.		
DR	PIR: S13301; S13301.		
DR	InterPro: IPR001073; C1q.		
DR	InterPro: IPR000087; Collagen.		
DR	Pfam: PF00386; C1q; 1.		
DR	Pfam: PF01391; Collagen; 9.		
DR	PRINTS: PR00007; COMPLEMENTC1Q.		
DR	ProDom: PD000007; Collagen; 1.		
DR	SMART: SM00110; C1Q; 1.		
DR	PROSITE: PS01113; C1Q; 1.		
KW	Extracellular matrix; Connective tissue; Repeat; Hydroxylation;		
KW	Cartilage; collagen; Signal; Glycoprotein.		
FT	SIGNAL	1	18
FT	CHAIN	19	674
FT	DOMAIN	19	56
FT	DOMAIN	57	519
FT	DOMAIN	520	674
FT	DOMAIN	539	674
FT	DISULFID	194	197
FT	MOD_RES	460	460
FT	MOD_RSS	463	463
FT	CARBOHYD	611	611
SO	SEQUENCE	674 AA;	65546 MM; CD4CA73A03E0D04A CRC64;
Query Match	31.18;	Score 411.5;	DB 1; Length 674;
Best Local Similarity	34.98;	Pred. No. 1.1e-21;	

	Matches	96;	Conservative	34;	Mismatches	84;	Indels	61;	Gaps	6;
QY	15	GSPRLDDKKISLRC	HPGLPSTP	RHHSOGILP	RGDGDGRD	GAAGAGEK	EGGRPLP	74		
		I::I::	I::I::I::	I::I::I::	I::I::I::	I::I::I::	I::I::I::			
Db	401	GNPGLPGPKGDP	GIAGSPGL	PVPGPACAKG	APGHNAGAP	PGVGLITK	PLIPG	460		
QY	75	-----	GRGDGPGPGEA	-----	GPAGTGGPAGCS	99				
Db	461	GPSPSGDVGTP	PPPGPAGI	AVKGLNGT	PGPPGPGNAG	EPGLP	PPGPPGPGQVA	520		
QY	100	VP-----	-----	PRSAFSAR	SRESRV	PPSDAPL	PEPRVLVNEGH	438		
Db	521	LPEDFVCKAGQ	PPFVSANOG	VTGMPSAT	VLISKAY--	PAIGTPI	PEPKILLNKQ	458		
QY	139	VTGKTCQVP	GVYFAVAHAT	YRASLQ	EDLVKN	GESIA--	SEFOFGPPK	PKPASLES	197	
Db	579	RTGIFETCK	IPILYFYS	HIHWKGT	HAWGLV	KNGCPVM	YTDYIK	GLDA--	SGSAVI	636
QY	198	RLPEPDV	WVNOVG	VDYIGI	YASIKIT	DSFGELV	232			
Db	637	DLTENDV	WLDLPN	AGNSGL	ISPEYVHS	SGFELV	671			

RESULT	8
COT7_HUMAN	
ID	COT7_HUMAN
AC	O9BXJ2
DT	15-JUN-2002 (Rel. 41, Created)
DT	15-JUN-2002 (Rel. 41, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Complement-c1q tumor necrosis factor-related protein 7 precursor.
GN	C1QTNF7 OR CTSPR7.
OS	Homo sapiens (Human).
OC	Eumetazoa; Metacoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
CC	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Piddington C.S., Sheppard P.O., Bishop P., Lasser G.W.,
RT	"Homo sapiens complement c1q tumor necrosis factor-related protein."
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Testis;  
RA Strausberg R.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
CC  
-1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
CC  
-1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.

-----  
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CC -----  
DR EMBL; AF329839; AAK17963.1; -  
DR EMBL; BC022187; AAK22187.1; -  
DR Genew: HGNC:14342; C10T0NF7.  
DR InterPro; IPR001073; C1q.  
DR InterPro; IPR000087; Collagen.  
DR Pfam; PF00386; C1q; 1.  
DR Pfam; PF01391; Collagen; 2.  
DR PRINTS; PR00007; COMPLEMENTC1Q.  
DR SMART; SM00110; C1Q; 1.  
DR PROSITE; PS01113; C1Q; 1.  
KW Collagen; Signal.

FT	CHAIN	FT	DOMAIN	FT	DOMAIN	FT	DOMAIN
1	16	17	289	38	139	141	276
POTENTIAL.	COMPLEMENT-C10 TUMOR NECROSIS FACTOR			RELATED PROTEIN 7.		COLLAGEN-LIKE.	C10.

50	SEQUENCE	289	AA;	30683	MM;	A61609FF66D26946	CNC64;
	Query Match			31.0%;	Score	410.5;	DB 1; Length 289;
	Best Local Similarity			40.0%;	Pred. NO.	5.4e-22;	
	Matches	98;	Conservative	26;	Mismatches	84;	Indels 37; Gaps 7;

```
QY      24  I P S L - - C P G H P L G T P G H H S Q O G L P R G D R G D R G A P ----- G A P E K G    66
Db      36  I P L P R P P G P G A N S P C P H G R I G L P R G R G R G R G K E G E K T A G L R K G T P L I A E K G    95
QY      67  E G G R P G L P G R G D P G R G E A G A C P T G A G E ----- C - S V P R S F A S K R S   111
Db      96  D O G E T G K A G F I G P E G S K E Y E F I G P P R G D G E O G D G L P C V C R C G S I Y L K A S F S G I T   155
QY      .
Db      112 E S R V P P S D A P L F F D R V L N E O G H Y D A W T K E F T C V P G V Y Y F A V H A T Y R A S L O F D L V K N   171
QY      156 T S Y - - P E E R L P I F N K V L F E N E G E H N P A T K F I C A F P I Y F S Y D I T L A N K L A I G L V H N   213
Db      172 G E S I A F F O F G M W R P A S L S G G A W R L E P E D E Q W V O V G C D Y I G I Y A S I K - T D S T S G F   230
QY      214 G Q R I K T F A N T G N H D V A - - S S Y I Y I L O D E V U L E I F T D O N G L S D P G M A D S L E S G F   271
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RESULT 9	CA1A_MOUSE	STANDARD;	PRT;	680 AA.
ID	CA1A_MOUSE			

AC 005306; (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Collagen alpha 1(x) chain precursor.  
 GN COL10A1.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C;  
 RX MEDLINE=93143676; Pubmed=8424763;  
 RA Elima K., Gerola I., Rosati R., Metsaranta M., Garofalo S., Perala M.  
 RA de Crombrughe B., Vunorio E.  
 RT "The mouse collagen x gene: complete nucleotide sequence, exon  
 structure and expression pattern."  
 TL Biochem. J. 289:247-253(1993).

RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-129/SV; TISSUE=Liver;  
RX MEDLINE=93238750; Pubmed=8477738;  
RA Kong R.Y.C., Kwan K.M., Lau E.T., Thomas J.T., Boot-Handford R.P.,  
RG Grant M.E., Chah K.S.E.;  
RT "Intron-exon structure, alternative use of promoter and expression of  
RT the mouse collagen X gene, Col10a1-1,"  
RT Eur. J. Biochem. 213:99-111(1993).

RN [3]  
 RP SEQUENCE OF 51-680 FROM N.A.  
 RC STRAIN-DBA/2J;  
 RX MEDLINE=92267014; PubMed=1587271;  
 RA Apte S.S., Seldin M.F., Haysashi M., Olsen B.R.;  
 RT "Cloning of the human and mouse type X collagen genes and mapping of  
 RL the mouse type X collagen gene to chromosome 10.";  
 RN Eur. J. Biochem. 206:217-224 (1992).  
 [4]

RP SEQUENCE OF 385-62/ FROM N.A.  
RC STRAIN-C57BL/6;  
RX MEDLINE=92182017; PubMed=1543751;  
RA Elima K., Metsaseranta M., Kallio J., Peräläe M., Eerola I.,  
RA Garmelo S., de Crombrughe B., Vuorio E.;  
RT "Specific hybridization probes for mouse alpha 2(IX) and alpha 1(X)



RT collagen mRNAs.";  
 RL Biochim. Biophys. Acta 1130:78-80(1992).  
 CC -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTROPHIC  
 CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE  
 CC MINERALIZATION ZONES OF HYALINE CARTILAGE.  
 CC -1- SUBUNIT: HOMOTRIMER.  
 CC -1- PFM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING  
 CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.  
 CC -1- SIMILARITY: STRONG TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.  
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; X67348; CAA47763.1; -;  
 DR EMBL; X65121; CAA46237.1; -;  
 DR EMBL; X63013; CAA44741.1; -;  
 DR EMBL; Z21610; CAA79736.1; -;  
 DR PIR; S28807; S28807.  
 DR PIR; S31216; S31216.  
 DR PIR; S22215; S22215.  
 DR MGI; MGI:88445; COL10a1.  
 DR InterPro; IPR001073; C1q.  
 DR InterPro; IPR000087; Collagen.  
 DR Pfam; PF00386; C1q; 1.  
 DR Pfam; PF01391; Collagen; 9.  
 DR PRINTS; PR00007; COMPLEMENTC1Q.  
 DR PRODOM; PD000007; Collagen; 2.  
 DR SMART; SM00110; C1Q; 1.  
 DR PROSITE; PS01113; C1Q; 1.  
 DR KMW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;  
 RW Cartilage; Collagen; Signal.  
 FT SIGNAL 1 18  
 FT CHAIN 1 680  
 FT DOMAIN 19 56  
 FT DOMAIN 57 519  
 FT DOMAIN 520 680  
 FT DOMAIN 545 680  
 FT DOMAIN 248 248  
 FT CONFLICT 286 286  
 FT CONFLICT 306 306  
 FT CONFLICT 417 417  
 FT CONFLICT 451 451  
 FT CONFLICT 500 500  
 FT CONFLICT 567 567  
 FT CONFLICT 569 569  
 FT CONFLICT 571 572  
 FT CONFLICT 635 635  
 FT SEQUENCE 680 AA; 66775 MW; FE984CA99AF70BE2 CRC64;  
 Query Match 30.8%; Score 408; DB 1; Length 680;  
 Best Local Similarity 33.4%; Pred. No. 1.9e-21;  
 Matches 99; Conservative 34; Mismatches 75; Indels 88; Gaps 9;  
 QY 15 GSPPLDNNKIPSLCPGHPGLP-----GRPGHH-----GSQ 44  
 Db 392 GEPGLNGPK-----GNFGLPGQKGDPPGVGTPGLRGVPYAKGVGNGHGEAGPREP 445  
 QY 45 GLPGRDGDGDGAPGARGEGEGRGRLPGR-----GDPRGRCA----- 86  
 Db 446 GIPTRGPTGPGVPGFPGSGKDPNGAPGAPGATGKNGLPPTGPPGPGRGSGEPG 505  
 QY 87 --GPAGTGPAGGECVSP-----PRSAFSAKRSESRVVP 117  
 Db 506 LPGPFGPPGPGQAVMPDGFITKAGORPLSGMPLVSAHNGVTGMFVSFAFTYILSRAY--P 563  
 QY 118 PSDAPLPDRVLVNEQGHYDAVTKGFTCOVGVVYFAVHAATVYRASLOFDLVKNG-ESIA 176

Db 564 AVGAPIPEDEILYNNRQHYDPRSGIFTCKIPCIYFYSHVHKGTHVMWGLYKNGPTMY 623  
 QY 177 SFQFQFGMPRPAISGAMWLEPEDQWQVQGVYIGIYASIKTSTSGFLV 232  
 Db 624 TYDESKGYLDQA--SGSAIMELTENDQWLOLPAESNGIYSSBYVHSSFGFLV 677  
 RESULT 10  
 ID CQT2\_HUMAN STANDARD; PRT; 285 AA.  
 AC Q9BXJ5;  
 DT 15-JUN-2002 (Rel. 41, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Complement-c1q tumor necrosis factor-related protein 2 precursor.  
 GN C1QTNF2 OR C1RP2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Piddington C.S., Bishop P.;  
 RT "Homo sapiens complement-c1q tumor necrosis factor-related protein.";  
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Muscle;  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; AF329836; AAK17960.1; -;  
 DR EMBL; BC011699; AAK11699.1; -;  
 DR Genew; HGNC:14325; C1QTNF2.  
 DR InterPro; IPR001073; C1q.  
 DR InterPro; IPR000087; Collagen.  
 DR Pfam; PF00386; C1q; 1.  
 DR Pfam; PF01391; Collagen; 2.  
 DR PRINTS; PR00007; COMPLEMENTC1Q.  
 DR SMART; SM00110; C1Q; 1.  
 DR PROSITE; PS01113; C1Q; 1.  
 DR KMW Collagen; Signal.  
 FT SIGNAL 1 15  
 FT CHAIN 1 285  
 FT DOMAIN 16 141  
 FT DOMAIN 143 285  
 FT SEQUENCE 285 AA; 29952 MW; 7E31FE9868D4EDFA CRC64;  
 Query Match 30.4%; Score 403; DB 1; Length 285;  
 Best Local Similarity 36.3%; Pred. No. 1.8e-21;  
 Matches 98; Conservative 29; Mismatches 91; Indels 52; Gaps 8;  
 QY 9 LLGLAA-----GSPPLDNNKIPSLC-----PGHGLPSTRGHHSGQLPGRDGDG 54  
 Db 18 LLGAFARRDFRKSQPOL-----VCSLPDGPQGPAGAPGSPGSMRMGFPKDCGDG 70  
 QY 55 RDGAPGARGEGEGGRP-----GLPGRDGDGGRGEGVAPG---TGPAGECVSPPSASNA 108  
 Db 71 HDGDRGDSGEGSPRPGTGNRKGPGKAGAIGRAGPGRGVNTPGKHGTPGKKGPKG 130  
 QY 109 KRSESRVPPPSDA-----PLFDRVLVNEQGHYDAVTKGFTCQ 146

DB 131 KKEPGLPGSCSGSGHTKSAFSAVATKSPRERLPIKFDILNNEGHNASSGKFCVCG 190  
 QY 147 VPGVYFAVATVYRASIQLDLYKNGESIASFQFQGWMPASTSGGAWRLPEQOVW 206  
 DB 191 VPGIYTYTITLANKLALGLVINGQRIPTFANTGNHDA--SSSTIALKGGDEW 248  
 QY 207 VQVGVGDYIGI-VASIKTDSFSGFLVYSD 235  
 DB 249 LQIFYSQNGLEFYDPTWDSLFTGFLIYAD 278  
 RESULT 11  
 C1QC\_HUMAN STANDARD; PRT: 245 AA.  
 ID P02747; Q96DL2; Q96H05;  
 AC 21-JUL-1986 (Rel. 01, Created)  
 DT 15-JUN-2002 (Rel. 41, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Complement C1q subcomponent, C chain precursor.  
 GN C1QG OR C1QC.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Monocytes;  
 RX MEDLINE=91174759; PubMed=1706597;  
 RA Sellar G.C., Blake D.J., Reid K.B.M.;  
 RT "Characterization and organization of the genes encoding the A-, B-  
 RT derived amino acid sequence of human C1q. The complete  
 RL Biochem. J. 274:481-490(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cerebellum;  
 RA Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,  
 RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,  
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,  
 RA Kawakami B., Nagai K., Isogai T., Sugano S.;  
 RT "NDO human cDNA sequencing project."  
 RT submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE OF 29-122.  
 RX MEDLINE=80020137; PubMed=486087;  
 RA Reid K.B.M.;  
 RT "Complete amino acid sequences of the three collagen-like regions  
 RT present in subcomponent C1q of the first component of human  
 RT complement.";  
 RL Biochem. J. 179:367-371(1979).  
 RN [5]  
 RP REVIEW OF C1Q DEFICIENCY.  
 RX MEDLINE=98450587; PubMed=9777412;  
 RA Petry F.;  
 RT "Molecular basis of hereditary C1q deficiency.";  
 RL Immunobiology 199:286-294(1998).  
 CC -1- FUNCTION: C1Q ASSOCIATES WITH THE PROENZYMES C1R AND C1S TO YIELD  
 CC C1, THE FIRST COMPONENT OF THE SERUM COMPLEMENT SYSTEM. THE  
 CC COLLAGEN-LIKE REGIONS OF C1Q INTERACT WITH THE CA(2+)-DEPENDENT  
 CC C1R(2)C1S(2) PROENZYME COMPLEX, AND EFFICIENT ACTIVATION OF C1  
 CC TAKES PLACE ON INTERACTION OF THE GLOBULAR HEADS OF C1Q WITH THE  
 CC FC REGIONS OF IGG OR IGM ANTIBODY PRESENT IN IMMUNE COMPLEXES.  
 CC -1- SUBUNIT: C1 IS A CALCIUM-DEPENDENT TRIMOLECULAR COMPLEX OF C1Q, R  
 CC AND S IN THE MOLAR RATIO OF 1:2:2. C1Q SUBCOMPONENT IS COMPOSED  
 CC OF NINE SUBUNITS, SIX OF WHICH ARE DISULFIDE-LINKED DIMERS OF THE  
 CC A AND B CHAINS, AND THREE OF WHICH ARE DISULFIDE-LINKED DIMERS OF  
 CC THE C CHAIN.  
 CC -1- PTM: O-LINKED GLYCANS CONSIST OF GLC-GAL DISACCHARIDES.

CC -1- DISEASE: DEFECTS IN C1QG ARE A CAUSE OF C1Q DEFICIENCY. IT IS A  
 CC RARE GENETIC DISORDER WHICH IS ASSOCIATED WITH RECURRENT  
 CC INFECTIONS AND A HIGH PREVALENCE OF LUPUS ERYTHEMATOSUS-LIKE  
 CC SYMPTOMS. IT IS CHARACTERIZED BY A LOSS OF ACTIVATION OF THE  
 CC COMPLEMENT CLASSICAL PATHWAY.  
 CC -1- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.  
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 CC  
 DR EMBL: AK057792; BAB1575.1; -  
 DR EMBL: BC009016; AAR09016.1; -  
 DR PIR: A03207; C1HQC.  
 DR PIR: S14351; S14351.  
 DR GeneW: HGNC:1245; C1QG.  
 DR MIM: 120575; -  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF00386; C1q; 1.  
 DR Pfam: PF01391; Collagen; 1.  
 DR PRINTS: PR00007; COMPLEMENTC1Q.  
 DR SMART: SM0110; C1Q; 1.  
 DR PROSITE: PS01113; C1Q; 1.  
 KW Complement pathway; Plasma; Hydroxylation; Glycoprotein; Collagen;  
 KW Repeat; Signal; Disease mutation.  
 FT SIGNAL 1 28  
 FT CHAIN 29 245  
 FT DOMAIN 31 112  
 FT DOMAIN 113 245  
 FT DISULFID 32 32  
 FT MOD\_RES 36 36  
 FT MOD\_RES 39 39  
 FT MOD\_RES 42 42  
 FT MOD\_RES 45 45  
 FT MOD\_RES 54 54  
 FT MOD\_RES 57 57  
 FT MOD\_RES 63 63  
 FT MOD\_RES 66 66  
 FT MOD\_RES 71 71  
 FT MOD\_RES 75 75  
 FT CARBOHYD 75 75  
 FT MOD\_RES 81 81  
 FT MOD\_RES 84 84  
 FT CARBOHYD 84 84  
 FT MOD\_RES 93 93  
 FT MOD\_RES 96 96  
 FT MOD\_RES 99 99  
 FT MOD\_RES 105 105  
 FT VARIANT 43 43  
 FT CONFLICT 14 14  
 FT CONFLICT 23 23  
 FT CONFLICT 57 57  
 FT CONFLICT 66 66  
 FT CONFLICT 72 72  
 FT CONFLICT 84 84  
 FT CONFLICT 87 87  
 FT CONFLICT 90 90  
 FT CONFLICT 215 215  
 SO SEQUENCE 245 AA; 25774 MM; FA17117B7ABFC12 CRC64;  
 Query Match 30.0%; Score 397; DB 1; Length 245;  
 Best Local Similarity 39.8%; Pred. No. 4e-21;  
 Matches 100; Conservative 33; Mismatches 84; Indels 34; Gaps 10;  
 QY 1 MRPLVLLGLAGSPPLDKNIPSLC---PQHPGLGTPRHGSGGLPGRGGRGGRG 57  
 ::||:||||| : :| ||||| || | |||||

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Db 13 LKLLLLLLLPLR-----GQANTGCGIPIGMBGLPGAPGKDYGDLPGPKGPIGA 64
QY 58 APGARKEGEGRRPGLPGRDPRGRGARGAPRPGPGECEVPP-----RSASFA 108
Db 65 IPGIRPGQKGEPLPGHPRGNMGPMGPGVPGMIGPEPEEGRYKOKFOSVTV 124
QY 109 KRSESRVPPSPDAPLPFVIVNEQGHDAVYGFCTCOVPGVYFAVHATVYRASLOPDL 168
Db 125 TR-QTHOPPARPSLRNFANVLINPGODYDTSTGKFTCAVPLGYTVYHNS-HTANLCVIL 182
QY 169 VKNGESIASFPOFGGMPKPSL-SGAMVRLPEPDQVWVOYGVGDY--IGIVASIKTD 224
Db 183 YRSQGVYVY---FCGHTSKTNQVNSGVILRLQVGEVW--LAVNDYDMVGIGS---D 234
QY 225 STFGELVYSD 235
Db 235 SVFSGELLPD 245

RESULT 12
CA18_RABIT STANDARD: PRT: 744 AA.
ID CA18_RABIT STANDARD: PRT: 744 AA.
AC P14282:
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Collagen alpha 1(VIII) chain precursor (Endothelial collagen).
GN COL8A1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89380199; PubMed=2476437;
RA Yamaguchi N., Benya P.D., Van der Rest M., Ninomiya Y.;
RT "The cloning and sequencing of alpha 1(VIII) collagen cDNAs
RT demonstrate that type VIII collagen is a short chain collagen and
RT contains triple-helical and carboxyl-terminal non-triple-helical
RT domains similar to those of type X collagen."
RL J. Biol. Chem. 264:16022-16029(1989).
CC -1- FUNCTION: MAJOR COMPONENT OF THE DESCENDING MEMBRANE (BASEMENT
CC MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
CC -1- SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION
CC WITH ALPHA 2(VIII) TYPE COLLAGENS.
CC -1- UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- MISCELLANEOUS: FOUR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PRESENT
CC AT THE C-TERMINUS OF THE TRIPLE-HELICAL REGION. THESE MAY PROVIDE
CC HIGH THERMAL STABILITY OF THIS REGION OF THIS REGION.
CC -1- SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -----
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CC -----
DR EMBL: J05042; AAA31204.1;
DR PIR: A34246; A34246.
DR InterPro: IPR001073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; C1q; 1.
DR Pfam: PF01391; Collagen; 8.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q; 1.
DR PROSITE: PS01113; C1Q; 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Cell adhesion; Collagen; Signal.
FT SIGNAL 1 20

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FT CHAIN 21 744 COLLAGEN ALPHA 1(VIII) CHAIN.
FT DOMAIN 29 117 NONHELICAL REGION (NC).
FT DOMAIN 118 571 TRIPLE-HELICAL REGION.
FT DOMAIN 572 744 NONHELICAL REGION (NC1).
FT DOMAIN 609 744 C1Q.
SQ SEQUENCE 744 AA; 73358 MW; 2A8CEFE8274E99 CRC64;

Query Match 28.2%; Score 374; DB 1; Length 744;
Best Local Similarity 34.4%; Pred. No. 4.7e-19;
Matches 93; Conservative 36; Mismatches 79; Indels 62; Gaps 8;

QY 24 IPSLC--GHPPLPTPGHHSQGLPGRDGRGRCAGAPKEGEGRRPGLP-----74
Db 475 VPGLGPRGPRGPDPDGLQSGPRGIPGIGTSGPRIGRPGIRPKRPEGLPGRGPGYVK 534
QY 75 -----GPRGDP--GPRGE--AGAPRPGAGECVPPRS-----104
Db 535 PGVAGLHGPGRKPGALPGQGPGLPGPPGPPGPPAPVMPPTPAPGELYLPDMGLGIDG 594
QY 105 -----AFSAKRSESRVP-----PPSDALPLPDRVLVNEQGHDAVYGFKT 144
Db 595 VKTPHAYAAKKGKNGGPAVEMPATFALPTAPPVGAIRKDRLLYNGRONYNPOTGIFT 654
QY 145 COVPGVYFAVHATVYRASLOPDLVKNGESIA-SFOFGGMPKPSLSCGAMVRLPEPD 203
Db 655 CEVPGVYFAVHATVYRASLOPDLVKNGESIA-SFOFGGMPKPSLSCGAMVRLPEPD 203
QY 204 QVWVGVGVGYIGIVASIKTDSTFGSGFLVY 233
Db 713 RVFLQMPSEQAAGLVAGQYVHSSFGYLILY 742

RESULT 13
COLL_LEPMA STANDARD: PRT: 419 AA.
ID COLL_LEPMA STANDARD: PRT: 419 AA.
AC P98085; Q91080;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE Inner ear-specific collagen precursor (Saccular collagen).
OS Lepomis macrochirus (Bluegill).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Centrarchidae; Lepomis.
OX NCBI_TaxID=13106;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95167486; PubMed=7863331;
RA Davis J.G., Oberholzer J.C., Burns F.R., Greene M.I.;
RT "Molecular cloning and characterization of an inner ear-specific
RT structural protein."
RL Science 267:1031-1034(1995).
RN [2]
RP CONCEPTUAL TRANSLATION.
RA Gibson T.;
RT Submitted (MAR-1995) to the SWISS-PROT data bank.
CC -1- FUNCTION: FORMS A MICROSTRUCTURAL MATRIX WITHIN THE OTOLITHIC
CC MEMBRANE (PROBABLY).
CC -1- TISSUE SPECIFICITY: SPECIALIZED SECRETORY SUPPORTING CELLS AT THE
CC OUTER PERIMETER OF THE SACCULAR EPITHELIUM.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT HAD TO BE
CC INTRODUCED FOR POSITIONS 391-419 SO AS TO MAXIMIZE THE SIMILARITY
CC WITH OTHER SHORT-CHAIN COLLAGENS.
CC -----
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CC EMBL: U17431; AAA69978.1; ALT_FRAME.
DR InterPro: IPR001073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; C1q; 1.
DR Pfam: PF01391; Collagen; 3.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q; 1.
DR PROSITE: PS01113; C1Q; 1.
DR Extracellular matrix; Repeat; Collagen; Signal.
KW SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT DOMAIN 20 419 INNER EAR-SPECIFIC COLLAGEN.
FT DOMAIN 58 57 NONHELICAL REGION (NC2).
FT DOMAIN 275 274 TRIPLE-HELICAL REGION (COL1).
FT DOMAIN 272 419 NONHELICAL REGION (NC1).
FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 419 AA; 43634 MW; 570CDB9675FC0F39 CRC64;

Query Match 28.2%; Score 373; DB 1; Length 419;
Best Local Similarity 37.5%; Pred. No. 3.1e-19;
Matches 96; Conservative 23; Mismatches 99; Indels 38; Gaps 6;

QY 15 GSPFLDNNK--IPSLCFGHPGLPTPGHSGQLPGR--DGRDGDGAPGAPGEGSGR 70
DB 157 GEPGLNTKSGISIGREGPMGLAGTKGLKGQGLKGLQEGKEKRGPPGLRGEMGLNGT 216
QY 71 PGLGPRGDDPGR-----RGEAGPAGTGPAGGECV 100
DB 217 DGVNGEGERPGLGKGDGTGARGPPRGPGGKMGALGKGLKGVKRGKRGKGGESVE 276
QY 101 PPRSAFSARSRSESVPPPSDAPLPDRVLVNEGSHYDAVTGKTCQVPGVYFAVHAITY 160
DB 277 QIRSAFSGVLSPRSFPPSLPVPKFDYFVNGEHPDPLTKFNVYTPGVYLLFYHLTVR 336
QY 161 RASLPFLVKNK--ESINSPFPGGWRKPRASLSCGAWRLPEPDQVWVQVGVYIGIYA 219
DB 337 NRPRVALVYNGVKKLRDLSYGODIDQ--SNLALHLTDGQVWLET--LRDMNGKYS 393
QY 220 SIKTSTFGFLVSD 235
DB 394 SSEDDSTFGFLLPD 409

RESULT 14
CA18_HUMAN STANDARD: PRT; 744 AA.
AC P27658; O96D07;
DT 01-AUG-1992 (Rel. 23, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Collagen alpha 1(VIII) chain precursor (Endothelial collagen).
GN COL8A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91231001; PubMed=2029894.
RA Muraguchi Y., Mattei M.-G., Yamaguchi N., Olsen B.R., Ntomiya Y.;
RA "The complete primary structure of the human alpha 1 (VIII) chain and
RA assignment of its gene (COL8A1) to chromosome 3.";
RA Eur. J. Biochem. 197;615-622(1991).
RL [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
CC -1- FUNCTION: MAJOR COMPONENT OF THE DESCENDING MEMBRANE (BASEMENT
CC MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
CC -1- SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION

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CC WITH ALPHA 2(VIII) TYPE COLLAGENS.
CC -1- P-TM: PROLINES AT THE THIRD POSITION OF THE TRIPLE-REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- MISCELLANEOUS: FOUR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PRESENT
CC AT THE C-TERMINUS OF THE TRIPLE-HELICAL REGION. THESE MAY PROVIDE
CC THE HIGH THERMAL STABILITY OF THIS REGION.
CC -1- SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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CC
DR EMBL: X57527; CA40748.1; -.
DR EMBL: BC013581; AAH13581.1; -.
DR PIR: S15435; S15435.
DR Genew: HGNC:2215; COL8A1.
DR MIM: 120251; -.
DR InterPro: IPR001073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; C1q; 1.
DR Pfam: PF01391; Collagen; 8.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR PRODOM: PD000007; Collagen; 1.
DR SMART: SM00110; C1Q; 1.
DR PROSITE: PS01113; C1Q; 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Cell adhesion; Collagen; Signal.
FT CHAIN 1 28
FT SIGNAL 29 744
FT DOMAIN 29 117 COLLAGEN ALPHA 1(VIII) CHAIN.
FT DOMAIN 118 571 NONHELICAL REGION (NC2).
FT DOMAIN 572 744 TRIPLE-HELICAL REGION (COL1).
FT DOMAIN 609 744 NONHELICAL REGION (NC1).
FT DOMAIN 262 262 C1Q.
FT CONFLICT 297 297 P -> L (IN REF. 1).
FT CONFLICT 344 344 P -> R (IN REF. 1).
FT CONFLICT 344 344 P -> A (IN REF. 1).
FT CONFLICT 382 382 A -> S (IN REF. 1).
FT CONFLICT 388 388 P -> S (IN REF. 1).
FT CONFLICT 454 454 L -> F (IN REF. 1).
FT CONFLICT 464 464 A -> H (IN REF. 1).
FT CONFLICT 601 601 Y -> T (IN REF. 1).
FT CONFLICT 631 631 A -> G (IN REF. 1).
SQ SEQUENCE 744 AA; 73364 MW; 28C1B0955DE2C9A3 CRC64;

Query Match 27.8%; Score 368; DB 1; Length 744;
Best Local Similarity 33.3%; Pred. No. 1.2e-18;
Matches 90; Conservative 34; Mismatches 84; Indels 62; Gaps 6;

QY 24 IPSLC--PGRHGLPTGCHHSGGLPRGRDGDGDAAPGAPGEGSGRGLP----- 74
DB 475 VPGLLGKRGKGGIPGDGGLGPPGIPGIGSGGIPGPGILPGKGGELGPPGPGIGK 534
QY 75 -----GPRGDPGRGEGAPGAPGTPG-----AGECS 99
DB 535 PGVAGLGRPGKRPALGPGGGLPGRPGPGPRPAVMPPTPRPGEVLPKMGGLDIDG 594
QY 100 VPPRSASFARSRSESRV-----PPSDAPLPDRVLVNEGSHYDAVTGKFT 144
DB 595 VKPRHAYGAKKKGKNGPVEAPFAETALTAPFPVGAIVKFNKLLYNGRONYNPOTGIFT 654
QY 145 QVPGVYFAVHAITYVYASLQFDLYKNGESIA--SFQFPGGWRKPRASLSCGAWRLPEPD 203
DB 655 CEVPGVYFAVHACKKGGNVALEKKNPEVMTYDEYKKGFLDQA--SSAVALLRPGD 712
QY 204 QVWVGVGVYIGIYASIKTSTFGFLVY 233
DB 713 RVFLQMPSEDAAGLITAGQIYHSSFGYLL 742

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RESULT 15
CAL8_MOUSE
ID CAL8_MOUSE STANDARD: PRT: 743 AA.
AC 000780; Q9D2V4;
DT 01-NOV-1995 (Rel. 32, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Collagen alpha 1(VIII) chain precursor.
GN COL8A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c;
RX MEDLINE-92362626; PubMed-1499564;
RA Murogaki Y., Shiota C., Inoue M., Ooshima A., Olsen B.R.,
RA Nimomiya Y.;
RT "Alpha 1(VIII)-collagen gene transcripts encode a short-chain
RT collagen polypeptide and are expressed by various epithelial,
RT endothelial and mesenchymal cells in newborn mouse tissues.";
RL Eur. J. Biochem. 207:895-902(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; Tissue=Kidney;
RX MEDLINE-21085660; PubMed-11217851;
RA Kawai J., Shimagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Araiawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischer W., Gaasterland T., Gissi C., King B., Kochia H.,
RA Kuehl P., Lewis S., Matsuo Y., Nkaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga M., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Buit C., Fletcher C., Fujita S., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- FUNCTION: MAJOR COMPONENT OF THE DESCENDING MEMBRANE (BASEMENT
CC MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
CC -1- SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION
CC WITH ALPHA 2(VIII) TYPE COLLAGENS.
CC -1- TISSUE SPECIFICITY: HIGH LEVELS IN CALVARIUM, EYE & SKIN OF
CC NEWBORN MICE; ALSO IN VARIOUS EPITHELIAL, ENDOTHELIAL AND
CC MESENCHYMAL CELLS.
CC -1- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1- SIMILARITY: STRONG TO ALPHA 2 TYPES VIII AND X COLLAGENS.
CC -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
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CC -----
DR EMBL: X66976; CAA47387.1; -.
DR EMBL: X66977; CAA47387.1; JOINED.
DR EMBL: AK018742; BAB31383.1; -.
DR PIR: S23779; S23779.
DR MGI: MGI:88463; Col8a1.

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DR InterPro: IPR001073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; C1q; 1.
DR Pfam: PF01391; Collagen; 7.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q; 1.
DR PROSITE: PS01113; C1Q; 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Cell adhesion; Collagen; Signal.
FT SIGNAL 1
FT CHAIN 28
FT DOMAIN 29 743 COLLAGEN ALPHA 1(VIII) CHAIN.
FT DOMAIN 118 571 NONHELICAL REGION (NC2).
FT DOMAIN 572 743 TRIPLE-HELICAL REGION (COL1).
FT DOMAIN 608 743 NONHELICAL REGION (NC1).
FT DOMAIN 6 6 C1Q.
FT CONFLICT 6 6 G -> R (IN REF. 2).
FT CONFLICT 85 85 H -> Y (IN REF. 1).
FT CONFLICT 109 109 K -> KG (IN REF. 1).
FT CONFLICT 109 109 P -> L (IN REF. 2).
FT CONFLICT 248 248 P -> A (IN REF. 2).
FT CONFLICT 313 313 IP -> SR (IN REF. 1).
FT CONFLICT 323 324 D -> H (IN REF. 1).
FT CONFLICT 361 361 T -> P (IN REF. 2).
FT CONFLICT 596 596 T -> P (IN REF. 2).
FT CONFLICT 717 719 MPS -> NPF (IN REF. 1).
SQ SEQUENCE 743 AA; 73454 MW; F584D85BD53897F4 CRC64;

Query Match 27.7%; Score 366.5; DB 1; Length 743;
Best Local Similarity 32.8%; Pred. No. 1.5e-18;
Matches 90; Conservative 36; Mismatches 77; Indels 71; Gaps 7;

OY 29 PGHPPLPGPHHSGQGLPGRDGDRGDPAPGAPGEGKGRGRLPGRGDP----- 80
|||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 470 PGLPVPGLGKGGKGGPGIGDGLGPGPIGPIVGPSPGIPGIPGKGGGLGPGPGF 529
81 -----GPKGE--AGPAGTGPAGECVPPR----- 103
OY 530 PGVGRPVAGLHGPGRKPGALPGQGLPGPPGPPGPPVAPMPTSPGEGYLPDMGL 589
104 -----SAFAKR-----SESRRV-PPSDALPPDRVLVNGGHYDAVT 140
DB 590 GIDGVKTPHVAAGKKGKGGPAYEMPATFALTPTPPVGAIVKPKDKLLYNGRNVNPT 649
OY 141 GKFTGVPGVYFAFVAHATVYRASLQFDLYKNGESIA-SFPQFGMPKPRASLGGAMVRL 199
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 650 GIFTVEGVYTFALHVNCKGKNVWALFKNNRPMYTYDEYKKGFLDQA--SGSAVLLL 707
OY 200 EPEDGVWVQVGVGDYIGIVASIKTSTFSGFLVY 233
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 708 RPDGVFLVMPSEQAAGLYAGGYVHSSFSFGYLLY 741

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Job time : 23 secs

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OM protein - protein search, using sw model

Run on: June 13, 2003, 15:50:06 ; Search time 32 Seconds

(without alignments)  
1564.670 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325

Sequence: 1 MRPLVLLILGLAAGSPPLD.....DSTFGFLVYSDMHSPPYFA 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10%

Listing first 45 summaries

Database :

1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP virus:\*  
16: SP bacteriophage:\*  
17: SP archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1254	94.6	243	11 Q8R002	Q8R002 mus musculu
2	425.5	32.1	240	6 Q95M04	Q95M04 bos taurinu
3	422	31.8	243	6 Q95J07	Q95J07 macaca mula
4	415.5	31.4	675	6 Q9N178	Q9N178 sus scrofa
5	402	30.3	295	11 Q9ZK4	Q9ZK4 rattus norv
6	395	29.8	294	11 Q9D8U4	Q9D8U4 mus musculu
7	373.5	28.2	194	6 Q95J95	Q95J95 canis famli
8	370.5	28.0	744	11 Q9D2V4	Q9D2V4 mus musculu
9	370.5	28.0	744	11 Q921S8	Q921S8 mus musculu
10	368	27.8	744	4 Q96D07	Q96D07 homo sapien
11	363.5	27.4	705	4 Q8TEJ5	Q8TEJ5 homo sapien
12	314	23.7	245	11 Q9DCM6	Q9DCM6 mus musculu
13	270.5	20.4	196	11 Q9ES30	Q9ES30 mus musculu
14	266.5	20.1	246	11 Q920N0	Q920N0 tamias sibi
15	252.5	19.1	246	13 Q91907	Q91907 carassius a
16	247.5	18.7	256	13 Q91909	Q91909 cyprinus ca

17	241.5	18.2	347	4 Q961H6	Q961H6 homo sapien
18	238.5	18.0	583	4 Q96G58	Q96G58 homo sapien
19	238.5	18.0	992	4 Q96G76	Q96G76 homo sapien
20	238.5	18.0	1016	4 Q9Y6C2	Q9Y6C2 homo sapien
21	237	17.9	890	5 Q77087	Q77087 alvinella p
22	235	17.7	1017	11 Q99K41	Q99K41 mus musculu
23	234.5	17.7	173	6 Q62789	Q62789 sus scrofa
24	225	17.0	325	5 Q17036	Q17036 caenorhabd
25	223	16.8	281	11 Q9QXP7	Q9QXP7 mus musculu
26	222.5	16.8	322	5 Q01945	Q01945 meloidogyne
27	222	16.8	251	13 Q91908	Q91908 brachydanio
28	222	16.8	1378	5 Q97405	Q97405 halictus di
29	221.5	16.7	120	6 Q77782	Q77782 oryctolagus
30	221.5	16.7	248	6 Q9T706	Q9T706 ovis aries
31	220	16.6	341	5 Q20142	Q20142 caenorhabd
32	219.5	16.6	205	11 Q9D0M2	Q9D0M2 mus musculu
33	219.5	16.6	326	11 Q8R066	Q8R066 mus musculu
34	219.5	16.6	381	5 Q94399	Q94399 caenorhabd
35	219.5	16.6	589	11 Q99LJ6	Q99LJ6 mus musculu
36	219.5	16.6	1453	11 Q63079	Q63079 rattus norv
37	218	16.5	182	11 Q8RI2	Q8RI2 mus musculu
38	217	16.4	319	5 Q17038	Q17038 caenorhabd
39	217	16.4	1160	4 Q14046	Q14046 homo sapien
40	217	16.4	1344	13 Q93419	Q93419 gallus gall
41	217	16.4	1418	6 Q28396	Q28396 equus caball
42	217	16.4	1442	11 Q62031	Q62031 mus musculu
43	217	16.4	1442	11 Q62033	Q62033 mus musculu
44	217	16.4	1450	13 Q9YIB4	Q9YIB4 cynops pyr
45	217	16.4	1459	11 Q62032	Q62032 mus musculu

## ALIGNMENTS

RESULT 1	PRELIMINARY:	PRT:	243 AA.
Q8R002			
AC Q8R002:	01-JUN-2002 (TREMBLrel. 21, Created)		
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)			
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
DS Similar to DKFZP586B0621 protein (Hypothetical 25.4 kDa protein).			
OS Mus musculus (Mouse).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX NCBI_TaxID=10090;			
RM [1]			
RP SEQUENCE FROM N.A.			
RA Strausberg R.;			
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			
DR EMBL; BC023068; AAH23068.1; -			
DR EMBL; BC025174; AAH25174.1; -			
KW Hypothetical protein.			
SQ SEQUENCE 243 AA; 25420 MW; 498129CD051DB97B CRC64;			
Query Match	94.6%; Score 1254; DB 11; Length 243;		
Best Local Similarity	93.4%; Pred. No. 5.1e-100;		
Matches	227; Conservative 7; Mismatches 9; Indels 0; Gaps 0;		
QY	1 MRPLVLLILGLAAGSPPLDNRKIPSLCPGHPGLPCTPGHNGSGGLPGRDGRDGAAG 60		
DB	1 MRPLVLLILGLAAGSPPLDNRKIPSLCPGHPGLPCTPGHNGSGGLPGRDGRDGAAG 60		
QY	1 APGEKGEGRGRLPGRDPPRGAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAG 120		
DB	1 APGEKGEGRGRLPGRDPPRGAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAGPAG 120		
QY	121 APLPRDRLVNEGGHYDAVNTGFTKQGVGYGYFYFNAVHYRASLOFLVKNCESTASFP 180		
DB	121 APLPRDRLVNEGGHYDAVNTGFTKQGVGYGYFYFNAVHYRASLOFLVKNCESTASFP 180		





DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF00386; C1q; 1.  
 DR Pfam: PF01391; Collagen; 8.  
 DR PRINTS: PR00007; COMPLEMENTC1Q.  
 DR ProDom: PD000007; Collagen; 2.  
 DR SMART: SM00110; C1Q; 1.  
 DR PROSITE: PS01113; C1Q; 1.  
 DR Collagen.  
 KW SEQUENCE 675 AA; 65447 MW; 26397B10310383F9 CRC64;

Query Match 31.4%; Score 415.5; DB 6; Length 675;  
 Best Local Similarity 36.1%; Pred. No. 1.7e-27;  
 Matches 99; Conservative 34; Mismatches 82; Indels 59; Gaps 7;

QY 15 GSPFLDNNKIRSLCPGHGLPCTPEGHSGSLPGHDGDDGAPAGEKEGGEGPGLP 74  
 DB 402 GNPGLPGPKGDPGIGGPPGLPGVAGAKAGVPGHNGEAGPAGIPGTGPIGP 461  
 QY 75 -----GPRGDPGPRGA-----GPRGPTGPRGCS 99  
 DB 462 GPPSGKDPGNPGPPGPGAGIATKGLNGPTGPPGPGKGHAGEPGLPDPGPPGPGQ-A 520  
 QY 100 VPP-----RSAPSAKRSRSP-----PPSDAPLPFDRLVNEQGHYDAV 139  
 DB 521 VPPEGVKEGGRAFVSANQVYTGMPVSAFTVILSKAYPAIGAPIFPDKILVNGQHDYDK 580  
 QY 140 TGKTCQVPGYVYRAVATVYRASLQPLVNGESIA-SFQFEGGMPKPSLGGANVR 198  
 DB 581 TGIFTCRIPIGYFYFSYHIVHGTAWVGLYKNGTPVMYTYDEVYGVYLDQA--SSAILD 638  
 QY 199 LEPEQVWVGVGVDYIGIVASIKTDSFSGFLV 232  
 DB 639 LTNDQVWDLQLPNAGSNGLSISSEYVHSSFSGLV 672

## RESULT 5

Q9Z1K4 PRELIMINARY; PRT; 295 AA.  
 AC O9Z1K4;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Collagen alpha 1 type X (Fragment).  
 GN COL10A1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY;  
 RX MEDLINE=20310874; PubMed=10853827;  
 RA Marks S.A., Lundmark C., Christersson C., Wurtz T., Odgren P.R.,  
 RA Seifert M.F., Mackay C.A., Mason-Savay A., Popoff S.E.;  
 RT "Endochondral bone formation in toothless (osteopectrotic) rats:  
 RT failures of chondrocyte patterning and type X collagen expression.";  
 RL Int. J. Dev. Biol. 44:309-316(2000).  
 DR EMBL: AJ131848; CAAL0518.1;  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF00386; C1q; 1.  
 DR PRINTS: PR00007; COMPLEMENTC1Q.  
 DR SMART: SM00110; C1Q; 1.  
 DR PROSITE: PS01113; C1Q; 1.  
 DR NON\_TER 1  
 FT SEQUENCE 295 AA; 30012 MW; FF43B1548028813E CRC64;

Query Match 30.3%; Score 402; DB 11; Length 295;  
 Best Local Similarity 36.7%; Pred. No. 9.3e-27;  
 Matches 94; Conservative 31; Mismatches 79; Indels 52; Gaps 7;

QY 25 PSLCPGH-----PGLPGPPGHSGSLPGHRGRDRGDCAPGAPGE-----KGE 67  
 DB 41 PKGVPHNGEAGPRKEPPIGTGRTGPTGPIGPFPGSGKDGKPGAPAGIATKGLNCP 100  
 QY 68 GGRPLPGPR---GDPGPRGEGAPGPTGPAEGCSVP----- 101  
 DB 101 AGPGRPGPRGHTGPGPLPGPPGPGPPSQAVIYDPGFTKSGQRPLSGMPLVSANQ 160  
 QY 102 ----PRSAFSKRSRSPPSDAPLPDDRVLVNEQGHYDAVTKFTCOVGYVFAVHA 157  
 DB 161 VTGMPVSAFTVILSKAY--PAVGAPIPDELLYNNQOQHYDPRSGIFTCKIGIYFSYHI 218  
 QY 158 TVYRASLQFDLVKNG-ESIASFEPFGGMPAPASLGGAMVRLPEPDQVWVGVDYIG 216  
 DB 219 HVKGTWVWGLKKNTPMTYTYDETSKGLDQA--SSAILEDNDQVWDLQLPNAGSNG 276  
 QY 217 IYASIKTDSFSGFLV 232  
 DB 277 LYSSEYVHSSFSGLV 292

## RESULT 6

Q9DBU4 PRELIMINARY; PRT; 294 AA.  
 AC Q9DBU4;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE 1810033K05R1K protein.  
 GN 1810033K05R1K.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Atakawa T., Hara A., Fukunishi Y., Kono H., Aachii J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Buit C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyokawa K., Wang K.H., Wenz C., Whitaker C., Wilmink L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK007683; BAB25187.1;  
 DR MGP: MGI:1916433; 1810033K05R1K.  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF00386; C1q; 1.  
 DR PRINTS: PR00007; COMPLEMENTC1Q.  
 DR SMART: SM00110; C1Q; 1.  
 DR PROSITE: PS01113; C1Q; 1.  
 DR SEQUENCE 294 AA; 30865 MW; 6D3905AE7C19B6FA CRC64;

Query Match 29.8%; Score 395; DB 11; Length 294;  
 Best Local Similarity 35.9%; Pred. No. 3.7e-26;  
 Matches 94; Conservative 31; Mismatches 93; Indels 44; Gaps 6;

```

QY 3 PLVLLVLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHSOGLPGRDGRDGRGAPGAP 62
DB 41 POLVCSLPG-----PQGPBPAPGAPSSGVGRMGKPGKDGQGGQDGRDSD 87
QY 63 GEKEGGRR---GLPGRGDPGRGEGAPAP---TGRAGCSVPBPRAFAKSESSEVVP 116
DB 88 GEEBPGRGTGRNGKQGPGRKAGAIGRAPRGPBGVSGTPGHGTPGKGPGRKGEPLP 147
QY 117 PPSDA-----PLPDRVLVNEOGHYDAVTKFTCOVPGVYFA 154
DB 148 GPCGSGSSRAKSAFVAVTKSPRERLPKIKDKILMNGGHYKNSGKFTVCSVGIYFT 207
QY 155 VHAIVYRASLOFDLVKNGESIASFPQFGPWPKPASISGAMVRLPEPDQVVOVGYDY 214
DB 208 YDITLANKHLAIGLVHNGQYRIRTFEDANTGNHDVA--SGSTILAKEGDEVMQIDFYSEQ 265
QY 215 IGI-YASIKIDSTFSGFLVSD 235
DB 266 NGLEYDPWIDSLTGLITLAD 287

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## RESULT 7

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ID 095J95 PRELIMINARY: PRT: 194 AA.
AC 095J95.
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adiponectin (Fragment).
GN APM1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADIPPOSE TISSUE;
RA Kadir M., Anantharayan S., Ionut V., Kim S.P., Van Citters G.W.,
RA Dea M.K., Bergman R.N.;
RT "Regulation of Adiponectin gene expression in the fat-fed dog.";
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF417206; AL009702.1;
DR InterPro: IPR001073; Clq.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF01391; Collagen; 1.
DR PRODOM: PD000007; Collagen; 1.
DR PROSITE: PS01113; Clq; UNKNOWN_1.
FT NON_TER 1 194
SQ SEQUENCE 194 AA; 20890 MW; 3AA3D947D187AF9A CRC64;

```

Query Match 28.2%; Score 373.5; DB 6; Length 194;  
 Best Local Similarity 42.3%; Pred. No. 1.6e-24;  
 Matches 90; Conservative 22; Mismatches 66; Indels 35; Gaps 9;

```

QY 8 LLLGLAAGSPPLDNNKIPSLCPGHPGLPGTPGHHSOGLPGRDGRDGRGAPGAPGEG 66
DB 4 VLPLPRKA-----CPGMAGIPGHPGHNGT---PGRGRD-----GTPEKG 43
QY 67 EGGRPGILPGRGD-----PGRGEGAPGAGTGPAGGCSVPPRAFAKSESSEVVP 117
DB 44 EKGPGGLVGPGRGGETGVTVGEGRPGFPGKRGEGESAVYHRSASFV-GLSEITV 102
QY 118 PSDAPLPFDRVLVNEOGHYDAVTKFTCOVPGVYFAVHAIVYRASLOFDLVKNGESIAS 177
DB 103 P-NPIFTKIFLYMLQNHHTGCTCKFCNIPGLTYFSYHITIVYLKDVSLYKKDK--AM 159
QY 178 FFOFGGMPRA-SLSGAMVRLPEPDQVVOV 209
DB 160 LFTYDQYQEKKNVDAGSGSVLLHLEVGQVWMLQV 192

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## RESULT 8

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ID 09D2V4 PRELIMINARY: PRT: 744 AA.
AC 09D2V4.
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Procollagen, type VIII, alpha 1.
GN COL8A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
EX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldi M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamijo M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzailli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welter C., Whitaker C., Wilmink L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK018742; BAB31383.1;
DR MGD: MGI:88463; Col8a1.
DR InterPro: IPR001073; Clq.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; Clq; 1.
DR Pfam: PF01391; Collagen; 7.
DR PRINTS: PR000007; COMPLEMENTC1Q.
DR SMART: SM00110; Clq; 1.
DR PROSITE: PS01113; Clq; 1.
SQ SEQUENCE 744 AA; 73581 MW; C659BDCBCEB99C CRC64;

```

Query Match 28.0%; Score 370.5; DB 11; Length 744;  
 Best Local Similarity 34.6%; Pred. No. 1.4e-23;  
 Matches 93; Conservative 32; Mismatches 83; Indels 61; Gaps 7;

```

QY 24 IPSLCC-PGHPGLPGTPGHHSOGLPGRDGRDGRGAPGAPGEGGRRGLP----- 74
DB 476 VPSGLGPKGEGIPGDOGGLGPPGPIVGSIGTGPPIGPGKGPGLPGEFPGVGVK 535
QY 75 -----GPRDPPGRGEGAPGTP-----AGCSV 100
DB 536 PGVAGLGPGRKPGALGPGQGLPGRGPRGPRGPRPAVPTPSGGEYLIPDMGLGIDGV 595
QY 101 PPRSASFAR-----SESRVP-PPSDAPLPFDRVLVNEOGHYDAVTKFTC 145
DB 596 KPRPAVAGKKGKGGPAYEMPAPFAELTVPPPGAGVKKDKLLYNORQYINPQYGTFTC 655
QY 146 QVPGVYFAVHAIVYRASLOFDLVKNGESIA-SFPQFGGMPKPASISGAMVRLPEPDQ 204
DB 656 EVPGVYFAVHVNCKGNVAVALEKNNPMMYTYDERKKGLDQA--SGSAVLLLRPGDQ 713
QY 205 VWVQVGVGDYIGIYASIKIDSTFSGFLVY 233
DB 714 VFLQMPSEQAAGLYAGGYVHSSFSGYLLY 742

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Db 643 NPATYTYDEYKKYGLDQA--SGGAVILQLRPNDQVWVQMPDQANGLYSTXYIHSFSGF 700  
QY 231 LV 232  
Db 701 LL 702

## RESULT 12

Q9DCM6 PRELIMINARY; PRT: 245 AA.  
AC Q9DCM6: 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
DE Complement component 1, q subcomponent, alpha polypeptide.  
GN C1QA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Atakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann T., Gaasterland T., Gissi C., King B., Kochiya H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schiraldi L.M., Stauble F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Marzari J., Mombereis P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Winking L.,  
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 403:685-690(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AK002655; BAB2262.1; -  
DR EMBL: BC002086; AA02086.1; -  
DR MGD: MGI:88223; C1qa.  
DR InterPro: IPR001073; C1q.  
DR InterPro: IPR000087; Collagen.  
DR Pfam: PF00386; C1q; 1.  
DR PRINTS: PF00391; Collagen; 1.  
DR PRINTS: PR00007; COMPLEMENTC1Q.  
DR SMART: SM00110; C1Q; 1.  
DR PROSITE: PS01113; C1Q; 1.  
SQ SEQUENCE 245 AA; 25974 MW; 41C206D49592020 CRC64;

Query Match 23.7%; Score 314; DB 11; Length 245;  
Best Local Similarity 35.3%; Pred. No. 2.7e-19;  
Matches 79; Conservative 24; Mismatches 85; Indels 36; Gaps 6;

QY 29 PGHGLPTGPHHSGGLPGDGRDGAAGAPGEGEGGRPLPGPRDGPGRGEGP 88  
Db 36 PGNRGRRGRRGLKEERGPAGI--RTGIRGFGDGESEGPGRKPNVGLPGSGPLGD 93  
QY 89 AGPTGPAEGCSVP-----PSASAKRSRESRVPPDAPLPFRVLVNEGSHDAYTK 142  
Db 94 SGPGGLKGVKGNPNINDDPRPASAIKRN---PMTIGNVYIFPKVLTNDSFQNTGR 150  
QY 143 FTCCVPGVYFAVHATVYRASLQFDLVKNGESIASFQFTGQWPKPA----- 189

Db 151 FICAVPGFYF-----NFQVISKMPLCLFIKSSSGCGPRDSLFSNTNKKGLFQ 199  
QY 190 SLGGAWRLREPDQVWVQVGVYIGIYAIKRTDSTFSGFLY 233  
Db 200 VLAGTVLQLRRGDEWIEKDPKAG-RYQCTEADSIIFGFLIF 242

## RESULT 13

Q9ES30 PRELIMINARY; PRT: 246 AA.  
AC Q9ES30: 01-MAR-2001 (TREMblrel. 16, Created)  
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE Collagenous repeat-containing sequence of 26kDa protein.  
GN COR326.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC MEDLINE=21264842; PubMed=11071891;  
RX Maeda T., Abe M., Kurisu K., Utko A., Furukawa S.;  
RA "Molecular cloning and characterization of a novel gene, COR326,  
RT encoding a putative secretory protein and its possible involvement in  
RT skeletal development.";  
RL J. Biol. Chem. 276:3628-3634(2001).  
DR EMBL: AF246265; AAG33704.1; -  
DR MGD: MGI:1932136; Cors.  
DR InterPro: IPR001073; C1q.  
DR InterPro: IPR000087; Collagen.  
DR Pfam: PF00386; C1q; 1.  
DR Pfam: PF01391; Collagen; 1.  
DR PRINTS: PR00007; COMPLEMENTC1Q.  
DR SMART: SM00110; C1Q; 1.  
DR PROSITE: PS01113; C1Q; 1.  
SQ SEQUENCE 246 AA; 26828 MW; 42A481B3E9F48F7E CRC64;

Query Match 20.4%; Score 270.5; DB 11; Length 246;  
Best Local Similarity 31.8%; Pred. No. 1.5e-15;  
Matches 78; Conservative 33; Mismatches 107; Indels 27; Gaps 6;

QY 4 LVLVLLGLA-----AGSPPLDNDKIPSLCPGHPGLPCTPHHSGGLPGDGR 52  
Db 11 LPLPLFLPCLCQDEYVESPPAGGLPPDCSKCHGDFGFRGQGPGRPGPIGNHGN 70  
QY 53 DGRGAGAGAGGEGGRRPGLPGRDGPGRGEGAPGAPPGAGECVPPRSASFARSE 112  
Db 71 NGNNGATGHEGAKGE-----KDGKGLDGPGRGEGGKPGGKGPVPPPELQIAFNASL 124  
QY 113 SRVPPSDAPLPFRVLVNEGSHDAYTGKTCQVPGVYFAV----HATVYRASLQFDL 168  
Db 125 ATFFSNONSGLITFSVETNIGNFDVMTGRGAVSGVYFTFSMAKHEDVEEYV--L 182  
QY 169 VKNGESIASFQFGGPKRPASLSGGAWRLREPDQVWVQVGVYIGIYAIKRTDSTFS 228  
Db 183 MHNQNTVFSNMYSTTKKSDTS-SNNAVILAKGDEWILRNKNG--ALMGDHRFSTFA 238  
QY 229 GFLVY 233  
Db 239 GFLIF 243  
RESULT 14  
Q920NO PRELIMINARY; PRT: 196 AA.  
AC Q920NO: 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
DE HP-20.

GN HP-20.  
OS Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;  
OC Tamias.  
OX NCBI\_TaxID=64680;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21488336; PubMed=11602349;  
RA Ono M., Hosoe Y., Azuma S., Shoji M., Nara K., Kondo N., Shiba T.,  
Takamatsu N.;  
RT "HNF-1 regulates the liver-specific transcription of the chipmunk HP-  
RT 20 gene.";  
RL Gene 277:121-127(2001).  
DR EMBL; AB067779; BAB68362.1; -.  
DR InterPro; IPR001073; C1q.  
DR Pfam; PF00386; C1q; 1.  
DR Pfam; PF01391; Collagen; 1.  
DR PROSITE; PS01113; C1Q; UNKNOWN\_1.  
SQ SEQUENCE 196 AA; 21330 MW; B07D17BFA94D2FD CRC64;  
  
Query Match 20.1%; Score 266.5; DB 11; Length 196;  
Best Local Similarity 37.4%; Pred. No. 2.5e-15;  
Matches 70; Conservative 23; Mismatches 67; Indels 27; Gaps 7;  
  
QY 60 GAPGKGGGRRGLRPGDPRGEA---GPAQTPGAGGCSVPPRPAFAKRSRVP 116  
DB 25 GPPGVGVYRPGVGPGRPGPQPAAGRPDPGRPSVKPCRSRSPFYKFS-GRIP 83  
QY 117 PPSDAPLPEDRVLVNEQGHDAVTKFTQVPGVYFAVHATYRASIQFDLVKNGESIA 176  
DB 84 PPSE-PVVFTEVLVNTQNRKLKASTGVFNVEPGRNHFSDVLYLCKKVIIGLKKHIGVM 142  
QY 177 SFQFGGMPKPAASISGGAMR-LEPEDQVWVQVGVGDIYIASIKTDST-----F 227  
DB 143 EKHQLSKNEYENAS---GAMIMPLRQGDKWLE-----ADVEEPEPQAKVYIF 189  
QY 228 SGFLVYS 234  
DB 190 SGFLISS 196  
  
RESULT 15  
Q91907 PRELIMINARY; PRT; 246 AA.  
AC Q91907.  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Mannose binding-like lectin precursor (Fragment).  
GN MBL.  
OS Carassius auratus (goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=20456722; PubMed=11003389;  
RA Vilved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjoldt K.;  
RT "The homologue of mannose-binding lectin in the carp family Cyprinidae  
RT is expressed at high level in spleen, and the deduced primary  
RT structure predicts affinity for galactose.";  
RL Immunogenetics 51:955-964(2000).  
DR EMBL; AF227739; AAF63470.1; -.  
DR HSSP; P35247; 1B08.  
DR InterPro; IPR000087; Collagen.  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF01391; Collagen; 2.  
DR Pfam; PF00059; Lectin\_C; 1.  
DR SMART; SM00034; CLECT; 1.

DR PROSITE; PS00615; C\_TYPE\_LLECTIN\_1; UNKNOWN\_1.  
DR PROSITE; PS50041; C\_TYPE\_LLECTIN\_2; 1.  
KW Lectin; Signal; 1.  
FT NON\_TER 1 1  
FT SIGNAL <1 13 POTENTIAL.  
FT VARIANT 145 145 S->F.  
SQ SEQUENCE 246 AA; 25709 MW; AB692282D289D0D5 CRC64;  
  
Query Match 19.1%; Score 252.5; DB 13; Length 246;  
Best Local Similarity 31.9%; Pred. No. 5.2e-14;  
Matches 80; Conservative 33; Mismatches 73; Indels 65; Gaps 14;  
  
QY 4 LILVLLILGAGSPPLDDKIPSLCPGHPGLPTEGHHSOGILPGRDGDRGDGAPGARG 63  
DB 2 LILQPALQLLDGAEFQNLN-----CPAYGVFGTGHN---GLPGRDGDGDAIGPKG 53  
QY 64 EKGGG---GRRGLRPGDPRGEAGPAGTGPAGCSVPPRPAFAKRSRSPVP 118  
DB 54 EKGGSVSVQGPGRKAGPPTAGKEGERSPGSPGSESVLESLSKSEIQDLKKAKI--- 110  
QY 119 SDAPLPEDRVLVNEQGHDAVTKFTQVPGVYFAVHATYRASIQFDLVKNGESIASF 178  
DB 111 ---ATFEK--VSSVCHFRKV-----GKYYITDGVVG---NFD-----QGLKSC 146  
QY 179 PPFQGMMPKPAASISGGAMR--RLEPEDQVWVQV---GVGD---YIGIYASIKTDSTF-- 227  
DB 147 MEF-----GTMVSPRTSAENQALLLVYSSGIGSKKPIYIGV-TDKRTGQFVD 194  
QY 228 --SGFLVYS 236  
DB 195 TEGKQLTFTNW 205

Search completed: June 13, 2003, 16:01:17  
Job time : 34 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: June 21, 2003, 16:33:24 ; Search time 1719 Seconds

(without alignments)

2289,414 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325

Sequence: 1 MRPLVLLGLGIAAGSPPLD.....DSFSGRLVYSDMHSVPFA 243

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_plus\_p2n\_model -DEV=xlh  
-Q=/cgn2\_1/USP10.spool/US09944944/runal\_13062003\_150047\_24252/app\_query.fasta.1.391  
-DB=EST -QFMT=fastlap -SUFFIX=first -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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-NO\_MMAP -LARGESODURY -NEG SCORES=0 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :

EST:  
1: em\_estba:  
2: em\_esthum:  
3: em\_estlin:  
4: em\_estmu:  
5: em\_estov:  
6: em\_estpl:  
7: em\_estro:  
8: em\_hlc:  
9: gb\_est1:  
10: gb\_est2:  
11: gb\_hlc:  
12: gb\_est3:  
13: gb\_est4:  
14: gb\_est5:  
15: em\_estfun:  
16: em\_estom:  
17: gb\_gss:  
18: em\_gss\_hum:  
19: em\_gss\_inv:  
20: em\_gss\_pln:  
21: em\_gss\_vrt:  
22: em\_gss\_fun:  
23: em\_gss\_mam:  
24: em\_gss\_mus:  
25: em\_gss\_other:  
26: em\_gss\_pro:  
27: em\_gss\_rtd:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1164.5	87.9	844	10	BE309370 601094718
2	1138	85.9	1093	14	BM924569 AGENCOURT
3	1125	84.9	1045	14	BM920874 AGENCOURT
4	1062.5	80.2	778	12	BF098614 601750614
5	1034	78.0	1154	13	BM547549 AGENCOURT
6	1024.5	77.3	869	13	BF763193 AGENCOURT
7	1019	76.9	941	13	BF1821899 AGENCOURT
8	1006	75.9	879	13	BF1820945 AGENCOURT
9	984	74.3	887	13	BF1490062 AGENCOURT
10	982.5	74.2	842	13	BF1688017 AGENCOURT
11	917	69.2	846	13	BF145845 AGENCOURT
12	895	67.3	1623	14	BM926477 AGENCOURT
13	873.5	65.9	567	13	BM021381 AGENCOURT
14	868.5	65.5	936	12	BF540263 AGENCOURT
15	827	62.4	870	9	AF451167 AGENCOURT
16	806	60.8	702	12	BF055285 AGENCOURT
17	754	56.9	649	13	BM427498 AGENCOURT
18	717	54.1	660	13	BM488918 AGENCOURT
19	713	53.8	630	12	BF706609 AGENCOURT
20	703	53.1	792	13	BF1770921 AGENCOURT
21	677	51.1	565	12	BF088379 AGENCOURT
22	674	50.9	801	13	BF1490880 AGENCOURT
23	673	50.8	628	13	BM426563 AGENCOURT
24	668.5	50.5	867	13	BF1818537 AGENCOURT
25	631	47.6	532	12	BF724241 AGENCOURT
26	623	47.0	664	14	BQ419058 AGENCOURT
27	612.5	46.2	564	14	BQ419213 AGENCOURT
28	609	46.0	655	14	BQ285731 AGENCOURT
29	593	44.8	410	12	BE861753 AGENCOURT
30	582	43.9	547	12	BE722922 AGENCOURT
31	575	43.4	735	14	BF0208555 AGENCOURT
32	573	43.2	634	14	BQ449252 AGENCOURT
33	568	42.9	630	12	BF046067 AGENCOURT
34	567.5	42.8	418	9	AA510952 AGENCOURT
35	567	42.8	628	14	BF0285387 AGENCOURT
36	553.5	41.8	535	13	BF705095 AGENCOURT
37	549	41.4	613	13	BF1842952 AGENCOURT
38	545	41.1	613	13	BF1842844 AGENCOURT
39	530	40.0	517	14	BM966954 AGENCOURT
40	530	40.0	521	14	BM966810 AGENCOURT
41	520.5	39.3	606	14	BQ260266 AGENCOURT
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43	515	38.9	1349	14	BF073882 AGENCOURT
44	502	37.9	325	9	A1070779 AGENCOURT
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#### ALIGNMENTS

RESULT 1  
LOCUS BE309370 844 bp mRNA linear EST 26-OCT-2000  
DEFINITION 601094718P1 NCI\_CGAP\_Mam5 Mus musculus cDNA clone IMAGE:3489340 5', mRNA sequence.  
ACCESSION BE309370  
VERSION BE309370.1 GI:9167454  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 844)  
NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)







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Db	753	TTCATCCGACGACAGACAGCCCTTCTCCGCGGATTTCTGGTGAACCTCCGACTGGGCGAGAGCT	812
QY	239	rPro	240
Db	813	CCCC	816

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DEFINITION  
601750614F1 NCI-GAP\_Mam1 mRNA  
musculus CDNA clone IMAGE:3978387 5',  
778 bp  
BF098614  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
EST.  
house mouse.

REFERENCE  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Scleroptera; Muridae; Mus  
1 (bases 1 to 778)  
NIH-MGC <http://mgc.nhl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLM9170 row: 1 column: 04  
High quality sequence stop: 708.

**FEATURES**  
**SOURCE**

Plate: LLAM9170 row: 1 column: 04  
High quality sequence stop: 708.  
Location/Qualifiers  
1. .778

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/note="Organ: mammary; Vector: PCMV-SPOB6; Site:1: Saliv
Site:2: Notti; Cloned unidirectionally. Primer: Oligo dT
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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Alignment Scores:	
Prod. No.:	1,09e-67
Score:	1062.50
Percent Similarity:	90.83%
Best Local Similarity:	87.77%
Query Match:	80.19%
DB:	12
US-09-944-944-42 (1-243) x BFO98614 (1-778)	
	Length: 778
	Matches: 201
	Conservative: 7
	Mismatches: 18
	Indels: 3
	Gaps: 1

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Db 92 ATGAGGCACCTCTTGCCCTTCTGCTCTGGGTCTGGGTGTCAGAGCTCTCCCTCTTGAC 152  
QY 21 AspAsnLysIleProSerLeuGlyProGlyHisProGlyLeuProGlyThrProGlyHis 40  
Db 152 GACAAACAAATCCCAAGCCTGTGTCTCCGGGGCAGCCGGGCTTCACAGGACACACAGGTAC 211

QY	41	HisGlySerGlnGlyLeuProGlyTrpArgSerGlyArgAspGlyValArgProGly	60
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QY	61	AlaProGlyGluGlyGlyGluGlyValArgTrpProGlyLeuProGlyProArgLysPro	80
Db	272	GCCCCGGGAGAAAGGACGAGGGCGGGAGACCGGGACATACCTGGGGCACAGTGGGAGCC	331
QY	81	GlyProArgGlyGlyGluAlaGlyProAlaGlyProIleArgProAlaGlyLysSerVal	100
Db	332	GGGGCGGCTGGAGAGGCGACGGGCCCTATGGGGGCTATCGGGCCCGGGGAGTGTGCGTA	391
QY	101	ProProArgSerAlaPheSerAlaLysArgSerGlyUserArgValProProSerArg	120
Db	392	CCCCACGATAGCCTTCATGTGCCAAGGATCCGAGAGCGGGATACCTCCGGCACCGGAC	451
QY	121	AlaProLeuProPheAspArgValLeuValAsnGlnGlnGlyAsnGlyTrpAspAlaValThr	140
Db	452	ACACCCCTACCTTTGACCGCTGTGCTGCTAATGACAGAGGCCATTTCGACCCCACTACT	511
QY	141	GlyLysPheThrCysGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyr	160
Db	512	GGCAAGTGCACCTGGCAAGCTGCTGGCTGTACTCTTGGCTGTACAGCCCACTGTACAC	571
QY	161	ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyUserIleAlaSerPheHeGln	180
Db	572	CGGGCGACCTTGACCTTGATCTTGTCAAAAACGGGAGCTCATGGCTCTTCTTCCAG	631
QY	181	PhePheGlyGlyTrpProLysProAlaSerLeuSer-GlyGlyAlaMetValArgLeuGln	200
Db	632	TCATTAAGGGGGGTGGCCCAAGCACGCCCTCGCTCAGGAGAGTGGAGATGAAGCTAGA	691
QY	200	uProGluAspGlnValTrpVal-GlnValGlyValGlyAspTyrIleGlyIleTyrAlas	220
Db	692	ACCTGAGGACCAAGGTGTGGCTTGACAGTGGGGCTGGTGAATACATGGGATCTATGAGAG	751
QY	220	erIleLysThrAspSerThrPhe	227
Db	752	AT---TACACAGACCGTACTTTC	771

RESULT 5	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	
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		CDNA Library Preparation: Life Technologies, Inc.						Contact: Robert Strausberg, Ph.D.					
		Email: cgabbs@remail.nih.gov						Tissue Procurement: Invitrogen					
		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)						DNA Sequencing by: Agencourt Bioscience Corporation					
		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:						<a href="http://image.llnl.gov">http://image.llnl.gov</a>					
		Plate: LRAM12713	row: 0	column: 19				High quality sequence, stop: 591.					

## FEATURES

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5724522"
/clone_1lb="NIH_MGC_125"

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/lab\_host="DHI0B"  
/site="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;  
Site\_1: EcoRV (destroyed); Site\_2: NotI; RNA source pool  
of three ovaries, from females ranging in age from 38 to  
49 yo. Library is oligo-dT primed and directionally cloned  
(EcoRV site is destroyed upon cloning). Average insert  
size 2.1 kb, insert size range 1-3.5 kb. Library is  
normalized and enriched for full-length clones and was  
constructed by C. Gruber (Invitrogen). Research Genetics  
Tracking code 036."

BASE COUNT      178 a    382 c    401 g    193 t

ORIGIN

Alignment Scores:

Pred. No.:                  1,79e-65                  Length:                  1154

Score:                     1034.00                  Matches:                 202

Percent Similarity:       88.89%                  Conservative:            6

Best Local Similarity:    86.32%                  Mismatches:            23

Query Match:              78.04%                  Indels:                 4

DB:                         13                                  Gaps:                    1

US-09-944-944-42 (1-243) x BM547549 (1-1154)

OY    1 MetarproleuleuValLeuleuleuLengilyLeulaAlaglySerProProleuasp 20

Db    188 ATGAGGCCACACTCTCGTCCTCCTCCTCGTGAGCCCTGGCGGCCTGCCCCCACTGGAC 247

OY    21 AspasnlyslieProserleucySProgllystProglyleuProglyThProglyHls 40

Db    248 GACAACAAAGATCCCAGCTCTGCCCGGGGACCCCGGCTTCCAGGCACCGCGGGCAC 307

OY    41 HisglyserglnGlyleuProgllyArgaspglylArqaspglylArqaspglylAprogly 60

Db    308 CATGGACGCCAGGGCTTCCGGCGCGCATGTGGCGACGGCCCGACGGCGCCGCCCGG 367

OY    61 AlaproglyludysglynglylglylYargProglyleuProglyProatrglyAspPro 80

Db    368 GCTCCGGGAGAAAAGGCGAGGGGGGCGGGGAGCTGCCGGGACCTCGAGGGGACCCC 427

OY    81 GlyProatrglyGluAlaglProalaglProthrghlyProalaglGluCyseVal 100

Db    428 GGCGCCCGAGAGAGCGCGGACCCCGGGGCCACCAGGCTGCCGGGGAETGCTCGGTG 487

OY    101 ProProARgserralapheserialAlysArgsergluSerArvalProProPsoerASP 120

Db    488 CCTCCGGGATCCGCTTCAGCGCCAACGGCTCCAGAGCGCGGGTGCCTCCGCGTGCAC 547

OY    121 AlaProleuProphesAPARGValLeuValnsnGlnglnglyHstYrAspalavalThr 140

Db    548 GCACCCCTGGCCCTTCGACCGGGCTGTGGTAACGACGGGACACTTACGAGCGCGTACC 607

OY    141 GlylspPhethrcysglnValProgllyVallytTyrrphealaValAlhsAlathValtyr 160

Db    608 GGCAAGTTCACTCCAGGTGCTCGGGGTCTACTACTTGGCGGTCANCCACCGCTCAC 667

OY    161 ArgAlaserleuglnPheaspleuVallysasnlygluserrlleiaserPhepegln 180

Db    668 CGGGCCAGCCGCACTTGTATCCGGGAGAGATGGCANATCCTT-GCCTCTTCTTAGT 726

OY    181 PheheglnGlyTTPProlyProAlaserleuSergergylGlyAlametalValArgleuIn 200

Db    727 TTTTTCGGGGGGGGGCCCAAGCCCCCCTGCTCTCGGGGGGGGCGACGTGTAAGTGGAA 786

OY    201 -ProgluaspGlnValtrpValGlnValGlyValGly--AspyrlleeglyletyAl 219

Db    787 CCCCTGAGGACCAATGTGGGGGACCGGGGTGCGAGGTTCAGCTCCTGGGAGCCTATGC 846

OY    219 aser-IlelysthrAspserrhrPheSergergylPheleu 231

Db    847 CAGCGGTCCGAACGAAACAGACTTCTTCTGTGGAAATTGG 884

RESULT 6  
11763193

LOCUS	869 bp	mRNA	linear	EST-25-sep-2001
DEFINITION	603049929F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5190222 5' , mRNA sequence.			
ACCESSION	BI763193			
VERSION	BI763193.1	GI:15754771		
KEYWORDS	EST .			
SOURCE	human.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
AUTHORS	1 (bases 1 to 869)			
TITLE	NIH-MGC http://mgc.nci.nih.gov/.			
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgaps@remail.nih.gov Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LRAM1475 row: 1 column: 07 High quality sequence stop: 777. Location/Qualifiers 1..869			
FEATURES				
source				

		/organism="Homo sapiens"		
		/db_xref="taxon:9606"		
		/clone_image="IMAGE:5190222"		
		/clone_lib="NIH_MGC_116"		
		/lab_host="DH10B"		
		/note="Organ: pooled colon, kidney, stomach; Vector: pCMV-SPORT6; Site_1: NotI; site_2: EcoRV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of stomachs, 62 yo male and 70 yo female. Library is Oligo-dT primed and directionally cloned (fcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C Gruber (Invitrogen).. Research Genetics tracking code 023. Note: This is a NIH_MGC Library."		
BASE COUNT	133 a	277 c	339 g	120 t
ORIGIN				
Alignment Scores:				
Score No.:	6,74e-65	Length:	869	
Score:	1024.50	Matches:	208	
Percent Similarity:	95.48%	Conservative:	3	
Best Local Similarity:	94.12%	Mismatches:	6	
Query Match:	77.32%	Indels:	7	
DB:	13	Gaps:	0	
US-09-944-944-42 (1-243) x B1763193 (1-869)				
QY	1	MetArgProLeuLeuValLeuDeuDeuLeuGlyLeuAlaAlaGlySerProProLeuAsp	20	
Db	217	ATGAGGCCACTCTCGTCGTCTGCTCCTGGGCCCTGGGGCCGTGCCCCCACTGGAC	276	
QY	21	AspAsnLysIleProSerLeuCysProGlyHisProGlyLeuProGlyTyhrProGlyHis	40	
Db	277	GACAACAGAGNTCCACAGCCTTGCCCAGGGGACACCCCGCGCTTCACAGACGACGCGGCAC	336	
QY	41	HISgLysercInGlyLeuProGlyLyrArgApGlyLyrArgApGlyLyrArgApGlyAlaProGly	60	
Db	337	CATGGCAGCCA-GGCTTGCCGGGGCCGCATGGCCGCGCGCCGCGACGGCGCCCGGG	395	
QY	61	AlAProGlyLyuLeGlyGlyuGlyLyrtrPProGlyLeuProGlyLyrProArGlyLYASPPro	80	
Db	396	GCTCCGGAGAGAAGGCGGAGGGCGGAGGCCGGGAACTCGCGGGAACCTCTCAGGGGACCCC	455	
QY	81	GlyProArGglyLyuLaGlyProAlaGlyProThrGlyProAlaGlyGluCySserVal	100	

D	b		456	GGGCGGAGAGAAGCGGGACCCGCCGGGGCCTGCCTCGGGGAATGTCGGTG	515
O	y		101	ProPtoAargSerAlaphSeSerAlalysArSergIuseRary-VAlProProPSerAs	120
D	b		516	CCTCGCGCATCGCGCTTCAAGCGCCAAAGCGCTCCGAGACCAGGGGGCTCCGCGCTCYGA	575
O	y		120	pAlaProleubProPhaeASparGVallLeuVal-AsnGIunGLyIsrTyraSpAlaVal-	139
D	b		576	CGCACCCCTTGCCTTCGACCGCGTGTGTAATAAGACAGACAGGAGATTACGACGCCGTTC	635
O	y		140	ThrGIlySPheHnCYSglInVaIProGIlyValTYrTYrPheaAlaValHisAlathrVal	159
D	b		636	ACCGGCAAGTTACACTGCGCAGGTGGCTGGGTCTACTTCTTCGCCGTCAATGCCACCGTG	695
O	y		160	TyrTrgAlaSerleugInPheaspleuVAlllysAnsngIjuseRIleaLaseRPhephe	179
D	b		696	TACCGGGGACAGCTGACAGTGTGACTGTGAANAATGCGAATCATTTGGGTC-TTCCTC	754
O	y		180	GlInPhePnegIylGYTPPrPolysProAlaSerleuSERglylAlameTVAlrgleu	199
D	b		755	CAGTTTTACGGGGGGGTGGCCAAAGCC--AGCTCGCTCTCGGGGGGGCCATGGTAGCGTG	812
O	y		200	GIuProGIuaSPGlnValITrpValGIhValGIlyVal-clYasprrylliegyllE	217
D	b		813	GAGCCTGAGGACAAGtGTGGGTGCGAGGTGTGTGGGTGACTACgtTGGGCATC	867
R	E	S	B1821899	941 bp	mRNA linear EST 04-OCT-2001
L	O	C	B1821899	LOCUS	NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176967 5'
D	E	F			mRNA sequence.
A	C	V	B1821899		B1821899
K	E	X	B1821899.1	GI:15933449	EST.
S	O				human.
O	R		Homo sapiens:		
J			Eukaryaota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
R			Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
A			1 (bases 1 to 941)		
T			NIH-MGC http://mgc.nci.nih.gov/.		
I			National Institutes of Health, Mammalian Gene Collection (MGC)		
J			Unpublished (1999)		
C			Contact: Robert Strausberg, Ph.D.		
O			Email: csapbs@email.nih.gov		
M			Tissue Procurement: Life Technologies, Inc.		
			cDNA Library Preparation: Life Technologies, Inc.		
			DNA Sequencing by: Incyte Genomics, Inc.		
			Clone distribution: MGC clone distribution information can be		
			found through the I.M.A.G.E. Consortium/LNLN at:		
			http://image.lnl.gov		
			plate: LHAM1440 row: p column: 24		
			High quality sequence stop: 779.		

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Location/Qualifiers
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/clone_image="51/6967"
/clone_id="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
pCMV-SPORT6; Site:1; NotI; Site:2; EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: This is a NIH_MGC Library."
BASE COUNT
130 a 320 c 329 g 162 t
ORIGIN

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Alignment Scores:	
Pred. No.:	1,816-64
Score:	1019.00
Percent Similarity:	90.40%
Best Local Similarity:	89.20%
Query Match:	76.91%
DB:	13
Length:	941
Matches:	223
Conservative:	3
Mismatches:	13
Indels:	14
Gaps:	0

US-09-944-944-42 (1-243) x BI821899 (1-941)

Oy	3	ProteinLeuValIleuLeuLeuLeuLeuIlyleuAlaIaglySerProProleuaspaspasn	22
Db	179	CCACTCCCTGCTCTCTCTCTCTCTGGGCTGGGGCCGGCTGCCCCCCACTGGACACAAAC	238
Oy	23	LysIleProSerIleuCySProGIyH1aSProGIyleuProGIyThPProGIyH1aShagly	42
Db	239	AAGATCCCCACGCTCTGCGCGGGAGCACCCCGGCTTCCAGGACGACCGGGCCACCATGAGC	298
Oy	43	Ser-GInglyleuProGIyArGaspGlyArGaspGlyArGaspGlyAlaPProGly-AlaP	62
Db	299	AGCCATGGGCTTGGCGGGCCCGAGAGGCGGACGCGGACGCGGCGGGCCGGCGGGCTC	358
Oy	62	roGIyGLyLysGIyGLyGLyArGArGPProGIyleuProGIyProArGGLyASPProGIyP	82
Db	359	CGGAGAGAAAGCGGAGGGCGGGAGGCCGGGACTCTCGGAGACTTGAGAGGAGACCCCGGGC	418
Oy	82	roArGglyGLyAlaGLyProAlaGLyProThr-GlyProAla-GlyGLyCySerValP	101
Db	419	CGCGAGGAGAGCGGGGACCCCGGGGCCACCGGGGCCCTGCCGGGGAGTGCTCGGTGCC	478
Oy	101	oProArGserAlaPheSerAlaLysArGSerGIuSer--ArgValPProProSerasp	120
Db	479	TCCGCGATCCGGCTTCAAGCCGACGCTCCGAGAGCCTGGGTTGCTTCCGCGCTGAC	538
Oy	121	AlaPProleu-ProPheaspArGValLeuValaSnGLyInGLyH1sTyraSPalaValTh	140
Db	539	GCACCCCTTGCCTTCGACCCGCTGCTGTGAACAGACGAGGACATYTAACAGCGCGGTAC	598
Oy	140	rgLyLysPheThrCys-GInValProGIyValTYTtyrPhalaValaHis-AlaThrVal	159
Db	599	CGGGAAGTCACTGCGCCAGGTGCTGGGGTCTTACTTGTGGCCCTCATTTGCCACCGTC	658
Oy	160	TyTrGAlaSerLeuGInPheaspLeuValLysaSnGLyGIuSerTlAlaSerPhePhe	179
Db	659	TACCGGGCCACCTGCACTTGATCTGTTGAAGAATGGCAATTCATTGCTCTTCTTTC	718
Oy	180	GInPhePheGLyGIyTTPProLysPProAlaSerLeuSerGIyGLyAlaMetValArgLeu	199
Db	719	CAGTT-TTCGGGGCAGTGGCCCAAGCAGACCTGCTCTCGGGGGGGCCATGGTGAGGCTG	777
Oy	200	GIu-ProGIuaspGlnValITTPValGlnVal-GlyValGLyASPtyrTlIleGIyleTyra	219
Db	778	GAGCCCTGAGACCAAGTGTGGTTCGCTGGGGGTGGTGACACTTGTGGCTTCTTGT	837
Oy	219	IaSerTlIysThrAspSerThrPheSerGIyPheLeuValTySeraspTTPHISers	239
Db	838	CCAGCATCAGGCA-GACAGGACCTTCTCGGATTTCTG-GTGTACTCCGACTGGCACAGTC	895
Oy	239	erProVal 241	
Db	896	CCGAGGTC 903	
RESULT 8			
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DEFINITION	603033989F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:515070 5',		
ACCESSION	B1820945		
VERSION	B1820945.1	GI:15932495	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		





Db 632 ACCGGCCAGCTGTGAGTTCATGTCACAAAGGCGAGCATCCGCTTCTTCC 691  
 QY 180 InPhepGlyGlyTTP-ProlySProAlaSerLeuSerglyGlyAlaMetValArgLeu 199  
 Db 692 AGTATTTGGGGGGGGTGGCCAAAGCAGCCTGCTCTCAGG-GGTGCGAAGGTAAAGGCTA 750  
 QY 200 Glu-ProGlu-AspGlnValTTPValGlnValGlyValGlyAspPyr---IleGlyIleT 218  
 Db 751 GAACCTGAGAGACCAAGCGTGTGGTGCAGGTGGGGTGGTGAATTACCATTTGATTCTT 810  
 QY 218 YrAlaSerIleLeuThrAspSerThrPheSer 228  
 Db 811 ATGCCAGCATCATGAGCAGCAGTACCTCTCG 842  
 RESULT 11  
 B1458455 846 bp mRNA linear EST 21-AUG-2001  
 LOCUS 603198837F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:5278184 5',  
 DEFINITION mRNA sequence.  
 ACCESSION B1458455  
 VERSION B1458455.1 GI:15249111  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 846)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshitsuki and Piero Carninci (RIKEN)  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM1702 row: j column: 09  
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 /note="Organ: brain; Vector: pBluescript (modified  
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 size-selected for average insert size 2.3 kb and  
 normalized to 40x. This is a primary library enriched  
 for full-length clones and constructed using the  
 cap-trapper method (Carninci, in preparation). Library  
 constructed by M. Brownstein (NHGRI/NHGRI, National  
 Institutes of Health). Note: this is a NIH-MGC Library."  
 BASE COUNT 129 a 271 c 330 g 115 t 1 others  
 ORIGIN  
 Alignment Scores:  
 Pred. No.: 3.97e-57 Length: 846  
 Score: 917.00 Matches: 189  
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 Best Local Similarity: 91.30% Mismatches: 12  
 Query Match: 69.21% Indels: 7  
 Gaps: 13  
 US-09-944-944-42 (1-243) x B1458455 (1-846)

QY 1 MetArgProLeuLeuValIleuLeuLeuEnglyLeuAlaIleGlySerProProLeuasp 20  
 Db 239 ATGAGGCCACTCTCTGCTCTGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 298  
 QY 21 AspaAnlySileProSerLeuCySProGlyHisPProGlyLeuProGlyThrProGlyHis 40  
 Db 299 GACAAACAGATCCCAAGCCTCTGCGCGGGGACCCCGGCTCTCAAGGACGCGGGGCCAC 358  
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 Db 359 CATGCCAGCGCGGGGCTTGGCGCGCGCGATGCGCGCGCGCGCGCGCGCGCGCGCGCGG 418  
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 Db 419 GCTCCGGGAGAAAGGCGAGGCGGAGGCGGAGGCGGAGCTGCGGAGCTTGAGAGGAGACCC 478  
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 Db 479 GGGCGCGGAGAGAGGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGG 537  
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 QY 121 AlaProLeuProPheAspArgValLeuValAsnGlyGlnGlyHisTyrAspAlaValThr 140  
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 QY 160 InPheGlySerLeuGlnPheAspLeuValLysAsnGlyGlySerIleAlaSerPhePheGly 180  
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 DEFINITION 5', mRNA sequence.  
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 VERSION BM926477.1 GI:19376856  
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 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 1623)  
 NIH-MGC http://mgc.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LHAM12824 row: d column: 01  
 High quality sequence stop: 558.  
 Location/Qualifiers  
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 source 1..1623







AUTHORS Sharma,S., Chang,J.T., Della,N.G., Campochiaro,P.A. and Zack,D.J.  
TITLE Identification of novel bovine RPE and retinal genes by subtractive  
hybridization  
JOURNAL Mol. Vis. 8, 251-258 (2002)  
COMMENT Contact: Sharma S  
Ophthalmology  
Flinders University  
Flinders Drive, Bedford Park, SA 5042, Australia  
Email: shivani.sharma@flinders.edu.au

FEATURES  
SOURCE 1. 870  
/organism="Bos taurus"  
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amplify bovine target cDNA"

BASE COUNT 171 a 251 c 265 g 183 t  
ORIGIN

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Score: 827.00 Matches: 154  
Percent Similarity: 98.73% Conservative: 1  
Best Local Similarity: 98.09% Mismatches: 2  
Query Match: 62.42% Indels: 0  
DB: Gaps: 9

US-09-944-944-42 (1-243) x AF451167 (1-870)

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QY 87 G1PProAlaGlyProThrGlyProAlaGlyGluCysSerValProProArgSerAlaPhe 106
   ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 GGACCCATGGGGGCAACGGGGCCGGCGGAGAGTCGCGCTCCGCGCTCCGCTTC 61

QY 107 SerAlaLysArgSerGluSerArgValProProProSerAspAlaProLeuProPheAsp 126
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Db 62 AGCGCTAAGCGCTCTGAGAGCGGGTCCCGCCGCGGAGCGGCCCTACCTTCGAC 121

QY 127 ArgValLeuValAsnGluGlnGlyHisTyrAspAlaValThrGlyLysPheThrCysGln 146
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Db 122 CCGGTCTGCTGTAACGAGCAGGAGGACTACGACGCCCTCAACGGCAAGTTCACCTGCCAG 181

QY 147 ValProGlyValTyrTyrPheAlaValHisAlaThrValTyrArgAlaSerLeuGlnPhe 166
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Db 182 GTGCCCGGGGTCTACTACTTCGCGCTCACGCCACCGCTTACCGGCTAGCCTGCAGTTT 241

QY 167 AspLeuValLysAsnGlyGluSerIleAlaSerPhePheGlnPhePheGlyTyrPro 186
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Db 242 GATCTGCTCAAGAAATGGCGAGCTATCGCCTTTCTTCAGTTCTTGGAGGGTGGCCC 301

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   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 302 AAGCGACGCTCGCTCTCCGGGGGGCCATGTGAGGCTGGAGCCTGAAGACAGGTGTGG 361

QY 207 ValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSerIleLysThrAspSerThr 226
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Db 362 GTACAGGTGGCGGTGGGAGTATATATGTCATCAGCCAGCATCAAGACAGACAGCACC 421

QY 227 PheSerGlyPheLeuValTyrSerAspTrpHisSerSerProValPheAla 243
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Db 422 TTCTCTGATTTTCTAGTGTATTTCTGACTGGACACTCCCTGTGTCTTGCT 472
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Search completed: June 21, 2003, 18:00:05  
Job time : 1733 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: June 13, 2003, 15:58:21 ; Search time 41 Seconds

(without alignments)  
569.772 Million cell updates/sec

Title: US-09-944-944-42

Perfect score: 1325  
Sequence: 1 MRPLVLLLLGLAAGSPPLD.....DSTFSGFLVSDMHSPPVFA 243Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summariesDatabase :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1207	91.1	219	2	TJ4782
2	424	32.0	244	2	JC4708
3	418.5	31.6	680	1	CGHUIB
4	416.5	31.4	674	2	S23297
5	412	31.1	246	2	S29328
6	411.5	31.1	674	2	S13301
7	408	30.8	680	2	S31216
8	399	30.1	245	1	C1HUOC
9	374	28.2	744	1	A34246
10	370	27.9	744	1	S23298
11	363.5	27.4	743	1	S23779
12	363	27.4	635	2	A57131
13	362	27.3	253	1	C1HUOB
14	360.5	27.2	253	2	S49158
15	359	27.1	744	2	S15435
16	351	26.5	253	2	A5797
17	316	23.8	423	2	A55797
18	314	23.7	245	1	C1HUOA
19	314	23.7	245	2	S19018
20	280.5	21.2	215	2	B48150
21	277.5	20.9	215	2	C48150
22	261.5	19.7	196	2	A48150
23	238.5	18.0	992	2	T08772
24	230.5	17.4	1049	1	CG8075
25	227.5	17.2	248	2	S11921
26	225	17.0	248	1	LNHUP1
27	225	17.0	325	2	T32248
28	224	16.9	636	2	S41067
29	223	16.8	1464	2	S59856

30	222.5	16.8	1758	2	T29350	hypothetical prote
31	222.5	16.8	1759	2	T29351	collagen alpha 2(I
32	222	16.8	360	2	T37285	collagen dpy-2 - C
33	221.5	16.7	170	2	B57131	collagen alpha 2(V
34	221	16.7	886	2	I50694	collagen alpha 1(I
35	221	16.7	1019	1	A32856	collagen alpha 1(V
36	220	16.6	248	1	LNDSPS	pulmonary surfacta
37	220	16.6	341	2	T16296	hypothetical prote
38	220	16.6	380	2	T28888	cuticle collagen d
39	219.5	16.6	247	1	LNDRPS	pulmonary surfacta
40	219.5	16.6	381	1	T27806	hypothetical prote
41	219.5	16.6	673	1	CGBO6C	collagen alpha 1(I
42	219.5	16.6	1466	1	CGHUI7L	collagen alpha 1(I
43	219	16.5	671	1	CGRTIS	collagen alpha 1(I
44	218.5	16.5	1453	1	S21626	collagen alpha 1(I
45	217	16.4	283	2	T29980	hypothetical prote

## ALIGNMENTS

RESULT 1  
TJ4782  
hypothetical protein DKFZp586B0621.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 02-Sep-2000  
C:Accession: TJ4782  
R:Ottewill, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, August 1999  
A:Reference number: 218184  
A:Accession: TJ4782  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-219 <OT>  
A:Cross-references: EMBL:AL110261  
A:Experimental source: adult uterus; clone DKFZp586B0621  
A:Genetics:  
A:Note: DKFZp586B0621.1  
C:Superfamily: complement C1q carboxyl-terminal homology

Query Match 91.1%; Score 1207; DB 2; Length 219;  
Best Local Similarity 100.0%; Pred. No. 1.3e-77;  
Matches 219; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 PSLCGHGLDPTREPHHSGGLPGDGDGAGAGGEGGGRPGPRG 84  
DB 1 PSLCGHGLDPTREPHHSGGLPGDGDGAGAGGEGGGRPGPRG 60  
QY 85 EAGPAGPTGPAEGECVPPRSAPSAKRSRVPDPDAPLPDRVLYVNOGHDAVTGKT 144  
DB 61 EAGPAGPTGPAEGECVPPRSAPSAKRSRVPDPDAPLPDRVLYVNOGHDAVTGKT 120  
QY 145 CQVPGVYFAVHATYRASLOFDLVKNESIASFPQFGMPKPSLSGAMVRLPEPDQ 204  
DB 121 CQVPGVYFAVHATYRASLOFDLVKNESIASFPQFGMPKPSLSGAMVRLPEPDQ 180  
QY 205 VVWVGVDYDGYTASITDSTFSGFLVSDMHSPPVFA 243  
DB 181 VVWVGVDYDGYTASITDSTFSGFLVSDMHSPPVFA 219

RESULT 2  
JC4708  
gelatin-binding 28k protein precursor - human  
N:Alternate names: adipose specific collagen-like factor  
C:Species: Homo sapiens (man)  
C:Date: 10-May-1996 #sequence\_revision 19-Jul-1996 #text\_change 20-Sep-1999  
C:Accession: JC4708; J04944  
R:Maeda, K.; Okubo, K.; Shimomura, I.; Funahashi, T.; Matsuzawa, Y.; Matsubara, K.  
Biochem. Biophys. Res. Commun. 221, 286-289, 1996  
A:Title: cDNA cloning and expression of a novel adipose specific collagen-like factor  
A:Reference number: JC4708; MUID:96224171; PMID:8619847  
A:Accession: JC4708







F:29-245/Product: complement subcomponent C1q chain B #status predicted <MAT>  
 F:31-114/Domain: collagenous, triple helix <COL>  
 F:121-244/Domain: complement C1q carboxyl-terminal homology <C1Q>  
 F:32/Disulfide bonds: interchain #status experimental  
 F:36,39,42,45,54,63,81,93,96,99,105/Modified site: 4-hydroxyproline (Pro) #status experimental  
 F:57,72,75/Modified site: 5-hydroxylysine (Lys) #status experimental  
 F:75/Binding site: carbohydrate (Lys) (covalent) #status experimental

Query Match 30.1%; Score 399; DB 1; Length 245;  
 Best Local Similarity 39.8%; Pred. No. 4.3e-21;  
 Matches 100; Conservative 33; Mismatches 84; Indels 34; Gaps 10;

QY 1 MRPLVLLILGLAASPLDDKRTSLIC---PGHGLPCTPGHSGSLGPRGDRGRG 57  
 DB 13 LKLLILLILLALR-----GQANTGCGITGMPGLPAPRGDITGLPRKGEPTA 64  
 QY 58 APGARDEGEGRPLPGRGDPGRGEGAPGPTGPAECVPP-----RSAPSA 108  
 DB 65 IPGIRGPKGQKGEPLGPHGKNKMPGPMGVPQPMGIPGEPGEGRYKQKFGSVFTV 124  
 QY 109 KRSESRVPPSPAPRPDRVLYNEGCHDAVTGKFTCOVPGYTVRAVATVTRASIQFDL 168  
 DB 125 TR-QTHQPPAPNLSLRFAVILNPGQDVTSTGKFTCKVPGLYFYVTHAS-HTANLCVLL 182  
 QY 169 VNGESIASFEQFGMPKPAFL-SGAMVRLPEPDQVWVGVDPY---IGIYASIKTD 224  
 DB 183 YRSQVKKVY---FCHTSTKTNQVNSGVLRLQVGEFVW--LAANDYIMVGIOGS---D 234  
 QY 225 STFGSFLYSD 235  
 DB 235 SVFSGFLRFPD 245

## RESULT 9

A34246  
 collagen alpha 1(VIII) chain precursor - rabbit  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: A34246  
 R.Yamaguchi, N.; Benya, P.D.; van der Rest, M.; Ninomiya, Y.  
 J. Biol. Chem. 264, 16022-16029, 1989  
 A:Title: The cloning and sequencing of alpha1(VIII) collagen cDNAs demonstrate that type  
 omalis similar to those of type X collagen.  
 A:Reference number: A34246; MUID:89380199; PMID:2476437  
 A:Accession: A34246  
 A:Molecule type: mRNA  
 A:Residues: 1-744 <YAM>  
 A:Cross-references: GB:J05042; NID:G164895; PIDN:AAA31204.1; PID:G164896  
 C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>  
 F:21-117/Region: amino-terminal nonhelical  
 F:118-571/Region: interrupted helical  
 F:572-744/Region: carboxyl-terminal nonhelical  
 F:617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 28.2%; Score 374; DB 1; Length 744;  
 Best Local Similarity 34.4%; Pred. No. 7.6e-19;  
 Matches 93; Conservative 36; Mismatches 79; Indels 62; Gaps 8;

QY 24 IPSLC--PGHGLPCTPGHSGSLGPRGDRGAPARPEKSGRGRPLP----- 74  
 DB 475 VPGILGPKGERPLPDGQGLGPRGIGITGPGSGIPGPKERPLGPRGPGVGR 534  
 QY 75 -----GPRGP---GPRGE---AGPAGPTGPAECVPPS----- 104  
 DB 535 PGVAGLHGPGRKPGALGPGQGLGPRGPPPPAPPAVMPPTPAPOGEYLRDMGLGIDG 594  
 QY 105 -----AFSAKRESRNP-----PPSDAPLPDRVLYNEGCHDAVTGKFT 144  
 DB 595 VTPHAYAAKKKNGKNGPRAYEMPAFTALTPAPPVGAIPKFTRLNLNGQNTNPOTGIT 654  
 QY 145 CQVPGVYFAVHATVYRASLQFDLVKNGESIA-SFGQFGMPKPAISGAMVRLPEPD 203

DB 655 CEVPGYTVRAVHNGCKGAVWVWALFKNNRPVATVTEYKKGFLDQA--SGSAVLLRPPD 712  
 QY 204 QVWVGVGDYIGITASIKTDSTFSGFLY 233  
 DB 713 RVFLQMPSEQAAGLVAGQYVHSSFSGLLY 742

## RESULT 10

S23298  
 collagen alpha 1(VIII) chain - chicken  
 C:Species: Gallus gallus (chicken)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
 C:Accession: S23298  
 R.Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jasenko, O.; Luvalle, P.;  
 maguchi, N.; Olsen, B.R.  
 In Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic  
 A:Title: The molecular biology of collagens with short triple-helical domains.  
 A:Reference number: S22243  
 A:Accession: S23298  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-744 <NIN>  
 C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology  
 F:617-743/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 27.9%; Score 370; DB 1; Length 744;  
 Best Local Similarity 34.4%; Pred. No. 1.4e-18;  
 Matches 93; Conservative 35; Mismatches 80; Indels 62; Gaps 8;

QY 24 IPSLC--PGHGLPCTPGHSGSLGPRGDRGAPARPEKSGRGRPLP----- 74  
 DB 475 VPGILGPKGERPLPDGQGLGPRGIGITGPGSGIPGPKERPLGPRGPGVGR 534  
 QY 75 -----GPRGP---GPRGE---AGPAGPTGPAECVPPS----- 104  
 DB 535 PGVAGLHGPGRKPGALGPGQGLGPRGPPPPAPPAVMPPTPAPOGEYLRDMGLGIDG 594  
 QY 105 -----AFSAKRESRNP-----PPSDAPLPDRVLYNEGCHDAVTGKFT 144  
 DB 595 VTPHAYAAKKKNGKNGPRAYEMPAFTALTPAPPVGAIPKFTRLNLNGQNTNPOTGIT 654  
 QY 145 CQVPGVYFAVHATVYRASLQFDLVKNGESIA-SFGQFGMPKPAISGAMVRLPEPD 203  
 DB 655 CEVPGYTVRAVHNGCKGAVWVWALFKNNRPVATVTEYKKGFLDQA--SGSAVLLRPPD 712  
 QY 204 QVWVGVGDYIGITASIKTDSTFSGFLY 233  
 DB 713 RVFLQMPSEQAAGLVAGQYVHSSFSGLLY 742

## RESULT 11

S23779  
 collagen alpha 1(VIII) chain - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Jun-2000  
 C:Accession: S23779  
 R.Muragaki, Y.; Shiota, C.; Inoue, M.; Ooshima, A.; Olsen, B.R.; Ninomiya, Y.  
 Eur. J. Biochem. 207, 895-902, 1992  
 A:Title: Alpha-1(VIII)-collagen gene transcripts encode a short-chain collagen polypep  
 C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology  
 F:616-742/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 27.4%; Score 363.5; DB 1; Length 743;  
 Best Local Similarity 32.8%; Pred. No. 4.1e-18;  
 Matches 90; Conservative 35; Mismatches 78; Indels 71; Gaps 7;

QY 29 PGRHGLPCTPGHHSQGLPGRDGRDGPAGAPGEGKGRPGLPGRGDP----- 80  
 Db 470 PGLGIVGVLLGLPKKEGPGIPGQGLGPGIGIVPSPBPPIPGKGPGLPGPGF 529  
 QY 81 -----GPRGE---AGPAGPTGAGCSVPR----- 103  
 Db 530 PGVCKPGVAGLHGPPKRGALPGQGLPGPGRPGPPGPAWMPPTSPQGYLPDML 589  
 QY 104 -----SAFSAR-----SSRVP-PPSDAPLPEDRVLVNEQGHYDAVT 140  
 Db 590 GIDGVKTPHAYAGKKGKGPAYEMPATFALTVPEPVGAPVKEFKLLYGRQNYNQT 649  
 QY 141 GKFCQVPGVYFVAVHATVYRASLQFDLVKNGESA-SFQPFSGMPPASLSCGAWRL 199  
 Db 650 GIFCEVPGVYFVAVHCKGNVWALFKNNEPMYTYDEYKKGFLLDQA---SGSAVLL 707  
 QY 200 EPEDQVWVGVGDYIGIYASIKTDFSPSGFLVY 233  
 Db 708 RPDQVFLQNFPEQAGLITAGQYVHSSPSGTLTY 741

## RESULT 12

A57131  
 collagen alpha 2(VIII) chain - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 03-Nov-1995 #sequence, revision 03-Nov-1995 #text, change 13-Aug-1999  
 C:Accession: A57131  
 R:Muragaki, Y.; Juncenko, O.; Apte, S.; Mattei, M.G.; Ninomiya, Y.; Olsen, B.R.  
 J. Biol. Chem. 266, 7721-7727, 1991  
 A:Title: The alpha2(VIII) collagen gene, A novel member of the short chain collagen family  
 A:Reference number: A57131; MUID:91210292; PMID:2019595  
 A:Accession: A57131  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-635 <NR>  
 A:Cross-references: GB:M60832; NID:g177178; PID:AAA62822.1; PID:g177179  
 C:Genetics:  
 A:Gene: GDB:COL8A2  
 A:Cross-references: GDB:127812; OMIM:120522  
 A:Map position: 1p34.3-1p32.3  
 C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology  
 F:1-11/Domain: amino-terminal nonhelical (fragment) #status predicted <NC2>  
 F:12-468/Region: interrupted helical  
 F:469-635/Domain: carboxyl-terminal nonhelical #status predicted <NC7>  
 F:508-634/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 27.4%; Score 363; DB 2; Length 635;  
 Best Local Similarity 38.6%; Pred. No. 3,8e-18;  
 Matches 93; Conservative 25; Mismatches 95; Indels 28; Gaps 7;

QY 11 GLAAGSPPLDNDKIPSLCPGHPGLPGPHHSGQLPGRDGRDGPAGAPGEGKGR 70  
 Db 401 GLGPGAPGIPGQGLPGKGPGLPGKGPGLPGP-----EGRAGEPTAGPRGPGVSPGJTGP 455  
 QY 71 PGLPGPGRDGPGRGEAPAG---PTGRA-----GECVPPPSASAKRSE 112  
 Db 456 PGLPGPGAPGAPAFDETGTAGLHLPLNGVEGAVLKGKRPQGLDELTAHATPAFTAVLTS 515  
 QY 113 SRVPPSDAPLPEDRVLVNEQGHYDAVTGKFTCOVPGVYFVAVHATVYRASLQFDLVKNG 172  
 Db 516 PL--PASGMPVKFRTLYLNGHSGTNPATGIFTTCVGGVYFVAVHATVYRASLQFDLVKNG 573  
 QY 173 -ESIASFFQFGGMPKPSASLSCGAMVRLPEPDQVWVGVGDYIGIYASIKTDFSPSGFL 231  
 Db 574 VPATYTYDEYKKGYLLDQA---SGSAVLLDRPDQVWVQIIPDQANGLSTETIHSSFGFL 631  
 QY 232 V 232  
 Db 632 L 632

## RESULT 13

C1H00B

complement subcomponent C1q chain B precursor [validated] - human  
 N:Alternate names: complement subcomponent C1q beta chain  
 C:Species: Homo sapiens (man)  
 C:Date: 22-May-1981 #sequence, revision 31-May-1996 #text, change 08-Dec-2000  
 C:Accession: B23422; A23422; B90304; A90301; B90315; A03206  
 R:Reid, K.B.M.  
 Biochem. J. 231, 729-735, 1985  
 A:Title: Molecular cloning and characterization of the complementary DNA and gene cod  
 A:Reference number: A23422; MUID:86076906; PMID:3000358  
 A:Accession: B23422  
 A:Molecule type: DNA  
 A:Residues: 'HS', 1-32 <RE1>  
 A>Note: the authors translated the codon AGT for the second position as Arg; they wer  
 A:Accession: A23422  
 A:Molecule type: mRNA  
 A:Residues: 28-253 <RE1>  
 A:Cross-references: EMBL:X03084  
 A>Note: the authors translated the codon ACA for residue 46 as Ile  
 R:Reid, K.B.M.  
 Biochem. J. 179, 367-371, 1979  
 A:Title: Complete amino acid sequences of the three collagen-like regions present in  
 A:Reference number: A90304; MUID:80020137; PMID:486087  
 A:Accession: B90304  
 A:Molecule type: protein  
 A:Residues: 'E', 23-84, 'D', 86-99, 'P', 101-135 <RE5>  
 R:Reid, K.B.M.; Thompson, E.O.P.  
 Biochem. J. 173, 863-868, 1978  
 A:Title: Amino acid sequence of the N-terminal 108 amino acid residues of the B chain  
 A:Reference number: A90301; MUID:79041552; PMID:708376  
 A:Accession: A90301  
 A:Molecule type: protein  
 A:Residues: 28-99, 'P', 101-195 <RE3>  
 R:Reid, K.B.M.; Gagnon, J.; Frampton, J.  
 Biochem. J. 203, 559-569, 1982  
 A:Title: Completion of the amino acid sequences of the A and B chains of subcomponent  
 A:Reference number: A90315; MUID:82283890; PMID:6981411  
 A:Accession: B90315  
 A:Molecule type: protein  
 A:Residues: 136-253 <RE4>  
 A>Note: 176-Glx may also be present  
 C:Comment: The first component of complement is a calcium-dependent complex of the th  
 lation of C1r (enzyme), C1s (proenzyme), and the other eight components of complem  
 (see PIR:C1HUQC) chain. Equimolar amounts of the A, B, and C chains are found after r  
 C:Genetics:  
 A:Gene: GDB:C1QB  
 A:Cross-references: GDB:119043; OMIM:120570  
 A:Map position: 1p36.3-1p34.1  
 C:Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal  
 C:Keywords: complement pathway; glycoprotein; heterodimer; hydroxyllysine; hydroxyprol  
 F:1-27/Domain: signal sequence #status predicted <SIG>  
 F:28-253/Product: complement subcomponent C1q chain B #status experimental <MNT>  
 F:33-116/Domain: collagenous, triple helix <COL>  
 F:123-249/Domain: complement C1q carboxyl-terminal homology <C1Q>  
 F:28/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status expert  
 F:31/Disulfide bonds: interchain (to chain A-26) #status experimental  
 F:35,38,41,53,56,65,83,86,101,104,107/Modified site: 4-hydroxyproline (Pro) #status e  
 F:59,62,77,92,98,110/Modified site: 5-hydroxylysine (Lys) #status experimental  
 F:59,62,98,110/Binding site: carbohydrate (Lys) (covalent) #status experimental

Query Match 27.3%; Score 362; DB 1; Length 253;  
 Best Local Similarity 36.9%; Pred. No. 1.7e-18;  
 Matches 90; Conservative 36; Mismatches 100; Indels 18; Gaps 6;

QY 4 LTVLLGLGLAAGSPPLDNDKIPSLCPGHPGLPGPHHSGQLPGRDGRDGPAGAPG 63  
 Db 13 LMLLLGLGLDIDISQGLSTGTPRALPGIPGIPGPRDGPGRGTGIGKGLPLADHG 72  
 QY 64 EKGEGRPGILPGPRGDPGRGEAP-----AGTPGAGCSVPPPSASAKRSESR 114  
 Db 73 EFGKGPDPGIPGNGKGYKPKRPGAPGAPRPGSGDYKKAQKIAFSATRT-IN 131  
 QY 115 VPPSDAPLPEDRVLVNEQGHYDAVTGKFTCOVPGVYFVAVHATVYRASLQFDLVKNGE- 173



Db 132 VLRRDQITREDVITNNMNNPEPSGKFTCKVPLDYTTTAAAS-SRGLTCVNLKGRGR 190  
QY 174 --SIASFQFPGGKPKPASLSGAMVRLPEDDQVQVGVGYIGIVASIKTDSFSGFL 231  
Db 191 AOKVVTFCDY--AYMTFQVTTGGVNLKLEQGENVFLO--ATDKNSILGMEGANSJFSGFL 246  
QY 232 VYSD 235  
Db 247 LFDP 250

## RESULT 14

SA49158  
complement protein C1q beta chain precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 16-Feb-1995 #sequence\_revision 12-May-1995 #text\_change 20-Aug-1999  
C:Accession: S49158  
R:Schwaeble, W.; Petry, F.; Loos, M.  
submitted to the EMBL Data Library, March 1993  
A:Description: cDNA cloning and expression of the mRNA encoding the B-chain of rat C1q.  
A:Reference number: S49158  
A:Accession: S49158  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-253 <SCH>  
A:Cross-references: EMBL:X71127; NID:g510191; PIDN:CAA50440.1; PID:g510192  
C:Superfamily: complement subcomponent C1q chain A; complement C1q carboxyl-terminal hom  
F:121-249/Domain: complement C1q carboxyl-terminal homology <C1q>

Query Match 27.2%; Score 360.5; DB 2; Length 253;  
Best Local Similarity 36.1%; Pred. No. 2,2e-18;  
Matches 95; Conservative 43; Mismatches 76; Indels 49; Gaps 13;

QY 1 MRPLVLLILGLAAGSPPLDNKIPSLC---PGHGLPPTGHHSGQLPGRDGDRG 57  
Db 9 LTPLL-LILLGL-----LHWSMAOSCTGSPGIPGVDPGIPGSDKPKPGIKGEG 61  
QY 58 APGAP-----GEGEGGRPGLP---GPRGDPGPRGEGAPGPTP---AGECVPPRSA 105  
Db 62 LPGLAGDHGELGEGKDGAGIPGIPGVGPKGAPGAPGPRGPKGSGSDYKATOKVA 121  
QY 106 FSAKRSERVPSPDAPLPFPRVLVNEQGHYDAVTKQVPGVYFAVNAHTVYRASLQ 165  
Db 122 FSALETVNSALRPNA--IRFEKIVTNVNDNPEPSGKFTCKVGLYFTTAAAS-SRGLNC 179  
QY 166 FDLVANG-----ESIASF-----FQFFGKPKPASLSGAMVRLPEDDQVQVQ-VGVG 212  
Db 180 VNIVGRDRDRMOKVLTFCDYAQNTEFYQ-----TTGGVVLTKLEQEVVHLQATDKN 230  
QY 213 DYIGIVASIKTDSFSGFLVYSD 235  
Db 231 SLGVEGA---NSITGFLFPD 250

## RESULT 15

SA15435  
collagen alpha 1(VIII) chain precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Aug-1999  
C:Accession: S15435  
R:Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Nimmiya, Y.  
Eur. J. Biochem. 197, 615-622, 1991  
A:Title: The complete primary structure of the human alpha-1(VIII) chain and assignment  
A:Reference number: S15435; MUID:91231001; PMID:2029894  
A:Accession: S15435  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-744 <MUR>  
A:Cross-references: EMBL:X57527; NID:g30081; PIDN:CAA40748.1; PID:g30082  
C:Genetics:  
A:Gene: GDB:COL8A1  
A:Cross-references: GDB:128104; OMIM:120251

A:Map position: 3q11.1-3q13.2  
C:Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homolog  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-744/Product: collagen alpha 1(VIII) chain #status predicted <MAT>  
F:21-117/Region: amino-terminal nonhelical  
F:118-571/Region: interrupted helical  
F:572-744/Region: carboxyl-terminal nonhelical  
F:617-743/Domain: complement C1q carboxyl-terminal homology <C1q>

Query Match 27.1%; Score 359; DB 2; Length 744;  
Best Local Similarity 33.0%; Pred. No. 8.5e-18;  
Matches 89; Conservative 33; Mismatches 86; Indels 62; Gaps 6;

QY 24 IPSLC--PGHGLPPTGHHSGQLPGRDGDRGAPGEGEGGRPGLP----- 74  
Db 475 VPLGLPKGPEIPDQGIQGGPPGIGIGSGSPGIPGPKGEPGLPGRPPGIGK 534  
QY 75 -----GPRGDPGPRGEGAPGPTP-----AGCS 99  
Db 535 PGVAGLHGPFGKPGALGFGQDGLPGRPPGPRGPRPAVMPTPPPGETLPDMGLGIDG 594  
QY 100 VPPRSAPFAKRSERVP-----PSDAPLPDRLVNEQGHYDAVTKGFT 144  
Db 595 VKPPHATGAKKKGNGCPAYEMPAFTAEILAPPPGVGPKFKLLYNGRQNYNPQTGIFT 654  
QY 145 QVPGVYFAVNAHTVYRASLQFDLYKNGESIA-SFQFFGKPKPASLSGAMVRLPEDD 203  
Db 655 CEVPGVYFAVNAHTVYRASLQFDLYKNGESIA-SFQFFGKPKPASLSGAMVRLPEDD 203  
QY 204 QVAVGVGVGYIGIVASIKTDSFSGFLVY 233  
Db 713 RYFLQMPBQAGLTAAGQYVHSSFSGYLLX 742

Search completed: June 13, 2003, 16:02:34  
Job time : 42 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: June 13, 2003, 15:59:26 ; Search time 15 Seconds

476.651 Million cell updates/sec

Title: US-09-944-944-42

Sequence: 1 MRPLLVLGLGLAGSPPLD.....DSTFSGFLVYSDWHSSPVFA 243

Scoring table: BLOSUM62

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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Database : Issued\_patents\_AA:\*

- 1: /cgn2\_6/ptodata1/1/aa/5A.COMB.pcp: \*
- 2: /cgn2\_6/ptodata1/1/aa/5B.COMB.pcp: \*
- 3: /cgn2\_6/ptodata1/1/aa/6A.COMB.pcp: \*
- 4: /cgn2\_6/ptodata1/1/aa/6B.COMB.pcp: \*
- 5: /cgn2\_6/ptodata1/1/aa/PTCUS.COMB.pcp: \*
- 6: /cgn2\_6/ptodata1/1/aa/Backfiles.pcp: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution..

## SUMMARIES

Result No.	Score	Query	Length	DB	ID	Description
1	1325	100.0	243	4	US-09-140-804-2	Sequence 2, Appli
2	1325	100.0	243	4	US-09-336-536-3	Sequence 3, Appli
3	1271	95.9	243	4	US-09-188-930-295	Sequence 295, Appli
4	1258	94.9	243	4	US-09-336-536-10	Sequence 10, Appli
5	1256	94.8	228	4	US-09-336-536-4	Sequence 4, Appli
6	1200	90.6	228	4	US-09-336-536-11	Sequence 11, Appli
7	675	50.9	128	4	US-09-336-536-7	Sequence 7, Appli
8	650	49.1	128	4	US-09-336-536-14	Sequence 14, Appli
9	433.5	32.7	247	4	US-08-463-911-2	Sequence 2, Appli
10	428.5	32.3	247	4	US-09-140-804-8	Sequence 8, Appli
11	428.5	32.3	247	4	US-09-118-408-3	Sequence 3, Appli
12	428.5	32.3	247	4	US-09-506-855-3	Sequence 3, Appli
13	424	32.0	244	2	US-08-463-911-7	Sequence 7, Appli
14	424	32.0	244	4	US-09-140-804-3	Sequence 3, Appli
15	424	32.0	244	4	US-09-140-804-3	Sequence 20, Appli
16	424	32.0	244	4	US-09-336-536-20	Sequence 2, Appli
17	417	31.5	231	4	US-09-530-423-1	Sequence 1, Appli
18	412	31.1	246	2	US-09-530-423-2	Sequence 2, Appli
19	399	30.1	294	4	US-08-463-911-4	Sequence 4, Appli
20	347	26.2	60	4	US-09-188-930-294	Sequence 294, Appli
21	324	24.5	60	4	US-09-336-536-6	Sequence 6, Appli
22	316	23.8	423	1	US-09-336-536-13	Sequence 13, Appli
23	316	23.8	423	2	US-08-383-744-2	Sequence 2, Appli
24	316	23.8	423	5	US-08-999-336-2	Sequence 2, Appli
25	314	23.7	245	4	PCT-US96-01427-2	Sequence 2, Appli
26	280.5	21.2	215	4	US-09-140-804-4	Sequence 4, Appli
27	277.5	20.9	185	2	US-09-140-804-5	Sequence 5, Appli
					US-08-463-911-3	Sequence 3, Appli

## ALIGNMENTS

28	276	20.8	236	4	US-09-140-804-6	Sequence 6, Appl
29	266.5	20.1	198	4	US-09-188-930-18	Sequence 138, Appl
30	257.5	19.4	130	4	US-09-485-316A-13	Sequence 13, Appl
31	251.5	19.0	130	4	US-09-485-316A-12	Sequence 12, Appl
32	243.5	18.4	130	4	US-09-485-316A-11	Sequence 11, Appl
33	240	18.1	161	4	US-09-415-351-3	Sequence 3, Appl
34	229.5	17.3	260	4	US-09-475-155-18	Sequence 178, Appl
35	229.5	17.3	261	4	US-09-118-408-2	Sequence 2, Appl
36	229.5	17.3	281	4	US-09-506-885-2	Sequence 2, Appl
37	228	17.2	684	1	US-08-555-665-12	Sequence 12, Appl
38	228	17.2	684	1	US-08-073-663-12	Sequence 12, Appl
39	224	16.9	228	4	US-09-219-849-38	Sequence 38, Appl
40	223	16.8	281	4	US-09-118-408-4	Sequence 44, Appl
41	223	16.8	281	4	US-09-506-885-44	Sequence 44, Appl
42	221	16.7	134	4	US-09-485-316A-9	Sequence 9, Appl
43	219.5	16.6	1057	3	US-08-931-820-4	Sequence 4, Appl
44	219.5	16.6	1078	4	US-08-963-823-21	Sequence 21, Appl
45	219.5	16.6	1078	4	US-09-506-881-21	Sequence 21, Appl

## RESULT 1

```

? Sequence2, Application US/09140804
? Patent No. 6197930
? GENERAL INFORMATION:
? APPLICANT: Sheppard, Paul O.
? APPLICANT: Humes, Jacqueline M.
? FILE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
? FILE REFERENCE: 97-49
? CURRENT APPLICATION NUMBER: US/09/140,804
? CURRENT FILING DATE: 1998-08-26
? EARLIER APPLICATION NUMBER: 60/056,983
? EARLIER FILING DATE: 1997-08-26
? NUMBER OF SEQ ID NOS: 47
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 2
? LENGTH: 243
? TYPE: PRT
? ORGANISM: Homo sapiens
? OS-09-140-804-2

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	Best Local Similarity	100.0%	Pred. No. 9.5e-114		
	Matches 243	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1 MRPLLVLVLLGLAGSPPLDNNKTPSLCPGHPGLPCTGTGHHGSGCLPGRDGRDGDGAPG	60			
	1 MRPLLVLVLLGLAGSPPLDNNKTPSLCPGHPGLPCTGTGHHGSGCLPGRDGRDGDGAPG	60			
QY	61 APGKGGGGRGRLGPRGGDPGPRGEGAGPCTGPAGGCSVPPRSAFSAKRSESRVPPSD	120			
Db	61 APGKGGGGRGRLGPRGGDPGPRGEGAGPCTGPAGGCSVPPRSAFSAKRSESRVPPSD	120			
QY	121 APLEFDDVLVNEGCHYDAVTGKFTCCQVPGVYYPFVHATVYRASLOFEDLVKNGESTASFQ	180			
Db	121 APLEFDDVLVNEGCHYDAVTGKFTCCQVPGVYYPFVHATVYRASLOFEDLVKNGESTASFQ	180			
QY	181 FFGGMPKPRASLSGGAMVRLPEDDVWVVOVGADYIGIYASIKTDSFSGFLVYSPMHSP	240			
Db	181 FFGGMPKPRASLSGGAMVRLPEDDVWVVOVGADYIGIYASIKTDSFSGFLVYSPMHSP	240			
QY	241 VFA 243				
Db	241 VFA 243				

```
;; GENERAL INFORMATION:
;; APPLICANT: Leidy, K.
;; APPLICANT: McKay, C.
;; APPLICANT: Bossone, S.
;; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
;; FILE REFERENCE: 7853-144
;; CURRENT APPLICATION NUMBER: US/09/336, 536
;; CURRENT FILING DATE: 1999-06-18
;; NUMBER OF SEQ ID NOS: 75
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO: 3
;; LENGTH: 243
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; US-09-336-536-3
```

```
Query Match          100.0%; Score 1325; DB 4; Length 243;
Best Local Similarity 100.0%; Pred. No. 9.5e-114;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MRPLVLLGLAGSPPLDNDKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGPAG 60
  |||
DB 1 MRPLVLLGLAGSPPLDNDKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGPAG 60
QY 61 APGEKGGGRGRLPGPRGDPGPRGEGAGPAGTGPAGECVPPRSASFSAKRSSESVPPSD 120
  |||
DB 61 APGEKGGGRGRLPGPRGDPGPRGEGAGPAGTGPAGECVPPRSASFSAKRSSESVPPSD 120
QY 121 APLEPDRVLYNEQGHYAVTGKFTCOVPGVYFFAVHATVYRASIQFDLVKNGESIASFFQ 180
  |||
DB 121 APLEPDRVLYNEQGHYAVTGKFTCOVPGVYFFAVHATVYRASIQFDLVKNGESIASFFQ 180
QY 181 FFGGMPKPRASISGGAMVRLPEPDQVWVQVGVGDYIGIYASIKTSTSGFLVYSDMHSPP 240
  |||
DB 181 FFGGMPKPRASISGGAMVRLPEPDQVWVQVGVGDYIGIYASIKTSTSGFLVYSDMHSPP 240
QY 241 VFA 243
  |||
DB 241 VFA 243
```

```
RESULT 3
US-09-188-930-295
; Sequence 295, Application US/09188930A
; Patent No. 6150502
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James Greg
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE REFERENCE: 11000.1011c1
; CURRENT APPLICATION NUMBER: US/09/188, 930A
; CURRENT FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 295
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Rat
; US-09-188-930-295
```

```
Query Match          95.9%; Score 1271; DB 4; Length 243;
Best Local Similarity 95.1%; Pred. No. 8.2e-109;
Matches 231; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 1 MRPLVLLGLAGSPPLDNDKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGPAG 60
  |||
DB 1 MRPLVLLGLAGSPPLDNDKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGPAG 60
QY 61 APGEKGGGRGRLPGPRGDPGPRGEGAGPAGTGPAGECVPPRSASFSAKRSSESVPPSD 120
```

```
|||||
DB 61 APGEKGGGRGRLPGPRGDPGPRGEGAGPAGTGPAGECVPPRSASFSAKRSSESVPPSD 120
QY 121 APLEPDRVLYNEQGHYAVTGKFTCOVPGVYFFAVHATVYRASIQFDLVKNGESIASFFQ 180
  |||
DB 121 APLEPDRVLYNEQGHYAVTGKFTCOVPGVYFFAVHATVYRASIQFDLVKNGESIASFFQ 180
QY 181 FFGGMPKPRASISGGAMVRLPEPDQVWVQVGVGDYIGIYASIKTSTSGFLVYSDMHSPP 240
  |||
DB 181 FFGGMPKPRASISGGAMVRLPEPDQVWVQVGVGDYIGIYASIKTSTSGFLVYSDMHSPP 240
QY 241 VFA 243
  |||
DB 241 VFA 243
```

```
RESULT 4
US-09-336-536-10
; Sequence 10, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leidy, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336, 536
; CURRENT FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 10
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-336-536-10
```

```
Query Match          94.9%; Score 1258; DB 4; Length 243;
Best Local Similarity 93.8%; Pred. No. 1.3e-107;
Matches 228; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
```

```
QY 1 MRPLVLLGLAGSPPLDNDKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGPAG 60
  |||
DB 1 MRPLVLLGLAGSPPLDNDKIPSLCPGHPGLPGTPGHHGSGGLPGRDGRDGPAG 60
QY 61 APGEKGGGRGRLPGPRGDPGPRGEGAGPAGTGPAGECVPPRSASFSAKRSSESVPPSD 120
  |||
DB 61 APGEKGGGRGRLPGPRGDPGPRGEGAGPAGTGPAGECVPPRSASFSAKRSSESVPPSD 120
QY 121 APLEPDRVLYNEQGHYAVTGKFTCOVPGVYFFAVHATVYRASIQFDLVKNGESIASFFQ 180
  |||
DB 121 APLEPDRVLYNEQGHYAVTGKFTCOVPGVYFFAVHATVYRASIQFDLVKNGESIASFFQ 180
QY 181 FFGGMPKPRASISGGAMVRLPEPDQVWVQVGVGDYIGIYASIKTSTSGFLVYSDMHSPP 240
  |||
DB 181 FFGGMPKPRASISGGAMVRLPEPDQVWVQVGVGDYIGIYASIKTSTSGFLVYSDMHSPP 240
QY 241 VFA 243
  |||
DB 241 VFA 243
```

```
RESULT 5
US-09-336-536-4
; Sequence 4, Application US/09336536
; Patent No. 6406884
; GENERAL INFORMATION:
; APPLICANT: Leidy, K.
; APPLICANT: McKay, C.
; APPLICANT: Bossone, S.
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
; FILE REFERENCE: 7853-144
; CURRENT APPLICATION NUMBER: US/09/336, 536
; CURRENT FILING DATE: 1999-06-18
```

NUMBER OF SEQ ID NOS: 75  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 4  
LENGTH: 228  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-336-536-4

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.8e-107;  
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SPPLDNNKIPSLCPGHPGLPTGPHHSGGLPGRDGRDGDAPGAPGEGGGRPLPG 75  
DB 1 SPPLDNNKIPSLCPGHPGLPTGPHHSGGLPGRDGRDGDAPGAPGEGGGRPLPG 60  
QY 76 PGDGPGRGEAGPAPPTGAGGECVPPRSASFSAKRSSESVPPSDAPLPFDRLVNEQGH 135  
DB 61 PGDGPGRGEAGPAPPTGAGGECVPPRSASFSAKRSSESVPPSDAPLPFDRLVNEQGH 120  
QY 136 YDAVTKGFTCOVPGYFFAVHATYVRASLQFDLVNKGESIASFFQFGGMPKPAISLSGA 195  
DB 121 YDAVTKGFTCOVPGYFFAVHATYVRASLQFDLVNKGESIASFFQFGGMPKPAISLSGA 180  
QY 196 MYRLPEPDQVWVQVGVGDIYIGIYASIKTDSTFSGFLVYSDMHSSPVFA 243  
DB 181 MYRLPEPDQVWVQVGVGDIYIGIYASIKTDSTFSGFLVYSDMHSSPVFA 228

RESULT 6  
US-09-336-536-11  
Sequence 11, Application US/09336536  
Patent No. 6406884

GENERAL INFORMATION:  
APPLICANT: Leiby, K.  
APPLICANT: McKay, C.  
APPLICANT: Bossone, S.  
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
FILE REFERENCE: 7853-144  
CURRENT APPLICATION NUMBER: US/09/336,536  
NUMBER OF SEQ ID NOS: 75  
CURRENT FILING DATE: 1999-06-18  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 11  
LENGTH: 228  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-336-536-11

Query Match  
Best Local Similarity 94.7%; Pred. No. 2.4e-102;  
Matches 216; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 16 SPPLDNNKIPSLCPGHPGLPTGPHHSGGLPGRDGRDGDAPGAPGEGGGRPLPG 75  
DB 1 SPPLDNNKIPSLCPGHPGLPTGPHHSGGLPGRDGRDGDAPGAPGEGGGRPLPG 60  
QY 76 PGDGPGRGEAGPAPPTGAGGECVPPRSASFSAKRSSESVPPSDAPLPFDRLVNEQGH 135  
DB 61 PGDGPGRGEAGPAPPTGAGGECVPPRSASFSAKRSSESVPPSDAPLPFDRLVNEQGH 120  
QY 136 YDAVTKGFTCOVPGYFFAVHATYVRASLQFDLVNKGESIASFFQFGGMPKPAISLSGA 195  
DB 121 YDAVTKGFTCOVPGYFFAVHATYVRASLQFDLVNKGESIASFFQFGGMPKPAISLSGA 180  
QY 196 MYRLPEPDQVWVQVGVGDIYIGIYASIKTDSTFSGFLVYSDMHSSPVFA 243  
DB 181 MYRLPEPDQVWVQVGVGDIYIGIYASIKTDSTFSGFLVYSDMHSSPVFA 228

RESULT 7  
US-09-336-536-7  
Sequence 7, Application US/09336536

Patent No. 6406884  
GENERAL INFORMATION:  
APPLICANT: Leiby, K.  
APPLICANT: McKay, C.  
APPLICANT: Bossone, S.  
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
FILE REFERENCE: 7853-144  
CURRENT APPLICATION NUMBER: US/09/336,536  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 7  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-336-536-7

Query Match  
Best Local Similarity 100.0%; Pred. No. 1.2e-54;  
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 105 AFSAKRSSESVPPSDAPLPFDRLVNEQGHDAVTKGFTCOVPGYFFAVHATYVRASL 164  
DB 1 AFSAKRSSESVPPSDAPLPFDRLVNEQGHDAVTKGFTCOVPGYFFAVHATYVRASL 60  
QY 165 QFDLVNKGESIASFFQFGGMPKPAISLSGAMVRLPEPDQVWVQVGVGDIYIGIYASIKTD 224  
DB 61 QFDLVNKGESIASFFQFGGMPKPAISLSGAMVRLPEPDQVWVQVGVGDIYIGIYASIKTD 120  
QY 225 STFSGFLV 232  
DB 121 STFSGFLV 128

RESULT 8  
US-09-336-536-14  
Sequence 14, Application US/09336536  
Patent No. 6406884

GENERAL INFORMATION:  
APPLICANT: Leiby, K.  
APPLICANT: McKay, C.  
APPLICANT: Bossone, S.  
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
FILE REFERENCE: 7853-144  
CURRENT APPLICATION NUMBER: US/09/336,536  
NUMBER OF SEQ ID NOS: 75  
CURRENT FILING DATE: 1999-06-18  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO 14  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-336-536-14

Query Match  
Best Local Similarity 94.5%; Pred. No. 2.3e-52;  
Matches 121; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 105 AFSAKRSSESVPPSDAPLPFDRLVNEQGHDAVTKGFTCOVPGYFFAVHATYVRASL 164  
DB 1 AFSAKRSSESVPPSDAPLPFDRLVNEQGHDAVTKGFTCOVPGYFFAVHATYVRASL 60  
QY 165 QFDLVNKGESIASFFQFGGMPKPAISLSGAMVRLPEPDQVWVQVGVGDIYIGIYASIKTD 224  
DB 61 QFDLVNKGESIASFFQFGGMPKPAISLSGAMVRLPEPDQVWVQVGVGDIYIGIYASIKTD 120  
QY 225 STFSGFLV 232  
DB 121 STFSGFLV 128

RESULT 9  
US-08-463-911-2



OY 166 FDLYKNGESIASFQFGGMPKPSASGAMVRLPEDDQVWVOY-GVGDYIGIYASIKTD 224  
| | : : : : | | : : : : | | : : : : | | : : : : |  
DB 176 VSLRKKDKAVLFTTDQIOE-KNVDAQSGSVLLHLEVGQVWLQYVGGDGHGLADNVND 234  
OY 225 STFGFLYSD 235  
| | : : : : | | : : : : | | : : : : | | : : : : |  
DB 235 STFGFLYHD 245

RESULT 12  
US-09-506-855-3  
; Sequence 3, Application US/09506855  
; Patent No. 6448221  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Lasser, Gerald W.  
; APPLICANT: Bishop, Paul D.  
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND  
; FILE REFERENCE: 99-12  
; CURRENT APPLICATION NUMBER: US/09/506,855  
; CURRENT FILING DATE: 2000-02-17  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-506-855-3

Query Match 32.3%; Score 428.5; DB 4; Length 247;  
Best Local Similarity 40.2%; Pred. No. 9.7e-32;  
Matches 101; Conservative 32; Mismatches 93; Indels 25; Gaps 8;

OY 1 MRPLVLLLL-LGLAASPLLDNKKIPSLCPHSG- - - -LPQTPGHHSQGLPRGRDGD 54  
| | : : : : | | : : : : | | : : : : | | : : : : |  
DB 4 LQALLFLILPSHAEDVDYTEELAPALVPPPKGICAGMAGIPGHPGHNTPGRDGD- 62  
OY 55 RDGAGARGEGEGRRPLPGRDPRGRGAGPAGP- - - - -TPPAGECSVPPPSA 105  
| | : : : : | | : : : : | | : : : : | | : : : : |  
DB 63 - - - - -GTPEGEGEGDAGLLGPKGTGVMTGAGPGRFPOTPRKGEPEAAVMTSA 117  
OY 106 FSAKSESRRPPSPDAPLPFDRLVNEQGHDAVTKFTCOVPGVYPAVATVYRASLO 165  
| | : : : : | | : : : : | | : : : : | | : : : : |  
DB 118 FSV-GLERYTVIP-NVPIRTFKIFYNQNMHTDGSIGKYYCAIPGLYIYSHIYYMAKYK 175  
OY 166 FDLYKNGESIASFQFGGMPKPSASGAMVRLPEDDQVWVOY-GVGDYIGIYASIKTD 224  
| | : : : : | | : : : : | | : : : : | | : : : : |  
DB 176 VSLRKKDKAVLFTTDQIOE-KNVDAQSGSVLLHLEVGQVWLQYVGGDGHGLADNVND 234  
OY 225 STFGFLYSD 235  
| | : : : : | | : : : : | | : : : : | | : : : : |  
DB 235 STFGFLYHD 245

RESULT 13  
US-08-463-911-7  
; Sequence 7, Application US/08463911  
; Patent No. 5869330  
; GENERAL INFORMATION:  
; APPLICANT: Scherer, Philipp E.  
; APPLICANT: Lodish, Harvey F.  
; TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Millita Drive  
; CITY: Lexington  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/463,911  
FILING DATE:  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WHI95-05  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-463-911-7

Query Match 32.0%; Score 424; DB 2; Length 244;  
Best Local Similarity 40.5%; Pred. No. 2.5e-31;  
Matches 106; Conservative 26; Mismatches 72; Indels 58; Gaps 10;

OY 6 VLLIGLAAASPLLDNKKIPSLCPH- - - - -PG- - - - -LPQTPGHHSQ 44  
| | : : : : | | : : : : | | : : : : | | : : : : |  
DB 7 VLLILAL- - - - -PGHDETTTQGGVLLPLPKGACGTGMAGIPGHPGN 50  
OY 45 GLPGRDGDGRDAGAPARGEGEGRRPLPGRD- - - - -PGRGEGAPRGPRPA 95  
| | : : : : | | : : : : | | : : : : | | : : : : |  
DB 51 GAPGRDGD- - - - -GTPEGEGEGDPELIGPKDIGETGVPAAGPGRPGIGRKEP 104  
OY 96 GECVPPRSASRSRPPSPDAPLPFDRLVNEQGHDAVTKFTCOVPGVYPAV 155  
| | : : : : | | : : : : | | : : : : | | : : : : |  
DB 105 GEGAVVYSASFV-GLERYTVIP-NVPIRTFKIFYNQNMHTDGSIGKYYCAIPGLYIY 162  
OY 156 HATVYRASLOFDLYKNGES-IASFQFGGMPKPSASGAMVRLPEDDQVWVOY-GVGD 213  
| | : : : : | | : : : : | | : : : : | | : : : : |  
DB 163 HITVYMKDVKYSLEFKKRAMLFTYDYOENNVDQ- - -SGSVLLHLEVGQVWLQYVGGEGE 220  
OY 214 YIGIYASIKTSTFGFLYSD 235  
| | : : : : | | : : : : | | : : : : | | : : : : |  
DB 221 RNLGYADNDSTFGFLYHD 242

RESULT 14  
US-09-140-804-3  
; Sequence 3, Application US/09140804  
; Patent No. 6197930  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Humes, Jacqueline M.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
; FILE REFERENCE: 97-49  
; CURRENT APPLICATION NUMBER: US/09/140,804  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: 60/056,983  
; EARLIER FILING DATE: 1997-08-26  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 244  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-140-804-3

Query Match 32.0%; Score 424; DB 4; Length 244;  
Best Local Similarity 40.5%; Pred. No. 2.5e-31;  
Matches 106; Conservative 26; Mismatches 72; Indels 58; Gaps 10;

```
OY 6 VLLLLGLAAGSPPLDNNKIPSLCPGH-----PG-----LPDTPGHHSQ 44
    ||||| |
Db 7 VLLLLAL-----PGHDETTTGGPGLPLPKGACTGMMAGITPGHPGN 50
OY 45 GLPGRDGRDGDAPGAPGEGGRRGLPGRGD-----PGPRGEGAPGPTGPA 95
    ||||| |
Db 51 GAPGRDGRD-----GTPGEGKEGKDPGLIGPKDIGETGVPAEGPRGPGIQRKGP 104
OY 96 GECVPPRSAPSAKRSRVPSPDAPLPFDRLVNEQGHYDAVTKFTCOVPGVYFAY 155
    ||: ||||| |
Db 105 GEGAYVYRSASFV-GLETYYTIP-NMPIRFTKIIFYNOQNHYDGSSTGKFCNIPGLYFAY 162
OY 156 HATVYRASLOFDLVKNES-IASFFQFFGWPKPASLSGAMVRLPEPDQVYQV-GVGD 213
    ||||| |
Db 163 HITVYMDVKVSLFKKDKAMLFYDQYQENNVDQ--SGSVLLHLEVGDQVWLQVYGE 220
OY 214 YIGIYASIKTDSFSGFLYSD 235
    ||: ||||| |
Db 221 RNLGYADNDNDSTFTGFLYHD 242
```

## RESULT 15

```
US-09-336-536-20
: Sequence 20 Application US/09336536
: Patent No. 6406884
: GENERAL INFORMATION:
: APPLICANT: Leidy, K.
: APPLICANT: McKay, C.
: APPLICANT: Bosson, S.
: TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
: FILE REFERENCE: 7853-144
: CURRENT APPLICATION NUMBER: US/09/336, 536
: CURRENT FILING DATE: 1999-06-18
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 20
: LENGTH: 244
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-336-536-20
```

## Query Match

37.0%; Score 424; DB 4; Length 244;

Best Local Similarity 40.5%; Pred. No. 2.5e-31;

Matches 106; Conservative 26; Mismatches 72; Indels 58; Gaps 10;

```
OY 6 VLLLLGLAAGSPPLDNNKIPSLCPGH-----PG-----LPDTPGHHSQ 44
    ||||| |
Db 7 VLLLLAL-----PGHDETTTGGPGLPLPKGACTGMMAGITPGHPGN 50
OY 45 GLPGRDGRDGDAPGAPGEGGRRGLPGRGD-----PGPRGEGAPGPTGPA 95
    ||||| |
Db 51 GAPGRDGRD-----GTPGEGKEGKDPGLIGPKDIGETGVPAEGPRGPGIQRKGP 104
OY 96 GECVPPRSAPSAKRSRVPSPDAPLPFDRLVNEQGHYDAVTKFTCOVPGVYFAY 155
    ||: ||||| |
Db 105 GEGAYVYRSASFV-GLETYYTIP-NMPIRFTKIIFYNOQNHYDGSSTGKFCNIPGLYFAY 162
OY 156 HATVYRASLOFDLVKNES-IASFFQFFGWPKPASLSGAMVRLPEPDQVYQV-GVGD 213
    ||||| |
Db 163 HITVYMDVKVSLFKKDKAMLFYDQYQENNVDQ--SGSVLLHLEVGDQVWLQVYGE 220
OY 214 YIGIYASIKTDSFSGFLYSD 235
    ||: ||||| |
Db 221 RNLGYADNDNDSTFTGFLYHD 242
```

Search completed: June 13, 2003, 16:02:56  
Job time : 17 secs



Query Match	94.8%;	Score 1305;	DB 4;	Length 1347;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1305;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	44	AGGAGCGAACACAGGACTGGGGGTGACGGCAGGAGGAGGGGCGCCCTGGCCGGGGAGAAAGCG	103	
Db	15	AGGAGCGAACACAGGACTGGGGGTGACGGCAGGAGGAGGGGCGCCCTGGCCGGGGAGAAAGCG	74	
QY	104	CGGGGGCTGGAGGCACACCAACTGGAGGGGTCCGGAGTACGACGCGCCCGGAAAGAGGCCA	163	
Db	75	CGGGGGCTGGAGGCACACCAACTGGAGGGGTCCGGAGTACGACGCGCCCGGAAAGAGGCCA	134	
QY	164	TCGGGGAGCCCGGAGGGGGGACTGGAGAAAGAACCCGGCGTTCGGGGTCCCGATCCCAAGC	223	
Db	135	TCGGGGAGCCCGGAGGGGGGACTGGAGAAAGAACCCGGCGTTCGGGGTCCCGATCCCAAGC	194	
QY	224	GCTATTAGAGCCACTCTCTGCTCTGCTCTCTGGGCGTGGGCGGGGCTCGCCCCACTTG	283	
Db	195	GCTATTAGAGCCACTCTCTGCTCTGCTCTCTGGGCGTGGGCGGGGCTCGCCCCACTTG	254	
QY	284	GACACACAACAAGATCCCAAGCCTTGCCCGGGGGCAACCCCGGCGCTTCACAGCACAGCGCGGC	343	
Db	255	GACACACAACAAGATCCCAAGCCTTGCCCGGGGGCAACCCCGGCGCTTCACAGCACAGCGCGGC	314	
QY	344	CACCATGGACGCCAGGGGCTTGGCCGGGGCGCGATGGCGCGACGCGCGCGAGCGGGCGGCC	403	



QY	897	ACAGACACTTCTCCGGATTTCTGGGTACTCCGACTGGCACAGCTCCCAGCTTTGCTT	956
Db	857	ACAGACACTTCTCCGGATTTCTGGGTACTCCGACTGGCACAGCTCCCAAGCTTTGCTT	916
QY	957	AGTGCCACTGCAAGTAGAGCTCATGCTCTCACTCCTAGAAAGAGAGGTGTGAGGCTGACA	1011
Db	917	AGTGCCCACTGCAAGTAGAGCTCATGCTCTCACTCCTAGAAAGAGAGGTGTGAGGCTGACA	976
QY	1017	ACCAAGTCATCCAGAGAGGGCTGGCCCCCTGGATATTGTGATGACTAGGAGGTGGGG	107
Db	977	ACCGTGTATCCAGAGAGGGCTGGCCCCCTGGAAATATTGTGATGACTAGGAGGTGGGG	1033
QY	1077	TAGAGCACTGCCGTCGTCGTCGTCGGCAAGAAATGGGAAACTGGCTGTCCTCGAATCAGG	1133
Db	1037	TAGAGCACTGCCGTCGTCGTCGTCGGCAAGAAATGGGAAACTGGCTGTCCTCGATCAGG	1099
QY	1137	TCTGGCAGCATGGGGCAGTGGCTGGATTCTCCGCCAAGACCAGAGAGAGTGTCTGTCTG	1199
Db	1097	TCTGGCAGCATGGGGCAGTGGCTGGATTCTCCGCCAAGACCAGAGAGAGTGTCTGTCTG	1155
QY	1197	GCAGTGTAAATCCCCCAAGTGCCTGTGTGTCACAGAGACCACGGTGGGGTCTCTCTCT	1255
Db	1157	GCAGTGTAAATCCCCCAAGTGTCTGTGTGTCACAGAGACCACCGTGGGGTCTCTCTCT	1211
QY	1257	GGTCCCTGCTTCTGTGATCCTCCCAACCCCTCTGCTCTGTGGGCGGGGCCCTTTTCT	1311
Db	1217	GGTCCCTGCTTCTGTGATCCTCCCAACCCCTCTGCTCTGTGGGCGGGGCCCTTTTCT	1277
QY	1317	CAGAGATCACTCATATAAACCTAAGAACCCCTC	1347
Db	1277	CAGAGATCACTCATATAAACCTAAGAACCCCTC	1307

```

RESULT 3
US-09-336-536-2
: Sequence 2, Application US/09336536
: Patent No. 6406884
: GENERAL INFORMATION:
: APPLICANT: Leiby, K.
: APPLICANT: McKay, C.
: APPLICANT: Bossons, S.
: TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
: FILE REFERENCE: 7853-144
: CURRENT APPLICATION NUMBER: US/09/336,536
: CURRENT FILING DATE: 1999-06-18
: NUMBER OF SEQ ID NOS: 75
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 728
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-09-336-536-2

```

Query Match	44.28;	Score 608;	DB 4;	Length 728;
Best Local Similarity	99.98;	Pred. No. 4.9e-236;		
Matches 728; Conservative	0;	Mismatches 0;	Indels 1;	Gaps 1;

[illegible]

QY	467	GGGCGCGAGAGAGAGCGGGACCCGCGGGGCCACCGGGCCCTCCGGGAGTGTCTGGTg	526
Db	240	GGGCGCGAGAGAGAGCGGGACCCCGGGGCCACCGGGCCCTCCGGGAGTGTCTGGTg	299
QY	527	CCTCGGCGATCCGCTTCAGGGGSCAAGGGCTCCGAGGCGGGGTGCTCGGCGCTGAG	586
Db	300	CCTCGGCGATCCGCTTCAGGGGSCAAGGGCTCCGAGGCGGGGTGCTCGGCGCTGAG	359
QY	587	GCACCCCTTGCCCTTGACCGCGCGTGTGTGTAACGAGCAGGACATTACGACGCGCTAC	646
Db	360	GCACCCCTTGCCCTTGACCGCGCTGTGTGTAACGAGCAGGACATTACGACGCGCTAC	419
QY	647	GGCAAGTTACCTGCGAGGTGCTGGGGTCTACTACTTGCGCGTCATGCCACCGTCTAC	706
Db	420	GGCAAGTTACCTGCGAGGTGCTGGGGTCTACTACTTGCGCGTCATGCCACCGTCTAC	479
QY	707	CGGGCCAGCTGCATTTGATCTGTGTGAAGAAATGGCGAAATCCATTGCTCTTCTCCAG	766
Db	480	CGGGCCAGCTGCATTTGATCTGTGTGAAGAAATGGCGAAATCCATTGCTCTTCTCCAG	539
QY	767	TTTTTCGGGGGGTGGCCCCAAGCCAGCCTCGCTCGGGGGGGGCCATTGGTGAAGGCTGGAG	826
Db	540	TTTTTCGGGGGGTGGCCCCAAGCCAGCCTCGCTCGGGGGGGGCCATTGGTGAAGGCTGGAG	599
QY	827	CCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGATCTACATTGGCATCTTATGGCAC	886
Db	600	CCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGATCTACATTGGCATCTTATGGCAC	659
QY	887	ATCAAGACAGACAGCACCTTCTCCGGATTGTGTGTACTCCGACTGGACAGCTCCCA	946
Db	660	ATCAAGACAGACAGCACCTTCTCCGGATTGTGTGTACTCCGACTGGACAGCTCCCA	719
QY	947	GTCTTGTCT 955	
Db	720	GTCTTGTCT 728	

```

RESULT 4
US-09-140-804-28
: Sequence 28, Application US/09140804
: Patent No. 6197930
: GENERAL INFORMATION:
: APPLICANT: Sheppard, Paul O.
: APPLICANT: Humes, Jacqueline M.
: TITLE OF INVENTION: ADIPOCTE-SPECIFIC PROTEIN HOMOLOGS
: FILE REFERENCE: 97-49
: CURRENT APPLICATION NUMBER: US/09/140,804
: CURRENT FILING DATE: 1998-08-26
: EARLIER APPLICATION NUMBER: 60/056,983
: EARLIER FILING DATE: 1997-08-26
: NUMBER OF SEQ ID NOS: 47
: SOFTWARE: FASTSEQ For Windows Version 3.0
: SEQ ID NO 28
: LENGTH: 144
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: N-terminal untagged linker
US-09-140-804-28

```

Query Match	5.3%	Score 73	DB 4	Length 144
Best Local Similarity	100.0%	Pred. No. 1.2e-20		
Matches 73; Conservative	0	Mismatches 0	Indels 0	Gaps 0

Oy	280	ACGAGGACGAACAATAATCCCAAGCCTCTGCCCCGGGGGACCCCGGCGCTTCCAGGCACAGCC	339
Db	72	ACTGAGCAGCAATAAATCCCAAGCCTCTGCCCCGGGGACCCCGGCGCTTCCAGGCACAGCC	131
Oy	340	GGGCGCACCATGGC	352
Db	132	GGGCGCACCATGGC	144

RESULT 5  
US-09-140-804-29  
; Sequence 29, Application US/09140804  
; Patent No. 6197930  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Humes, Jacqueline M.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
; FILE REFERENCE: 97-49  
; CURRENT APPLICATION NUMBER: US/09/140,804  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: 60/056,983  
; EARLIER FILING DATE: 1997-08-26  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 29  
; LENGTH: 144  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: N-terminal Glu-Glu tag linker  
US-09-140-804-29

Query Match 5.2%; Score 72; DB 4; Length 144;  
Best Local Similarity 100.0%; Pred. No. 3.2e-20;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 281 CTGAGCAGACAAGATCCAGCCTGCGCGGGGACCCGGGCTTCAGGACGCGG 340  
DB 73 CTGAGCAGACAAGATCCAGCCTGCGCGGGGACCCGGGCTTCAGGACGCGG 132

OY 341 GGGCACCATTGCG 352  
DB 133 GGGCACCATTGCG 144

RESULT 6  
US-09-140-804-31  
; Sequence 31, Application US/09140804  
; Patent No. 6197930  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Humes, Jacqueline M.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
; FILE REFERENCE: 97-49  
; CURRENT APPLICATION NUMBER: US/09/140,804  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: 60/056,983  
; EARLIER FILING DATE: 1997-08-26  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 31  
; LENGTH: 144  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: C-terminal Glu-Glu tag linker  
US-09-140-804-31

Query Match 5.2%; Score 72; DB 4; Length 144;  
Best Local Similarity 100.0%; Pred. No. 3.2e-20;  
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 884 AGCATCAGACAGACAGACCTTCGCGATTCTGTGATCTGACCTCCAGCTGCGACAGCTCC 943  
DB 1 AGCATCAGACAGACAGACCTTCGCGATTCTGTGATCTGACCTCCAGCTGCGACAGCTCC 60  
OY 944 CCAAGCTTTGCT 955  
DB 61 CCAAGCTTTGCT 72

RESULT 7  
US-09-140-804-30  
; Sequence 30, Application US/09140804  
; Patent No. 6197930  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Humes, Jacqueline M.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
; FILE REFERENCE: 97-49  
; CURRENT APPLICATION NUMBER: US/09/140,804  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: 60/056,983  
; EARLIER FILING DATE: 1997-08-26  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 30  
; LENGTH: 147  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: C-terminal untagged linker  
US-09-140-804-30

Query Match 3.9%; Score 54; DB 4; Length 147;  
Best Local Similarity 100.0%; Pred. No. 5.5e-13;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 905 TTCTCCGATTCTGTGATCTGCTGACTGCGACTGCGACAGCTCCAGCTTTGCTTAG 958  
DB 22 TTCTCCGATTCTGTGATCTGCTGACTGCGACTGCGACAGCTCCAGCTTTGCTTAG 75

RESULT 8  
US-09-140-804-35/c  
; Sequence 35, Application US/09140804  
; Patent No. 6197930  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Humes, Jacqueline M.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
; FILE REFERENCE: 97-49  
; CURRENT APPLICATION NUMBER: US/09/140,804  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: 60/056,983  
; EARLIER FILING DATE: 1997-08-26  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 35  
; LENGTH: 51  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC15273  
US-09-140-804-35

Query Match 3.7%; Score 51; DB 4; Length 51;  
Best Local Similarity 100.0%; Pred. No. 1e-11;  
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 300 CCAAGCTTTGCTGCGCGGACCCGCGCTTCAGGACGCGGGGCGCAACGATG 350  
DB 51 CCAAGCTTTGCTGCGCGGACCCGCGCTTCAGGACGCGGGGCGCAACGATG 1

RESULT 9  
US-09-140-804-43/c  
; Sequence 43, Application US/09140804  
; Patent No. 6197930  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Humes, Jacqueline M.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
; FILE REFERENCE: 97-49

```
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC15274
US-09-140-804-43
```

```
Query Match          3.7%; Score 51; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      300 CCAGCCTCTGCCCGGGGACCCCGGCTTCCAGGACGCGGCGCCACCATG 350
          |||
Db       51 CCAGCCTCTGCCCGGGGACCCCGGCTTCCAGGACGCGGCGCCACCATG 1
```

```
RESULT 10
US-09-140-804-36
; Sequence 36, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC15273
US-09-140-804-36
```

```
Query Match          3.6%; Score 50; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      886 CATCAGACAGACAGACCTTCTCCGATTTCTGCTGATCTCCGACTGGC 935
          |||
Db       1 CATCAGACAGACAGACCTTCTCCGATTTCTGCTGATCTCCGACTGGC 50
```

```
RESULT 11
US-09-140-804-44
; Sequence 44, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 44
; LENGTH: 50
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC15273
US-09-140-804-44
```

```
Query Match          3.6%; Score 50; DB 4; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      886 CATCAGACAGACAGACCTTCTCCGATTTCTGCTGATCTCCGACTGGC 935
          |||
Db       1 CATCAGACAGACAGACCTTCTCCGATTTCTGCTGATCTCCGACTGGC 50
```

```
RESULT 12
US-09-140-804-37
; Sequence 37, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC15724
US-09-140-804-37
```

```
Query Match          3.3%; Score 45; DB 4; Length 65;
Best Local Similarity 100.0%; Pred. No. 2.6e-09;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      914 TTCTGTGTACTCCGACTGGACAGCTCCCGAGTCTTGTGTTAG 958
          |||
Db       1 TTCTGTGTACTCCGACTGGACAGCTCCCGAGTCTTGTGTTAG 45
```

```
RESULT 13
US-09-140-804-45
; Sequence 45, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; EARLIER FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 45
; LENGTH: 68
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide ZC15267
US-09-140-804-45
```

```
Query Match          3.1%; Score 43; DB 4; Length 68;
Best Local Similarity 100.0%; Pred. No. 1.6e-08;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 913 ATTTCTGTGTCGACGTCGACGACAGCTCCCGAGCTCTTGTCT 955  
|||||  
Db 1 ATTTCTGTGTCGACGTCGACGACAGCTCCCGAGCTCTTGTCT 43

RESULT 14  
US-09-140-804-42/C  
; Sequence 42, Application US/09140804  
; Patent No. 6197930  
; GENERAL INFORMATION:  
; APPLICANT: Humes, Jacqueline M.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
; FILE REFERENCE: 97-49  
; CURRENT APPLICATION NUMBER: US/09/140,804  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: 60/056,983  
; EARLIER FILING DATE: 1997-08-26  
; NUMBER OF SEQ. ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 42  
; LENGTH: 63  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC15269  
US-09-140-804-42

Query Match 2.8%; Score 39; DB 4; Length 63;  
Best Local Similarity 100.0%; Pred. No. 6.7e-07;  
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 280 ACTGAGACACACAGATCCCGACGCTCTGCGCGGGGCA 318  
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Db 39 ACTGAGACACACAGATCCCGACGCTCTGCGCGGGGCA 1

RESULT 15  
US-09-140-804-33/C  
; Sequence 33, Application US/09140804  
; Patent No. 6197930  
; GENERAL INFORMATION:  
; APPLICANT: Humes, Jacqueline M.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
; FILE REFERENCE: 97-49  
; CURRENT APPLICATION NUMBER: US/09/140,804  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: 60/056,983  
; EARLIER FILING DATE: 1997-08-26  
; NUMBER OF SEQ. ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 33  
; LENGTH: 62  
; TYPE: DNA  
; ORGANISM: Oligonucleotide ZC15268  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide ZC15268  
US-09-140-804-33

Query Match 2.8%; Score 38; DB 4; Length 62;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 38 CTGAGACACACAGATCCCGACGCTCTGCGCGGGGCA 1

Search completed: June 21, 2003, 14:34:08  
Job time : 82 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 08:08:59 ; Search time 2191 Seconds  
(without alignments)  
10178.542 Million cell updates/sec

Title: US-09-944-944-41

Perfect score: 1377  
Sequence: 1 gactagctctcttgagctc.....aaaaaaaaaaaaaaaaaa 1377

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues  
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_man:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	767.8	55.8	869	13	BI763193 603049929
2	750.6	54.5	1154	13	BM547549 AGENCOURT
3	732.8	53.2	1093	14	BM924569 AGENCOURT
4	730.2	53.0	846	13	BI458455 AGENCOURT
5	712.6	51.8	801	13	BI490880 603031867
6	672.2	48.8	724	13	BI771879 603055280

Result No.	Score	Query Match	Length	ID	Description
7	671	48.7	1045	14	BM920874
8	660.4	48.0	792	13	BI770921
9	641.8	46.6	887	13	BI490062
10	631	45.8	1623	14	BM926477
11	607.2	44.1	630	12	BM706609
12	596	43.3	596	14	BM893587
13	586.4	42.6	541	13	BM544255
14	583.2	42.4	941	13	BI821899
15	578	42.0	878	14	BM893691
16	577.2	41.9	879	13	BI820945
17	572.4	41.6	574	13	BM021127
18	554	40.2	870	9	AF451167
19	551.4	40.0	553	12	BF882978
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21	521	37.8	521	14	BM966810
22	517	37.5	517	14	BM966954
23	507.8	36.9	574	10	AM150070
24	507.6	36.9	844	10	BE309370
25	489.4	35.5	567	13	BM021381
26	479	34.8	778	12	BF098614
27	463.4	33.7	867	13	BI818537
28	457.4	33.2	1349	14	BM073882
29	453.2	32.9	702	12	BF055285
30	452.4	32.9	454	9	AI805087
31	448.4	32.6	462	10	AM070344
32	440.2	32.0	445	14	BM673416
33	438.4	31.8	842	13	BI688017
34	426.4	31.0	449	13	BM668611
35	424.4	30.8	442	14	BM693336
36	423.4	30.7	548	12	BF906443
37	421.6	30.6	630	12	BF040667
38	409.8	29.8	413	9	AI083823
39	408.4	29.7	410	14	BM707291
40	405.4	29.4	408	9	AI083548
41	402.4	29.2	405	9	AI083824
42	395.6	28.7	547	12	BF722922
43	394.6	28.7	936	12	BF540263
44	392	28.5	392	10	BE138819
45	387.2	28.1	392	10	AM192716

## ALIGNMENTS

RESULT 1  
LOCUS BI763193 869 bp mRNA linear EST 25-SEP-2001  
DEFINITION 603049929F1 NIH\_MGC\_116 Homo sapiens CDNA clone IMAGE:5190222 5',  
mRNA sequence.  
ACCESSION BI763193  
VERSION BI763193.1 GI:15754771  
KEYWORDS  
SOURCE  
ORGANISM human.  
Tissue: c9apbs-r@mail.nih.gov  
REFERENCE  
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLM11475 row: 1 column: 07  
High quality sequence stop: 777.  
Location/Qualifiers

FEATURES  
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone IMAGE:5190222"
/clone_1fb="NIH_MGC_116"
/lab_host="DH10B"
/notes="Organ: pooled colon, kidney, stomach; Vector:
pCMV-Sports; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49
female, 71 yo male colon; 46 yo male kidney, and pool of
stomachs, 62 yo male and 70 yo female. Library is
oligo-dt primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb.
Insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber. (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."

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Query Match	55.8%	Score 767.8	DB 13	Length 869	
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				Indels	8
				Gaps	7
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QY	71	GCAGGGCAGGGGGCGCCCTGCGCGGGAGAGCGCGGGGGCTGGAGCACACCACTGGAG	130		
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Db	121	GGTCGGAGTAGCGGAGCGCCCCGAAAGAGGCGCTATCGGGGAGCCGGGAGAGGGGACTGCGA	180		
QY	191	GAGACACCCGGCGTCCGGGGCTCCCGGTGACAGCGCTATGAGGCCCTCGTGGCTGCG	250		
Db	181	GAGACACCCGGCGTCCGGGGCTCCCGGTGACAGCGCTATGAGGCCCTCGTGGCTGCG	240		
QY	251	CTCTGGGCGCTGGGGCGCGGCTCGCCCTGACGACCAACAGATCCAGCCTCTGCG	310		
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QY	311	CCGGGGCAGCCCGCGCTTCCAGGCGACCGCGGCCACATGCGAGCCAGGGCTTGCGGGCG	370		
Db	301	CCGGGGCAGCCCGCGCTTCCAGGCGACCGCGGCCACATGCGAGCA- GGCCTTGCGCGGGC	359		
QY	371	CGCATGGCGCGGACGGCGCGGAGGGCGCGCGGGGCTCCGGGAGAAAGCGGACGGCG	430		
Db	360	CGCATGGCGCGGACGGCGCGGAGGGCGCGCGGGGCTCCGGGAGAAAGCGGACGGCG	419		
QY	431	GGGAGCGCGGAGCTGCGGAGCACTGAGAGGAGACCCGGGCGCGGAGAGAGCGGGACCC	490		
Db	420	GGGAGCGCGGAGCTGCGGAGCACTGAGAGGAGACCCGGGCGCGGAGAGAGCGGGACCC	479		
QY	491	GCGGGGCCCAACCGGGGCTGCCGGGAGTGCTCGGTGCTCCGCAATCCGCTTAGCGCC	550		
Db	480	GCGGGGCCCAACCGGGGCTGCCGGGAGTGCTCGGTGCTCCGCAATCCGCTTAGCGCC	539		
QY	551	AAGGCGTCCGAGAGACC- GGGTGGCTCCGGCGCTTGAGCGACACCTTGCCCTTGACCGCGT	609		
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QY	610	GCTGGTG- AACGACAGGAGCAATTACGAGCGG- TCACCGGCAAGTTACCTGGCAGGTG	667		
Db	600	GCTGGTAAACGACAGGAGCAATTACGAGCGGCTTACCGGCAAGTTACCTGGCAGGTG	659		
QY	668	CTTGGGGTCTACTTCTGCGCGTGCATGCGCACGCTTACCGGGCAGCGCTCAGTTGAT	727		
Db	660	CTTGGGGTCTACTTCTGCGCGTGCATGCGCACGCTTACCGGGCAGCGCTCAGTTGAT	719		
QY	728	CTGGTGAAGATGGCGAATCCATTGCTCTTCTTCAGTTTTCGGGGGGTGCGCCAAAG	787		

Dd	720 CTGGTGAAGATGCGCAATTCATTGGGCTC-TTCTCCAGTTTACGGGGGGTGCC--AA	776
Oy	788 CCAAGCCTCCGTCTCCGGGGGGGGCCATGTAAGCGCTGAGCCTGAGAGACCMAAGTGTGGGTG	847
Dd	777 GCCAGCTCGCTCTCGGGGGGGGGGCATGTAAGCGCTGAGAGCCTGAGAGCACCAAGTGTGGGTG	836
Oy	848 CAGGTGGGTG-TGGTGACTACATGGCATCTTA	879
Dd	837 CAGGTGGGTGGTGGGAGACTAAGTCGACATCTTA	869
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LOCUS	AEENCOUPT_6507694 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5724522	
DEFINITION	5' mRNA sequence.	
ACCESSION	BMS47549	
VERSION	BMS47549.1	GI:18781410
KEYWORDS	EST.	
SOURCE	human.	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 1154)	NIH-MGC	<a href="http://mgc.nhl.nih.gov/">http://mgc.nhl.nih.gov/</a>	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	Contact: Robert Strassberg, Ph.D.			Email: <a href="mailto:cgabs-r@mail.nih.gov">cgabs-r@mail.nih.gov</a>
	Tissue Procurement: Invitrogen			
	CDNA Library Preparation: Life Technologies, Inc.			
	CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LNL)			
	DNA Sequencing By: Agencourt Bioscience Corporation			
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:			
	<a href="http://image.llnl.gov">http://image.llnl.gov</a>			
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	High quality sequence stop: 591.			

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/clone_1lb="NIR_MGC_125"	
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			Gaps	3
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QY	100	AGCGCGGGGGCTGGGAGCACACCAACCTGAGAGGTCCTCGAGACGAGGACCGCCGGAAGGAG	159	
Db	61	AGCGCGGGGGCTGGGAGCACACCAACCTGAGAGGTCCTCGAGACGAGGACCGCCGGAAGGAG	120	
QY	160	GCCATCGGGGAGCCCGGAGGGGGGACTCGAGAGGACCCGGGCTCCGGGCTCCCGATGC	219	
Db	121	GCCATCGGGGAGCCCGGAGGGGGGACTCGAGAGGACCCGGGCTCCGGGCTCCCGATGC	180	





[illegible][illegible]



OY	880	TGCCAGCATCAAGACAGACAGACACCTCTTCGGAATTTCTGGTATACACCCAGTGGACAG	939
Db	182	TGCCAGCATCAAGACAGACAGACACCTTCCTCGGATTTCTGGTATACCTCCAGTGGACAG	241
OY	940	CTCCCACTCTTTGCTTCTAGTGCACACAGTGCACAAAGTGAGCTCATGTCTCACTCTAGAAG	999
Db	242	CTCCCAAGCTTTTCTGTTAGTGTCCCACTGACCAAGTGAGCTCATGTCTCACTCTAGAAG	301
OY	1000	AGGCTGTGAGGCTTACAAACCAAGTTCATCCAGAGGCTGGCCCCCTGGAAATATTGTGAA	1059
Db	302	AGGCTGTGAGGCTTACAAACCAAGTTCATCCAGAGGCTGGCCCCCTGGAAATATTGTGAA	361
OY	1060	TGACTAGGAGAGTGGGATAGAGACACTCTCCCTGCTGTGCTGAGCAAGAAATGGAGACAGT	1119
Db	362	TGACTAGGAGAGTGGGATAGAGACACTCTCCCTGCTGTGCTGAGCAAGAAATGGAGACAGT	421
OY	1120	GCGTGTCTGCATCAGCTGTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACAG	1179
Db	422	GCGTGTCTGCATCAGCTGTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCAAGACAG	481
OY	1180	AGGATGTGCTGTCTGTGGCAGTGAATGCCAGTTGCTGTGCTGACAGAGCCACAGG	1239
Db	482	AGGATGTGCTGTCTGTGGCAGTGAATGCCAGTTGCTGTGCTGACAGAGCCACAGG	541
OY	1240	TGGGATGTCTCTTCTCTGCTGGTCTGTGCTTCTGTGATCTCTCCACCCCTCTGCTCT	1299
Db	542	TGGGATGTCTCTTCTCTGCTGGTCTGTGCTTCTGTGATCTCTCCACCCCTCTGCTCT	601
OY	1300	GGGGCGGGCCCTTTTCTCAGATCACTCAATAAACCCTAAGAACCTCTCATTAATAAAAAA	1359
Db	602	GGGGCGGGCCCTTTTCTCAGATCACTCAATAAACCCTAAGAACCTCTCAATAAAAAA	661
OY	1360	AAAAAAAAAAAAAAAAAAAA 1377	
Db	662	AAAAAAAAAAAAAAAAAAAA 679	
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LOCUS			
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ACCESSION	BM920874		
VERSION	BM920874.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 1045)		
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs@email.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	http://image.lnl.gov		
	Plate: L14M12785 row: n column: 14		
	High quality sequence stop: 415.		
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[illegible]

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B1770921	EST.
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SOURCE	Homo sapiens
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 792)
AUTHORS	NIH-MGC <a href="http://mgc.ncl.nih.gov/">http://mgc.ncl.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cga@bs-remail.nih.gov">cga@bs-remail.nih.gov</a> Tissue Procurement: Life Technologies, Inc.
COMMENT	cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.lnl.gov">http://image.lnl.gov</a> Plate: L1AM1524 row: J column: 10 High quality sequence stop: 782.
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	/note="Organ: pooled lung and spleen; Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed and directionally cloned (pcory site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIH-MGC Library."
BASE COUNT	142 a 232 c 237 g 180 t 1 others
ORIGIN	
Query Match	48.0%; Score 660.4; DB 13; Length 792;
Best Local Similarity	96.9%; Pred. No. 3.5e-81;
Matches 758; Conservative	0; Mismatches 16; Indels 8; Gaps 8;
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Db	1 GAGCGGGGTGCTCCGCCGCTGAACGACCCTTGCCATCAGCGCGCTGTAACA 60
OY	622 GCAGGACATTAGCAAGCGCGTCACCGCGCAATTGACCTGACAGTGCTGGGCTACTA 681
Db	61 GCAGGACATTAGCAAGCGCGTCACCGCGCAATTGACCTGACAGTGCTGGGCTACTA 120
OY	682 CTTCGCGGTGATGCAACCGTCTACCGGGCCAGCTGAGTTGATCTGTGAAGAATGG 741
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OY	742 CGAATTCATTCCTCTTTCTTCACAGTTTTTTGGGGGGGTGGCCAAAGCCAGCTCGCTTC 801
Db	181 CGAATTCATTCCTCTTTCTTCACAGTTTTTTGGGGGGGTGGCCAAAGCCAGCTCGCTTC 240
OY	802 GGGGGGGGCCATGTGTGAGGCTGTGAGAGCCATGAGTGTGGTGTGAGTGTGG 861
Db	241 GGGGGGGGCCATGTGTGAGGCTGTGAGAGCCATGAGTGTGGTGTGAGTGTGG 300
OY	862 TGACTACATTGGCATCTATGCGACAGATTAACAAGACAGCACCTTCTCCGGAATTTCTGGT 921
Db	301 TGACTACATTGGCATCTATGCGACAGATTAACAAGACAGCACCTTCTCCGGAATTTCTGGT 360
OY	922 GTACTCCGACGTGGACACAGCTCCCAGTCTTTGCTTAGTGCCCACTGCAAGATGAGCTCAT 981

Db	361	GTACTCCGACATGGGACACCTGCCAGCTCCAGCTGTTTGGCTTAGTGCCCACTGGCAAAAGTAGACATCAT	420
QY	982	GCTCTCACTCCTAGAAGAGGAGGTGTGAGGCTGACAAACCAGGTGATCCAGAGAGGC-TGGC	1040
Db	421	GCTCTCACTCCTAGAAGAGGAGGTGTGAGGCTGACAAACCAGGTGATCCAGAGAGGCTTGGC	480
QY	1041	CCCCCTGGAAATATTGTGAATGACTAGGAGAGGTGGGGTAGAGC-ACCTCCGCTCTGCTGC	1099
Db	481	CCCCCTGGAAATATTGTGAATGACTAGGAGAGGTGGGGTAGAGCACTCTCCGCTCTGCTGC	540
QY	1100	TGGCAGGAATGGGAAACAGTGGCTGTCTGCATCAGTCTGG-CAGCATGGGGCAGTGGC	1158
Db	541	TGGCAAGGAATGGGAAACAGTGGCTGTCTGCATCAGTCTGGCCAGCATGGGGCAGTGGC	600
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QY	1274	GATCCCTCCCAACCCCTCTGCTCTCTGGGGCCGGCCCTTTTCTCGAGATCACTCAATAA	1333
Db	721	GATCCCTCCCAACCCCTCTGCTCTCTGGGGCCGGCCCTTTTCTCGAGATCACTCAATAA	780
QY	1334	AC 1335	
Db	781	AC 782	

FEATURES	Source
RESULT 9	
LOCUS	B1490062
DEFINITION	B1490062 887 bp mRNA linear EST 28-AUG-2001
ACCESSION	603031867/1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5172880 5',
VERSION	B1490062
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE	1 (bases 1 to 887)
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
	Contact: Robert Strusberg, Ph.D. Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a> Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLM11430 row: f column: 17 High quality sequence stop: 815.
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	/note="Organ: pooled brain, lung, testis; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C.



[illegible]

	BASE COUNT	93 a	215 c	257 g	65 t	
ORIGIN						
Query Match	44.1%;	Score 607.2;	DB 12;	Length 630;		
Best Local Similarity	99.5%;	Pred. No. 7.le-74;				
Matches	609;	Conservative	0;	Mismatches	3;	Indels
					0;	Gaps
OY	7	TTCCTTGGAGATCTGAGAGAGAAAGCGGACGAGGAGACCAACAGACTGGGGT	66			
Dd	19	TCCTTTTGGAATCTGGGAGAGAAAAGCGGACCGGAGAGGACMACAGACTGGGGT	78			
OY	67	GACGCAGAGGAGGAGGGGCGCCTTGCGCCGGGAGAAAGCGGGGGGTGGAGCACCACT	126			
Dd	79	GACGGCAGAGGAGAGGGGGCGCTTGCGCCGGGAGAAAGCGGGGGGTGGAGCACCACT	138			
OY	127	GGAGGGTCCGAGTAGACGAGGCCCCGAGAAGAGGCCATCGGGGAGACCGGAGGGGGACT	186			
Dd	139	GGAGGGTCCGAGTAGAGAGAGCGCCCGAAGAGAGGCCATCGGGGAGACCGGAGGGGGACT	198			
OY	187	GCGAGAGAGACCCCGGCGCTCGGGGCTCCCGGTGCACGCGTATGAGGCCATCTCTGCT	246			
Dd	199	GCGAGAGAGACCCCGGCGCTCCGGGCTCCCGGTGCACGCGTATGAGGGCCATCTCTGCT	258			
OY	247	GCTGCTCTCGGGGCTGGGGCGCGGCGGCTCGCCCCCACTGGAGCAACAAGATCCCAGCT	306			
Dd	259	GCTGCTCTCGGGGCTGGGGCGCGGCGGCTCGCCCCCACTGGAGCAACAAGATCCCAGCT	318			
OY	307	CTGGCCGGGGGACACCCCGGCTTTCACAGCAGCAGCCGGGACCATGAGCAGCGGCTTGC	366			
Dd	319	CTGGCCGGGGGACACCCCGGCTTTCACAGCAGCAGCCGGGACCATGAGCAGCGGCTTGC	378			
OY	367	GGGCGCGGANTGGCGCGAGCGGCGCGAGCGGCGCCCGGGGCTCGGGAGAGAAAGCGGA	426			
Dd	379	GGGCGCGGANTGGCGCGAGCGGCGCGAGCGGCGCCCGGGGCTCGGGAGAGAAAGCGGA	438			
OY	427	GGGGGGGAGGCGGGGAGCTGCGGGGAGCTTCAGAGGGGAGACCCCGGGCCGAGAGAGCGGG	486			
Dd	439	GGGGGGGAGGCGGGGAGCTGCGGGGAGCTTCAGAGGGGAGACCCCGGGCCGAGAGAGCGGG	498			
OY	487	ACCGCGGGGAGCCACCGGAGCTTGC CGGGGAGATGCTCGGCTCGCGCATCGGCTTTCAG	546			
Dd	499	ACCGCGGGGAGCCACCGGAGCTTGC CGGGGAGATGCTCGGCTCGCGCATCGGCTTTCAG	558			
OY	547	CGCCAAGCGCTCGAGAGACGGGGTGCCTCGCGCTCTTCAGCGACACCTTGCCCTTCGACCG	606			
Dd	559	CGCCAAGCGCTCGAGAGACGGGGTGCCTCGCGCTCTTCAGCGACACCTTGCCCTTCGACCG	618			
OY	607	CGTCTGTGTGTA 618				
Dd	619	CGTCTGTGTGTA 630				
RESULT 12						
BMB93587/c						
LOCUS	BMB93587	596 bp	mRNA	linear	EST 29-APR-2002	
DEFINITION	1326g10.x1 Melton Normalized Human .islset 4 N4-HIS 1 Homo sapiens					
FEATURES	cDNA clone IMAGE:6136122 3' similar to TR:09UYX4 Q9UYX4					
HYPOTHEICAL	22.8 KD PROTEIN ; mRNA sequence.					
ACCESSION	BMB93587					
VERSION	BMB93587.1	GI:19349055				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE	1 (bases 1 to 596)					
AUTHORS	Melton,D., Brown,J., Kenty,G., Permult,A., Lee,C., Kaestner,K.,					
	Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,					
	Hallier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blisatn,A.,					
	Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas					
	,M., Gibbons,M., Mcann,R., Cole,R., Tsagarishvili,R., Williams,T.,					
	Jackson,Y. and Bowers,Y.					
	Endocrine Pancreas Consortium					
TITLE						



JOURNAL  
Unpublished (2000)  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
COMMENT

**FEATURES**  
**source**

BASE COUNT	139 a	183 c	169 g	105 t
ORIGIN				

Query Match	43.3%	Score 596	DB 14	Length 596
Best Local Similarity	100.0%	Pred. NO.	2.5e-72	
Matches	596	Conservative	0	Mismatches 0
				Indels 0
				Gaps 0

QY	752	GCCTCTTCTCCACAGTTTTTGGGGGGGGGCCCAAGCAGCTCGCTCTCGGGGGGGGCC	811
Db	596	GCCTCTTCTCCACAGTTTTTGGGGGGGGGCCCAAGCAGCTCGCTCTCGGGGGGGGCC	537
QY	812	ATGGTGAAGGCTGAGACCTGAGGACCAAGTGTGGGTGCGAGTGGGTGTGGGTACTACATTT	871
Db	536	ATGGTGAAGGCTGAGACCTGAGGACCAAGTGTGGGTGCGAGTGGGTGTGGGTACTACATTT	477
QY	872	GGCATCTATGCGACACATCAAGACACAGACACACCTTCTCCGGATTTCTGTGTACTCCGAC	931
Db	476	GGCATCTATGCGACACATCAAGACACAGACACCTTCTCCGGATTTCTGTGTACTCCGAC	417
QY	932	TGGCACAGCTCCCCAGTCTTGTGTTAGTGGCCACACGCAAGGAGACATGCTGCACATC	991
Db	416	TGGCACAGCTCCCCAGTCTTGTGTTAGTGGCCACACGCAAGTGAAGTATGCTCTCACTC	357
QY	992	CTAGAAAGAGGGGTGAGGCTGACACACCGAGTCACTCCAGAGGGCTGGCCCCCTCGAAT	1051
Db	356	CTAGAAAGAGGGGTGAGGCTGACACACCGAGTCACTCCAGAGGGGTGGCCCCCTCGAAT	297
QY	1052	ATTGTGAATGACTATAGGAGAGTGGGGGTAGAGCACTCTCGTCTGCTGGCAGGAATG	1111
Db	296	ATTGTGAATGACTATAGGAGAGTGGGGGTAGAGCACTCTCGTCTGCTGGCAGGAATG	237
QY	1112	GGAAACAATGGCTGCTCGATCAGGTCAGGTCGCGAGATGGGGAGAGGGCTGGAATTCCTGCC	1171
Db	236	GGAAACAATGGCTGCTCGATCAGGTCGCGAGATGGGGAGAGGGCTGGAATTCCTGCC	177

QY 1172 AAGACCGAGAGAGTGTGCTGCTGCGGCAAGGTAAATCCCCAGATGCTGAGTTCACAGA 1231

Db 176 AAGACCGAGAGAGTGTGCTGCTGCGGCAAGGTAAATCCCCAGATGCTGAGTTCACAGA 117

QY 1232 GCCACAGAGTGGGGGAGCTCTCTTCCTGGGCTCTGCTCTTCAGATATCCGCCACCCCTTC 1291

Db 116 GCCACAGAGTGGGGGAGCTCTCTTCCTGGGCTCTGCTCTTCAGATATCCGCCACCCCTTC 57

QY 1292 CTGCTCCTGGGGCGGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCTTC 1347

Db 56 CTGCTCCTGGGGCGGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCTTC 1

RESULT	13
LOCUS	BMS44255
DEFINITION	BMS44255 596 bp mRNA linear EST 20-FEB-2002
ACCESSION	AGNCOU027.6490655 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5587759
VERSION	5' mRNA sequence.
KEYWORDS	BMS44255 BMS44255.1 GI:18775356
SOURCE	EST.
ORGANISM	Human.

FEATURES	Location/Qualifiers
source	1. .596

BASE COUNT	138 a	158 c	172 g	127 t	1 others
ORIGIN					

Query Match	42.68;	Score 586.4;	DB 13;	Length 596;
Best Local Similarity	99.78;	Pred. No. 5e-71;		
Matches 587; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

QY	789	CAGCTTCGCTCTCGGGGGGGGGCCATGGTGTGAGGCTGAGACCTGAGACCAAGTGTGGGTGC	848
Db	1	CAGCTTCGCTCTCGGGGGGGGGCCATGGTGTGAGGCTGAGACCTGAGACCAAGTGTGGGTGC	60
QY	849	AGGGGGGTGGGGGAGTACATTTGGGCATTCATGGCAGATTCACACAGACAGACACTTCT	908
Db	61	AGGGGGGTGGGGGAGTACATTTGGGCATTCATGGCAGATTCACACAGACAGACACTTCT	120
QY	909	CCGGATTTCGTGTACTCCGACATGGGACAGACTCCCGACATCTTGTGTAAAGTGCCCACTGC	968



Db	121	CCGGATTTCTGTGTACTCCAGCTGGCAGACACTCCCAAGTCTTTGCTTAGTGCACACTGC	180
QY	969	AAAGTGAGCTCATGCTCTCACTCCTAGAGAGAGGGTGTGAGGCTGACAAACAGGTCATCC	1028
Db	181	AAAGTGAGCTCATGCTCTCACTCCTAGAGAGAGGGTGTGAGGCTGACAAACAGGTCATCC	240
QY	1029	AGGAGGGCTGGCCCCCTGGAAATTTGTGAATGACTAGGAGAGTGGGGTAGACACTCTC	1088
Db	241	AGGAGGGCTGGCCCCCTGGAAATTTGTGAATGACTAGGAGAGTGGGGTAGACACTCTC	300
QY	1089	CGTCCCTGCTGGTGGCAAGGAATGGGAACAGTGGCTGTGGATCAAGTCTGGCGAGCAT	1148
Db	301	CGTCCCTGCTGGTGGCAAGGAATGGGAACAGTGGCTGTGGATCAAGTCTGGCGAGCAT	360
QY	1149	GGGCAGTGGCTGGAATTTCTGCCCAAGACCAAGAGATGTGCTGTGGCAAGTAAAT	1208
Db	361	GGGCAGTGGCTGGAATTTCTGCCCAAGACCAAGAGATGTGCTGTGGCAAGTAAAT	420
QY	1209	CCCCCAGTGGCTGTGGTCCAGAGAGCCCAAGGTGGGGTGTCTCTTCCGTGCTCTGCTT	1268
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QY	1269	CTCTGGATCTCTCCCAACCCCTCCTGCTCTGTGGGGCGGGCCCTTTTCTCAAGATCACTC	1328
Db	481	CTCTGGATCTCTCCCAACCCCTCCTGCTCTGTGGGGCGGGCCCTTTTCTCAAGATCACTC	540
QY	1329	AATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1377
Db	541	AATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	589

RESULT	14
B1821899	
LOCUS	
DEFINITION	B1821899 941 bp mRNA linear EST 04-OCT-2001 603035796f1 NIH_MGC_115 Homo sapiens CDNA clone IMAGE:5176957 5', mRNA sequence.
ACCESSION	B1821899
VERSION	B1821899.1 GI:15933449
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 941) NIH-MGC http://mgc.nci.nih.gov/ National Institutes of Health, Mammalian Gene Collection (MGC)
AUTHORS	Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	Email: cgaabs+email.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL) CDNA Library Arranged by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> plate: LLAM1440 row: p column: 24 High quality sequence stop: 779.

**FEATURES**  
**source**

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/notes="Organ: pooled brain, lung, testis; Vector:
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source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dt primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 Kb,
insert size range 1-3 Kb. Library is normalized and

```

BASE COUNT	130 a	320 c	329 g	162 t	enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
ORIGIN					

Query Match	42.4%;	Score 583.2;	DB 13;	Length 941;
Best Local Similarity	94.3%;	Pred. No. 1e-70;		
Matches 758; Conservative	0;	Mismatches 28;	Indels 18;	Gaps 14;

OY	191	GAGGACCCCGGCGTCCGGGGCTCCCGGATGCCAGCGCTATGAG -GCCACTCTCTGCTCTGCT	249
Db	136	GAGGACCCCGGCGCTGCCGGGCTCCCGGATGCCAGCGCTATGAGTGCACATCTCTCTCTCTCT	195
OY	250	GCTCTGGGGCTTGGGGGCGCGGGCTGGCCCCCACTGGAGACAACAAGATCCCAAGCTCTGG	309
Db	196	GCTCTGGGGCTTGGGGGCGCGGGCTGGCCCCCACTGGAGACAACAAGATCCCAAGCTCTCTG	255
OY	310	CCCGGGGCGACCCCGGCTTTCACAGCAGCGCGGGCCACCATGGACAGCCA -GGGCTTGGCCGG	368
Db	256	CCCGGGGCGACCCCGGCTTTCACAGGAGCGCGGGCCACCATGGACAGCCATGGGGCTTGGCCGG	315
OY	369	GCCCGGATGGCCCGGAGCGCGCCGCGACGCGCGCCGG -GGCTCCGGGAGAGAAAGGCGAG	427
Db	316	GCCCGGATGGCCCGGAGCGCGCCGCGACGCGCGCCGGGGTCTCCGGGAGAGAAAGGCGAG	375
OY	428	GCGCGGAGCGCGGGGACTCCCGGACCTCGAGAGGGGAGCCCGGGCGCGAGAGAGGCGGGA	487
Db	376	GCGCGGAGCGCGGGGACTCCCGGACCTCGAGAGGGGAGCCCGGGCGCGAGAGAGGCGGGA	435
OY	488	CCCGCGGGGCGCACCGGG -CCTGCGGGGAGTGTCTGGTCTTCGCGGATCCGCTTCA	545
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OY	546	GCGCGAAGCGCTCCGAGAGAGC -GGGTGCTCTCCGGCGTACGAGCAGCCCTTG -CCCTTGG	602
Db	496	GCGCGAAGCGCTCCGAGAGAGCCTGGGTGCTCTCCGGCGTACGAGCAGCCCTTGCCCTTGG	555
OY	603	ACCGCGTCTGCTGTAAGAGAGGAGACATTAACGAGCGCGTACCGGCGAAGTCACTCTCC	662
Db	556	ACCGCGTCTGCTGTAAGAGAGGAGACATTAACGAGCGCGTACCGGCGAAGTCACTCTCC	615
OY	663	-AGGTGCTTGGGGTCTACTTCTGGCGCTCCA -TGCCACCGCTTACCGGGCGACGCTCGA	720
Db	616	GAGGTGCTTGGGGTCTACTTCTGGCGCTCCAATTCATTCGCAACGCTTACCGGGCGACGCTCGA	675
OY	721	GTTTGATCTGTGTAAGAAATGCGAATCATTTGCGCTTTCTTCCAGTTTTCGSGGGGTG	780
Db	676	GTTTGATCTGTGTAAGAAATGCGAATCATTTGCGCTTTCTTCCAG -TTTTCGSGGATG	734
OY	781	GCCCAAGCAGCCTTCGCTCTCGGGGGGGGCGCATGGTGAAGCTGGAG -CCTGAGAGCCAG	839
Db	735	GCCCAAGCAGCCTTCGCTCTCGGGGGGGGCGCATGGTGAAGCTGGAGGCGCTGAGGACCCAG	794
OY	840	TGTGGGTGCAAGT -GGGTGTTGGGTGACTACTTGGCATCTTATGGCAGCATCAAGACAGAC	898
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OY	899	AGCAGCTTCTCCGAGATTCTGTGTACTCCAGTCCAGTCCAGCAGCTCCCAAGTCTTGGCTTATG	958
Db	854	AGCAGCTTCTCCGGA -TTCTGTGTACTCCAGTCCAGTCCAGTCCCAAGTCTTGGCTTGTG	912
OY	959	TGCCCACTGCAGAAAGTGAAGCTATG 982	
Db	913	---CCCGTGTCAAGTGAAGCTCTCTG 933	

RESULT 15	LOCUS	DEFINITION
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BM893691	1128e08.x1	Melton Normalised Human Islet 4 N4-HIS 1 Homo sapiens
	CDNA clone IMAGE:6136046	3' similar to TR:090FX4 Q90FX4
	HP0THERICAL 2.8 KD PROTEIN	; mRNA sequence.

ACCESSION BM893691  
 VERSION BM893691.1 GI:19349159  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 (bases 1 to 578)  
 AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
 Lemishka,I., Scares,M., Brestelli,J., Gradwohl,G., Clifton,S.,  
 Hallier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blisstein,A.,  
 Schmitt,A., Theising,B., Ritter,E., Ronko,T., Bennett,J., Cardenas  
 ,M., Gibbons,M., McCann,R., Cole,K., Tsagarelshvili,R., Williams,T.,  
 Jackson,Y. and Bowers,Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 TITLE  
 JOURNAL  
 COMMENT  
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Library was constructed by Dr. Douglas Melton DNA sequencing by:  
 Washington University Genome Sequencing Center for information on  
 obtaining a clone please contact: Juliana Brown  
 (brown@efas.harvard.edu)  
 Seq primer: -40UP from Glbco  
 High quality sequence stop: 408.  
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 Location/Qualifiers  
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 /tissue\_type="Islets of Langerhans"  
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 Site:2: Sal 1; Starting library constructed using  
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 fractionation; average insert size 1.08 kb. Library was  
 amplified once on solid support and plasmid DNA from  
 library was prepared. The library DNA was normalized by  
 method #4 from Bonaldo, Lennon, and Soares 1996 genome  
 Research 6:791-806; 0.5 microgram single-stranded library  
 plasmid DNA was mixed with 5 micrograms PCR product  
 representing library inserts and hybridized to an EcoT of  
 20. Single-stranded (unhybridized) plasmids were isolated  
 by hydroxyapatite chromatography and used to make this  
 library."  
 BASE COUNT 130 a 181 c 163 g 104 t  
 ORIGIN  
 Query Match 42.0%; Score 578; DB 14; Length 578;  
 Best Local Similarity 100.0%; Pred. No. 7.1e-70;  
 Matches 578; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db |  
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 QY 830 GAGGACCAAGTGGGGGAGCGAGTGGGTGGGTGACATACATTTGGCATCTATGCCAGATC 889  
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 QY 890 AAGACAGACAGACCTTCTCGGATTTCTGGTACTCCAGCTGGACAGAGTCCCGAGTC 949  
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 QY 338 GCTGACAAACAGGTATCCAGGAGGCTGGCCCCCGGGAATATTGGAATGACTAGGA 279  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 21, 2003, 14:34:16 ; Search time 19.5 Seconds

(without alignments)  
5857.734 Million cell updates/sec

Title: US-09-944-944-41  
Perfect score: 2540  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 225784

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : SwissProt.40:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1325	52.2	243	1	COT5_HUMAN
2	458	18.0	680	1	CA1A_HUMAN
3	454	17.9	674	1	CA1A_BOVIN
4	451	17.8	674	1	CA1A_CHICK
5	448	17.6	680	1	CA1A_MOUSE
6	433.5	17.1	247	1	APM1_MOUSE
7	426.5	16.8	744	1	CA18_RABIT
8	424	16.7	244	1	APM1_HUMAN
9	417.5	16.4	635	1	CA28_HUMAN
10	417	16.4	289	1	COT7_HUMAN
11	417	16.4	743	1	CA18_MOUSE
12	415.5	16.4	744	1	CA18_HUMAN
13	412	16.2	246	1	C10C_MOUSE
14	407	16.0	419	1	COLE_LEPMA
15	403	15.9	285	1	COT2_HUMAN
16	397	15.6	245	1	COT2_HUMAN
17	362	14.3	251	1	C10B_HUMAN
18	360.5	14.2	253	1	C10B_RAT

19	350	13.8	253	1	C10B_MOUSE	P14106 mus musculus
20	328	12.9	1049	1	CA13_BOVIN	P04258 bos taurus
21	322	12.7	1464	1	CA11_HUMAN	P02452 homo sapien
22	318.5	12.5	1453	1	CA11_CHICK	P02457 gallus galli
23	314	12.4	245	1	C10A_HUMAN	P02747 homo sapien
24	314	12.4	245	1	C10A_MOUSE	P98086 mus musculus
25	313.5	12.3	1460	1	CA11_CANFA	O95317 canis famill
26	310.5	12.2	1459	1	CA12_MOUSE	P28481 mus musculus
27	309	12.2	1670	1	CA34_HUMAN	O01955 homo sapien
28	306.5	12.1	1262	1	CA13_CHICK	P12105 gallus galli
29	303.5	11.9	255	1	GLIC_MOUSE	O9684 mus musculus
30	302	11.9	636	1	CA13_RAT	P13941 rattus norv
31	302	11.9	1464	1	CA13_MOUSE	P08121 mus musculus
32	301.5	11.8	1418	1	CA12_HUMAN	P02458 homo sapien
33	300	11.8	747	1	CA12_BOVIN	P02459 bos taurus
34	300	11.8	1466	1	CA13_HUMAN	P02461 homo sapien
35	298.5	11.8	258	1	C1RF_HUMAN	O75973 homo sapien
36	298.5	11.8	258	1	C1RF_MOUSE	O88992 mus musculus
37	298.5	11.8	779	1	CA11_BOVIN	P02453 bos taurus
38	298	11.7	1453	1	CA11_MOUSE	P11087 mus musculus
39	297.5	11.7	1366	1	CA21_CANFA	O46392 canis famill
40	297	11.7	1364	1	CA21_BOVIN	P02465 bos taurus
41	296	11.7	1355	1	CA21_RANCA	O43350 rana catesb
42	295.5	11.6	671	1	CA11_RAT	P02454 rattus norv
43	294	11.6	1372	1	CA21_MOUSE	O01149 mus musculus
44	294	11.6	1838	1	CA15_HUMAN	P20908 homo sapien
45	293	11.5	1806	1	CA1B_HUMAN	P12107 homo sapien

## ALIGNMENTS

### RESULT 1

ID	COT5_HUMAN	STANDARD:	PRT:	243 AA.
AC	O9BXJ0: O9BXJ4;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Complement-c1q tumor necrosis factor-related protein 5 precursor.			
GN	C1QTNF5 OR CTRP5.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
RN	NCBI_Taxid=9606;			
RP	[1]			
RA	SEQUENCE FROM N.A.			
RA	Sheppard P.O., Humes J.M.;			
RT	"Homo sapiens complement-c1q tumor necrosis factor-related protein.";			
RL	Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.			
RC	[2]			
RC	SEQUENCE OF 25-243 FROM N.A.			
RA	TISSUE=uterus;			
RA	Otteenwelder B., Obermayer B., Mewes H.-W., Gassenhuber J.,			
RA	Wiemann S.;			
RL	- SIMILARITY: (AUG-1999) to the EMBL/Genbank/DBJ databases.			
CC	- SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.			
CC	- SIMILARITY: CONTAINS 1 C1Q DOMAIN.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
DR	EMBL: AF329841; AKK1965.1; -			
DR	EMBL: AL110261; CAB53702.1; -			
DR	GeneW: HGNC:14344; C1QTNF5.			
DR	InterPro: IPR01073; C1q.			
DR	InterPro: IPR000087; Collagen.			
DR	Pfam: PF00386; C1q; 1.			
DR	Pfam: PF01391; Collagen; 1.			



RT occur in two unrelated families with metaphyseal chondrodysplasia  
RT type Schmid.";  
RL Am. J. Hum. Genet. 54:169-178(1994).  
RN [10]  
RP VARIANT SMCD ARG-591.  
RX MEDLINE=94272470; PubMed=8004099;  
RA McIntosh I., Abbott M.H., Warran M.L., Olsen B.R., Francomano C.A.;  
RT "Additional mutations of type X collagen confirm COL10A1 as the  
RT Schmid metaphyseal chondrodysplasia locus.";  
RL Hum. Mol. Genet. 3:303-307(1994).  
RN [11]  
RP VARIANT SMCD VAL-618.  
RX MEDLINE=95181449; PubMed=7876225;  
RA Chan D., Cole W.G., Rogers J.G., Beteman J.F.;  
RT "Type X collagen multimer assembly in vitro, is prevented by a Gly618  
RT to Val mutation in the alpha 1(X) NC1 domain resulting in Schmid  
RT metaphyseal chondrodysplasia.";  
RL J. Biol. Chem. 270:4558-4562(1995).  
RN [12]  
RP VARIANTS SMCD ARG-545; GLU-595; HIS-597; LYS-617; ARG-644 AND GLY-648  
RX MEDLINE=95331767; PubMed=7607655;  
RA Bonaventure J., Chamblade F., Maroteaux P.;  
RT "Mutations in three subdomains of the carboxy-terminal region of  
RT collagen type X account for most of the Schmid metaphyseal  
RT dysplasias.";  
RL Hum. Genet. 96:58-64(1995).  
RN [13]  
RP VARIANT SMCD PRO-600.  
RX MEDLINE=96375754; PubMed=8782043;  
RA Wallis G.A., Rash B., Sykes B., Bonaventure J., Maroteaux P.,  
RA Zabel B., Wynne-Davies K., Grant M.E., Boot-Hanford R.P.;  
RT "Mutations within the gene encoding the alpha 1 (X) chain of type X  
RT collagen (COL10A1) cause metaphyseal chondrodysplasia type Schmid but  
RT not several other forms of metaphyseal chondrodysplasia.";  
RL J. Med. Genet. 33:450-457(1996).  
RN [14]  
RP VARIANTS SMCD GLU-18 AND ARG-18.  
RX MEDLINE=97220591; PubMed=9067753;  
RA Ikegawa S., Nakamura K., Nagao A., Haga N., Nakamura Y.;  
RT "Mutations in the N-terminal globular domain of the type X collagen  
RT gene (COL10A1) in patients with schmid metaphyseal  
RT chondrodysplasia.";  
RL Hum. Mutat. 9:131-135(1997).  
RN [15]  
RP VARIANTS SMD GLU-595.  
RX MEDLINE=99057503; PubMed=9837818;  
RA Ikegawa S., Nishimura G., Negai T., Hasegawa T., Ohashi H.,  
RA Nakamura Y.;  
RT "Mutation of the type X collagen gene 'COL10A1' causes  
RT Spondylometaphyseal dysplasia.";  
RL Am. J. Hum. Genet. 63:1659-1662(1998).  
RN [16]  
RP VARIANT SMCD CYS-597.  
RX MEDLINE=99069781; PubMed=9852679;  
RA Sasai H., Ida A., Nakata Y., Koyama K.;  
RT "Novel missense mutation resulting in the substitution of tyrosine by  
RT cysteine at codon 597 of the type X collagen gene associated with  
RT Schmid metaphyseal chondrodysplasia.";  
RL J. Hum. Genet. 43:259-261(1998).  
RN [17]  
RP -1- FUNCTION: TYPE X COLLAGEN IS A PRODUCT OF HYPERTHROPHIC  
CC CHONDROCYTES AND HAS BEEN LOCALIZED TO PRESUMPTIVE  
CC MINERALIZATION ZONES OF HYALINE CARTILAGE.  
CC  
CC -1- SUBUNIT: HOMOTRIMER.  
CC  
CC -1- PM: PROLINES ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.  
CC  
CC -1- DISEASE: DEFECTS IN COL10A1 ARE THE CAUSE OF SCHMID TYPE  
CC METAPHYSEAL CHONDRODYSPLASIA (SMCD), A DOMINANTLY INHERITED  
CC DISORDER OF THE OSSEOUS SKELETON. THE CARDINAL FEATURES OF THE  
CC PHENOTYPE ARE MILD SHORT STATURE, COXA VARA AND A WADDLING GAIT.  
CC RADIOGRAPHY USUALLY SHOWS SCLEROSIS OF THE RIBS, FLARING OF THE  
CC METAPHYSES, AND A WIDE IRREGULAR GROWTH PLATE, ESPECIALLY OF THE  
CC KNEES.  
CC  
CC -1- DISEASE: DEFECTS IN COL10A1 ARE THE CAUSE OF SPONDYLOMETAPHYSEAL

```

CC      DYSPLASIA (SMD) SMD COMPRISES A HETEROGENEOUS GROUP OF HERITABLE
CC      SKELETAL DYSPLASIAS CHARACTERIZED BY MODIFICATIONS OF THE
CC      VERTEBRAL BODIES OF THE SPINE AND METAPHYSES OF THE TUBULAR BONES.
CC      -1- SIMILARITY: STRONG, TO ALPHA 1 AND 2 TYPE VIII COLLAGENS.
CC      -1- SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaborative
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CC      entities requires a license agreement (See http://www.isb.ch/announce
CC      or send an email to license@isb.slb.ch).
CC      -----
DR      EMBL; X60382; CAA42933.1; -
DR      EMBL; X65120; CAA46236.1; -
DR      EMBL; X98568; CAA6178.1; -
DR      EMBL; A1121963; CAB87590.1; -
DR      EMBL; S68531; AAC60615.1; -
DR      EMBL; X58879; CAA11686.1; -
DR      EMBL; M74050; AAA61221.1; -
DR      EMBL; X72579; CAA51170.1; -
DR      EMBL; X72580; CAA51170.1; JOINED.
DR      PIR; S15826; S15826.
DR      PIR; S30086; S30086.
DR      PIR; A43901; A43901.
DR      PIR; S18249; S18249.
DR      PIR; S21856; S21856.
DR      PIR; S26396; S26396.
DR      Genew; HGNC:2185; COL10A1.
DR      MIM; 120110; -.
DR      MIM; 156500; -.
DR      MIM; 184250; -.
DR      InterPro; IPR001073; C1q.
DR      InterPro; IPR000087; Collagen.
DR      Pfam; PF00386; C1q; 1.
DR      Pfam; PF01391; Collagen; 8.
DR      PRINTS; PRO00007; COMPLEMENTC1Q.
DR      SMART; SM00110; C1Q; 1.
DR      PROSITE; PS01113; C1Q; 1.
KW      Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW      Cartilage; Collagen; Signal; Disease mutation; Polymorphism.
KW      CATALYTIC: 1
KW      CHAIN: 1
KW      CHAIN: 18
KW      CHAIN: 18
FT      FT CHAIN 19 680 COLLAGEN ALPHA 1(X) CHAIN.
FT      FT CHAIN 19 56 NONHELICAL REGION (NC2).
FT      FT DOMAIN 57 519 TRIPLE-HELICAL REGION.
FT      FT DOMAIN 520 680 NONHELICAL REGION (NC1).
FT      FT DOMAIN 545 680 C1Q.
FT      FT DOMAIN 18 18 G->E (IN SMD).
FT      FT VARIANT 18 18 /FTID=VAR_001838.
FT      FT VARIANT 18 18 /FTID=VAR_001839.
FT      FT VARIANT 545 545 /FTID=VAR_001840.
FT      FT VARIANT 591 591 C->R (IN SMD).
FT      FT VARIANT 591 591 /FTID=VAR_001841.
FT      FT VARIANT 591 591 /FTID=VAR_001841.

Alignment Scores:
Pred. No.: 2.24e-14
Score: 458.00
Percent Similarity: 42.78%
Best Local Similarity: 32.47%
Query Match: 18.03%
DB: 1 Gaps: 13

US-09-944-944-41 (1-1377) x CA1A_HUMAN (1-680)
QY      19 CTGCGAGAGGAGAAAGCGGAGCGAGCGAGGAGCAACAGACTGGGTGAGCGAGGCGCA 78
QY      111 111 111 111 111 111 111 111 111 111
Db      303 LeuProGlyLeuThySclYglValrGclYProAlaagLYleuProGlyYProGlyAlaIalys 3722
QY      79 GGG-----GGCGCCCTGGCGGGGAGAAAGCGGGGGGCTGGAGCAACA----- 120
QY      111 111 111 111 111 111 111 111 111 111

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[illegible]

DB	SEQUENCE	744 AA;	73358 MW;	2A8CFE1F8274E99	CRC64;
US-09-9444-9444-41	(1-1377) x CA18_RBDIT (1-744)				
QY	22 GGAGGAGGAAGCGGAGCGGAGGAGGAGCAACAGACTGGGTGATGCGGAGGCGAGG 81				
Db	349 GYGLALGLYLSPROGLYPHEPROGLYPROLYSGLYASPARIGLYLLEGLYGLYALPRO 368				
QY	82 GGGGCC-----TGCCGGGGAGAGCGCGGGGGCTGGAGCACA 120				
Db	369 GYALALGLYLSPROARGLYGLYGLYLSGLYPROVALGLYALAPROGLYMETGLYGLYPRO 388				
QY	121 CCA-----ACGCGAGGGTCGGAGATGAGGAC-----GCCCGAAGAGGAGCAATCGGG 168				
Db	389 PROGLYGLYLSPROGLYLSLEUPROGLYLSLEUPROGLYLSLEUPROGLYLSLEUPROGLY 408				
QY	169 GAGCCGGGA-----GGGGGGAAGTGGAGAGAGCAACCGCGGCTGGGCTCCCGG 216				
Db	409 PHEPROGLYLSLEUPROGLYLSGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLYGLY 427				
QY	217 TGCCAGGCGCTATGAGGCACTCTCTGCTGCTGCTCTCTGCGGCTGGCGGCGGCTCGCC 276				
Db	428 LYSGLYGLYLSLEUPROGLYLSLEUGLNGLYLPHLEPROGLYLSPROGLYLSLEUGLNGLY 447				
QY	277 CCGCATGGAGCAACAAGATCCCGAGCT----- 306				
Db	448 PROPROGLYLSLEUPROGLYLSLEUPROGLYLSLEUPROGLYLSLEUPROGLYLSLEUPROGLY 467				



	-	FUNCTION: IMPORTANT NEGATIVE REGULATOR IN HEMATOPOIETIS AND IMMUNE SYSTEMS; MAY BE INVOLVED IN ENDING INFLAMMATORY RESPONSES THROUGH ITS INHIBITORY FUNCTIONS. INHIBITS ENDOTHelial NF-KAPPA B SIGNALING THROUGH A CAMP-DEPENDENT PATHWAY. INHIBITS TNF-ALPHA-INDUCED EXPRESSION OF ENDOTHelial ADHESION MOLECULES. INVOLVED IN THE CONTROL OF FAT METABOLISM AND INSULIN SENSITIVITY.
CC	-	SUBUNIT: HOMODIMER (POTENTIAL).
CC	-	SUBCELLULAR LOCATION: SECRETED IN PLASMA.
CC	-	TISSUE SPECIFICITY: EXPRESSED ONLY IN THE ADIPOSE TISSUE.
CC	-	DISEASE: Defects in APPL are the cause of adiponectin deficiency, resulting in very low concentration of plasma adiponectin.
CC	-	Insulin resistance, and diabetes type 2.
CC	-	PHARMACEUTICAL: Adiponectin might be used in the treatment of diabetes type 2 and insulin resistance.
CC	-	SIMILARITY: CONTAINS 1 COLLAGENOUS DOMAIN.
CC	-	SIMILARITY: CONTAINS 1 C1Q DOMAIN.
CC	-	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isd-sdb.ch/announce/or_send_an_email_to_license@sdb-stb.ch">http://www.isd-sdb.ch/announce/or_send_an_email_to_license@sdb-stb.ch</a> ).
DR	EMBL;	D45371; BA08227.1; -
DR	EMBL;	AB012165; BAA6716.1; -
DR	EMBL;	AB012164; BAA6716.1; JOINED.
DR	EMBL;	AJ131460; CAB52413.1; -
DR	EMBL;	AJ131461; CAB52413.1; JOINED.
DR	MIM;	603441; -
DR	InterPro;	IPR001073; C1q.
DR	InterPro;	IPR000087; Collagen.
DR	Pfam;	PF00386; C1q; 1.
DR	Pfam;	PF01391; collagen; 1.
DR	PRINTS;	PR00007; COMPLEMENTC1Q.
DR	SMART;	SM00110; C1Q; 1.
DR	PROSITE;	PS01113; C1Q; 1.
KW	Hormone; Collagen; Signal; Repeat; Hydroxylation; Plasma; Polymorphism; Disease mutation; Obesity; Diabetes mellitus.	
FT	CHAIN	1 14
FT	DOMAIN	15 244
FT	DOMAIN	42 107
FT	DISULFID	108 244
FT	MOD_RES	36 36
FT	MOD_RES	44 44
FT	MOD_RES	47 47
FT	MOD_RES	53 53
FT	MOD_RES	62 62
FT	MOD_RES	71 71
FT	MOD_RES	76 76
FT	MOD_RES	86 86
FT	MOD_RES	95 95
FT	MOD_RES	104 104
FT	VARIANT	84 84
FT	VARIANT	112 112
FT	VARIANT	117 117
FT	VARIANT	164 164
FT	VARIANT	221 221
FT	VARIANT	241 241
SEQ	SEQUENCE	244 AA; 26414 MM; /FTTD=VAR_013278. C6C64;

Alignment Scores:

Pred. No.:	9.12e-13	Length:	244
Score:	424.00	Matches:	106
Percent Similarity:	50.38%	Conservative:	26

Best Local Similarity:	40.46%	Mismatches:	72
Query Match:	16.69%	Indels:	58
DB:	1	Gaps:	10
US-09-944-944-41 (1-1377) x APM1_HUMAN (1-244)			
QY	242	GMSCGSCGSCCTCTGGGCTGGGCGGCGGCTGGCCCCCACTGGACAGACAAGATCCCC	301
Db	7	ValLeuLeuLeuLeuLeuLeu-----	13
QY	302	AGCCTCTGCCCCGGGGCAC-----	325
Db	14	-----ProGlyHisAspGlnGlnuThrThrThnGlnGlyProGlyValLeuLeuPro	30
QY	36	-----CTTCCAGGCAGCCCGGGCCACCATGGACGCC	358
Db	31	LeuProGlyGlyAlaCysThrGlyTrpMetIaGlyIleProGlyHisProGlyHisAsn	50
QY	359	GGCTTGCCGGCGCGGAGTGGCCGACGGCCCGCGAGCGGCGCGCGGGCTCCGGAGAC	418
Db	51	GlyAlaProGlyAlaArgAspGlyArgAsp-----GlyThrProGlyGln	64
QY	419	AAAGCGAGGAGGCGGAGCGGAGCTCGGGACCTCGAGGGAC-----	463
Db	65	LysGlyGlnGlyAspProGlyLeuIleGlyProGlyGlyAspIleGlyGlnGly	84
QY	464	-----CCCGGGCGCGAGAGAGAGGGCGGACCCGCGGGCCACCGGCGCTGCC	511
Db	85	ValProGlyAlaGlnGlyProArgGlyPheProGlyIleGlnGlyArgGlyGlnPro	104
QY	512	GGGAGTCTCGGTGCTCCGCGATCCGCTTCAGCGCCAGAGCGCTCCAGAGCCGGTG	571
Db	105	GlyGlnGlyAlaTyrValTyrArgSerAlaPheSerVal--GlyLeuGlnThrTyrVal	123
QY	572	CTCCGCGCTGAGCAGCACTTGGCCCTTCAGACGCGCTGCTGGTGAACGAGAGACAT	631
Db	124	ThrIlePro--AsnMetProIleArgPheThrLysIlePheTyrAsnGlnAsnHis	142
QY	632	TACGAGCGCGTACCGGCAAGTTCACTGCAAGTCCGCGGTCTACTACTTGGCGTCC	691
Db	143	TyrAspGlySerThrGlyLysPheHisCysAsnIleProGlyLeuTyrTrpPheAlaTyr	162
QY	692	CATGCCACCGTCTACCGGGCCAGCTGCAAGTTGATCTGTGAAGAATGGCAATCC---	748
Db	163	HisIleThrValTyrMetLysAspValLysValSerLeuPheLysLysAspLysAlaMet	182
QY	749	ATTGCGCTCTCTTCAGATTTCGGGGGGTGGCCCAACGCAAGCTCGCTGGCGGGG	808
Db	183	LeuPheThrTyrAspGlnTyrGlnGlnAsnValAspGlnAla-----SerGlySer	200
QY	809	GCCATGCTGAGGCTGAGCGCTGAGGACCAAGTGTGGGTGCAAGTG---GGTGTGGTGC	865
Db	201	ValLeuLeuHisLeuGlnValGlyArgGlnValIlePheGlnValTyrGlnGlnGlyGln	220
QY	866	TACATTGCATCTATGCCAGATCAAGACAGACAGACACCTCTCCGATTTCTGTGTAC	925
Db	221	ArgAsnGlyLeuTyrAlaAspAsnAspSerThrPheThrGlyPheLeuLeuTyr	240
QY	926	TCCGAC 931	
Db	241	HisAsp 242	









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Db          725 uTYtAlAGlYcIotYrValHtHsSerPheSeCtYTYrIreUleuTYr 741
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          |||:|||||:|||||:|||||:|||||
RESULT 12
CA18_HUMAN STANDARD; PRT; 744 AA.
AC P27658; G96D07;
DT 01-AUG-1992 (Rel. 23, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Collagen alpha 1(VIII) chain precursor (Endothelial collagen).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RX MEDLINE=91231001; PubMed=2029894;
RA Muragaki Y., Mattei M.-G., Yamaguchi N., Olsen B.R., Nimomiya Y.;
RT "The complete primary structure of the human alpha 1 (VIII) chain and
RT assignment of its gene (COL8A1) to chromosome 3."
RL Eur. J. Biochem. 197:615-622(1991).
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
CC Submitted (SEP-2001) to the EMBL/GenBank/DDAJ databases.
CC -1 FUNCTION: MAJOR COMPONENT OF THE DESCENDING MEMBRANE (BASEMENT
CC MEMBRANE) OF CORNEAL ENDOTHELIAL CELLS.
CC -1 SUBUNIT: MAY FORM HOMOTRIMERS, OR HETEROTRIMERS IN ASSOCIATION
CC WITH ALPHA 2(VIII) TYPE COLLAGENS.
CC -1 PPM: PROLINS AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
CC UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
CC -1 MISCELLANEOUS: FOUR CONSECUTIVE GLY-PRO-PRO TRIPLETS ARE PRESENT
CC AT THE C-TERMINUS OF THE TRIPLE-HELICAL REGION. THESE MAY PROVIDE
CC THE HIGH THERMAL STABILITY OF THIS REGION.
CC -1 SIMILARITY: STRONG, TO ALPHA 2 TYPES VIII AND X COLLAGENS.
CC -1 SIMILARITY: CONTAINS 1 C10 DOMAIN.
CC -----
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CC -----
DR EMBL; X57527; CAA40748.1; -.
DR EMBL; BC013581; AAH13581.1; -.
DR PIR; S15435; S15435
DR GeneW; HGRC:2215; COL8A1.
DR MIM; 120251; -.
DR InterPro; IPR001073; C1q.
DR InterPro; IPR000087; Collagen.
DR Pfam; PF00386; C1q; 1.
DR Pfam; PF01391; Collagen; 8.
DR PRINTS; PR00007; COMPLEMENTC1Q.
DR ProDom; PD000007; Collagen; 1.
DR SMART; SM00110; C1Q; 1.
DR PROSITE; PS01113; C1Q; 1.
KW Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
KW Glycoprotein; Cell adhesion; Collagen; Signal.
FT SIGNAL 1 28
FT CHAIN 29 744 COLLAGEN ALPHA 1(VIII) CHAIN.
FT DOMAIN 29 117 NONHELICAL REGION (NC2).
FT DOMAIN 118 571 TRIPLE-HELICAL REGION (COL1).
FT DOMAIN 572 744 NONHELICAL REGION (NC1).
FT DOMAIN 609 744 C1Q.
FT CONFLICT 262 262- P->L (IN REF. 1).
FT CONFLICT 297 297 P->R (IN REF. 1).
FT CONFLICT 344 344 P->A (IN REF. 1).
FT CONFLICT 382 382 A->S (IN REF. 1).

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FT	CONFLICT	388	388	P -> S (IN REF. 1)	1
FT	CONFLICT	454	454	L -> F (IN REF. 1)	1
FT	CONFLICT	464	464	A -> H (IN REF. 1)	1
FT	CONFLICT	601	601	Y -> T (IN REF. 1)	1
FT	CONFLICT	631	631	A -> G (IN REF. 1)	1
SO	SEQUENCE	744 AA;	73364 MW;	2BC1B0955DE2C9A3 CRC64;	

  

Alignment Scores:		Pred. No.:	Score:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
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			415.50						
			41.46%						
			32.16%						
			16.36%						
DB:		1							

  

US-09-944-944-41 (1-1377) x CA18_HUMAN (1-744)									
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DB	349	G1Y1LDELyLysProGlyPheProGlyProLysG1YAspAsgGlyMetG1YValPro	366						
OY	82	GCGGCC-----TGGCCGGGAGAGAGCGCGGGCTGGAGCACCA	120						
DB	369	G1YAlALeUeUyProArGlyGlyLysG1YProIleG1YAlALeUyIleG1YPro	388						
OY	121	CCA-----ACGTGGAGGGrTCGAGAGAGCGAC-----GCCCGCAAGAGCGCATCGG	168						
DB	389	ProG1Ys1uProG1YLeuProG1YIleProG1YProMetG1YProProG1YAlIleG1Y	408						
OY	169	GAGCCGGGA-----GGGGGAGACTCGAGAGAGACCCCGGCGTCCGGCTCCGG	216						
DB	409	PheProG1YProLysG1YLeuG1YLeuG1YIleVal--G1YProG1YLeuG1YProG1YPro	427						
OY	217	TGCCAGCGCATATAGGCCCACTCTGCTGCTCTGCTGCTGGCGCGCGCGCGCTGCC	278						
DB	428	LysG1Ys1uProG1YLeuG1YLeuG1YLeuG1YLeuG1YLeuG1YLeuG1YLeuG1Y	447						
OY	277	CCCATCTGGAGAGCAACAATATCCCGACCT-----	306						
DB	448	ProProG1YMetArG1YLeuProG1YProIleG1YProLysG1YLeuAlaG1YLeuLys	467						
OY	307	-----CTGGCCGGGGCACCCCGGCTT-----CCAGGCAC	336						
DB	468	G1YValProG1YLeuProG1YVal-ProG1YLeuG1YProLysG1YLeuProG1YI	487						
OY	337	GCGGGGCAACATGGAGCCAG-----GGCTTGGCGCGCGCGCATGGCCCGCACGG	387						
DB	487	eProG1YAspG1YLeuG1YLeuG1YProProG1YIleProG1YIleG1YLeuG1YProSerG1	507						
OY	388	CCGCGACGGCGCGCGCGGCGTCCGGAGAGAAAGCAGAGGGCGGAGCGCGGATGCC	447						
DB	507	YProIleG1YProProG1YIleProG1YProLysG1YLeuProG1YLeuProG1YProPr	527						
OY	448	G-----	448						
DB	527	OG1YpHeProG1YIleG1YLysProG1YValAlaG1YLeuHisG1YProProG1YLysPr	547						
OY	449	-----GAGACTCGAGGGGAGCCCGCGCGGAGAGAGAGCGGAGCCCGGGGGCC	499						
DB	547	OG1YAlALeUeUyProG1YLeuG1YLeuProG1YLeuProG1YProProG1YProG1YPr	567						
OY	499	CACCGGGCC-----	508						
DB	567	OGProG1YProProAlALeUeUyMetProProArProProProProG1YLeuG1YLeuProAs	587						
OY	509	-----GCCGGGGAGTGTCTCGGTCTCCGATCCGCTTCAAGCCCAAGCGCTCCGA	561						
DB	587	pMetG1YLeuG1YIleAspG1YValLysProProHisAlaTyrG1YAlaLysLysG1Y	607						
OY	562	GAGCGGGGTCCT-----CC	576						
DB	607	Shsng1Yg1YProAlATyrG1YLeuMetProAlaPheThrAlaG1YLeuThrAlaProPhePr	627						



Db 129 ThrThrGlnTyr---ProGluAlaAsnAlaLeuValArgPheAsnSerValValThrAsn 147  
 QY 620 GAGCAGGAGCATTCAGCAGCCGCTCAGCCGCAAGTTACCTGCGAGGCTCGGGGTAC 679  
 Db 148 ProGlnGlnTyrAsnProSerThrGlyLysPheThrGlyValAlaProGlyLeuTyr 167  
 QY 680 TACTTCGCGTCATGACGCGCTGACCGGCGCAGCTGCAAGTTGATCGTGGAAGAT 739  
 Db 168 TyrPhe---ValTyrTyrThrSerHisThrAlaAsnLeuGlyValHisLeuAsnLeu 186  
 QY 740 GCGCAATCATGCTCTCTCTCTCCAGTTTTCGGGGGGTGGCCCAAGCCCTCGCTC 799  
 Db 187 LeuAlaArgValAlaSerPheCysAspHisMetPheAsn---SerLysGlnValSer--- 204  
 QY 800 TCGGGGGGGGCGCATGTCAGGCTGAGGCTGAGCCTGAGCAGCTGTGGTGGTGGTGG 859  
 Db 205 SerGlyGlyAlaLeuAlaSerGlyLeuAlaArgGlyAspGluValTyr-----LeuSerVal 222  
 QY 860 GGTGACATCATGTCATGTCAGCATCAAGACAGACAGACAGACCTTCCTCGGATTTCG 919  
 Db 223 AsnAspTyrAsnGlyMetValGlyLeuGlySerAsnSerValPheSerGlyPheLeu 242  
 QY 920 GTGACTCTCGAC 931  
 Db 243 LeuPheProAsp 246  
 RESULT 14  
 COLE\_LEPMA STANDARD: PRT; 419 AA.  
 AC P98085; Q91080;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Inner ear-specific collagen precursor (Saccular collagen).  
 OS Lepomis macrochirus (Bluegill).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 CC Acanthomorphi; Acanthopterygii; Perciformes; Percoidae;  
 CC Centrarchidae; Lepomis.  
 CC NCBI\_TaxID=1106;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95167486; PubMed=7863331;  
 RA Davis J.G., Oberholzer J.C., Burns F.R., Greene M.I.;  
 RT "Molecular cloning and characterization of an inner ear-specific  
 structural protein.";  
 RL Science 267:1031-1034(1995).  
 RN [2]  
 RP CONCEPTUAL TRANSLATION.  
 RA GIBSON T.;  
 RL Submitted (MAR-1995) to the SWISS-PROT data bank.  
 CC -I- FUNCTION: FORMS A MICROSTRUCTURAL MATRIX WITHIN THE OTOLITHIC  
 MEMBRANE (PROBABLY).  
 CC -I- TISSUE SPECIFICITY: SPECIALIZED SECRETORY SUPPORTING CELLS AT THE  
 OTHER PERIMETER OF THE SACCULAR EPITHELIUM.  
 CC -I- SIMILARITY: CONTAINS 1 C10 DOMAIN.  
 CC -I- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT HAD TO BE  
 INTRODUCED FOR POSITIONS 391-419 SO AS TO MAXIMIZE THE SIMILARITY  
 WITH OTHER SHORT-CHAIN COLLAGENS.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL: U17431; AA69978.1; ALT\_FRAME.  
 DR InterPro: IPR001073; C1q.  
 DR InterPro: IPR000087; Collagen.  
 DR Pfam: PF00386; C1q; 1.

DR Pfam: PF01391; Collagen; 3.  
 DR PRINTS: PR00007; COMPLENTECQ.  
 DR SMART: SM0110; C1Q; 1.  
 DR PROSITE: PS01113; C1Q; 1.  
 KW Extracellular matrix; Repeat; Collagen; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT DOMAIN 20 419 INNER EAR-SPECIFIC COLLAGEN.  
 FT DOMAIN 20 57 NONHELICAL REGION (NC2).  
 FT DOMAIN 58 274 TRIPLE-HELICAL REGION (COL1).  
 FT DOMAIN 275 419 NONHELICAL REGION (NC1).  
 FT DOMAIN 272 419 C1Q.  
 FT CARBOHYD 37 37 N-LINKED (GICNAC. . .) (POTENTIAL).  
 FT CARBOHYD 320 320 N-LINKED (GICNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 419 AA; 43634 MW; 570CDB9675FC0F39 CRC64;  
 Alignment Scores:  
 Pred. No.: 4,89e-12 Length: 419  
 Score: 407.00 Matches: 120  
 Percent Similarity: 44.38% Conservative: 26  
 Best Local Similarity: 36.47% Mismatches: 140  
 Query Match: 16.02% Indels: 43  
 DB: 1 Gaps: 11  
 US-09-944-944-41 (1-1377) x COLE\_LEPMA (1-419)  
 QY 28 GGAAGCGGAGCGCGGAGGAGCGAAGCAGCATGCGGGGAC-----GGCAGG 75  
 Db 97 GlyLeuProGlyAlaAsnGlyLeuAsnGlyAspIleGlyLysGlyAspGlnGlyPro 116  
 QY 76 GCAGG-----GGCGCTGCGCGGAGGAGCGCGGGGTGAGCAGCA----- 120  
 Db 117 ValGlyLeuProGlyValAlaProGlyLysProGlyLysGlyLysGlyAspProGly 136  
 QY 121 -----CCACTGAGGAGTCCGAGTAGCAGCGCGCCCGAAGAGGCC 162  
 Db 137 LeuLysGlyAspLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 156  
 QY 163 ATCGGGAGCGCGG-----GGGGGACTCGAGAGAGACCGCGCGCGGCTCCGCGGTC 219  
 Db 157 ---GlyGlyProGlyLeuAsnGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 172  
 QY 220 CAGCGCTATGAGGCGCATCT 279  
 Db 173 -----PrometGlyProGlyLeuAlaGlyThrLysGlyLeu 184  
 QY 280 ACTGACAGCAACAAGATCCCAAGCTCTGC---CCGGGACACCCCGCTTCAGGCAC 336  
 Db 185 LysGlyGlyGlnGlyLeuLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 204  
 QY 337 GCCGGCCACCATGACGAGCGAGGCTTCCGCGCGCGGAGCGCGCGCGCGCGCGCG 396  
 Db 204 ProGlyLeuArgGlyGlyMetGlyLeuAsnGlyLysAspGlyValLysGlyLysGly 224  
 QY 397 CGCGCCGCGGCGCTCCGCGGAGAGAGAGGCGCGGAGCGCGGAGCGCGGAGCT-- 454  
 Db 224 GlyLeuProGlyProLeuGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 244  
 QY 455 -----CGAGGGAGCCCGCGCGCGCGCGAGAGAGAGCGGAGC 489  
 Db 244 GglyGlyArgGlyMetAlaGlyLeuArgGlyLysGlyLysGlyLysGlyLysGlyLys 264  
 QY 490 CGCGGGCGCGACCGCGCGCTCCGCGGAGTGCCTGCTCCGCGAGTCCGCTTAAAGCG 549  
 Db 264 CArgGlyProLysGlyProProGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 284  
 QY 550 CAAGGCTCCGAGAGCGCGGTCGCTCCCGCTGACCACTGCGCTTCCGAGCGGCT 609  
 Db 284 GlyLeuPheProSerArgSerPheProProProSerLeuProValLysPheAspLys 304  
 QY 610 GCTGCTGACGAGCAGGAGCATTCAGCAGCGCGTCAAGGAGTTCACCTGCGAGGTC 669  
 Db 304 LpHeTyrAsnGlyGlyGlyLysThrPsrProThrLeuAsnLysPheAsnValThrTyrPr 324



GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 21, 2003, 15:31:46 ; Search time 92.5 Seconds  
(without alignments)  
6134.635 Million cell updates/sec

Title: US-09-944-944-41

Perfect score: 2540  
Sequence: 1 gactagctctcttgagctc.....aaaaaaaaaaaaaaaaaaaaa 1377

Scoring table:

BIOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODL=frame+ n2p model -DEV=xlh  
-DB=SPREMBL\_21 -OPMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blsum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR.SCORE=Pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTMT=pio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09944944\_QCGN\_1.1.79 @runat\_13062003\_145846\_22773 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGOQUERY -NEG.SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: SPREMBL\_21.\*  
2: sp\_archaea.\*  
3: sp\_bacteria.\*  
4: sp\_fungi.\*  
5: sp\_human.\*  
6: sp\_invertebrate.\*  
7: sp\_mammal.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp Vertebrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1254	49.4	243	11 08R002	08R002 mus musculi

2	457	18.0	675	6	09N178	09n178 sus scrofa
3	429	16.9	295	11	09Z1K4	09z1k4 rattus norv
4	425.5	16.8	240	6	095M04	095m04 bos taurus
5	423	16.7	243	6	095UD7	095ud7 macaca mula
6	418	16.5	744	11	09D2V4	09d2v4 mus musculi
7	418	16.5	744	11	0921S8	0921s8 mus musculi
8	415.5	16.4	744	4	096D07	096d07 homo sapien
9	414	16.3	705	4	08REJ5	08rej5 homo sapien
10	398	15.7	294	11	09D8U4	09d8u4 mus musculi
11	373.5	14.7	194	6	095J95	095j95 canis famill
12	325	12.8	1458	13	0910B9	0910b9 oncorhynch
13	322	12.7	1461	4	076045	076045 homo sapien
14	321.5	12.7	1450	13	09YIB4	09yib4 cynops pyrr
15	320	12.6	1419	11	0631Z3	0631z3 rattus norv
16	319.5	12.6	1445	13	0932S1	0932s1 rana catesb
17	317	12.5	678	13	0934B6	0934b6 oncorhynch
18	314	12.4	245	11	09DCM6	09dcm6 mus musculi
19	313.5	12.3	1442	11	062031	062031 mus musculi
20	313.5	12.3	1442	11	062033	062033 mus musculi
21	310.5	12.3	889	16	09F2N5	09f2n5 streptomyc
22	310.5	12.2	1459	11	062032	062032 mus musculi
23	308	12.1	902	5	016161	016161 mytilus edu
24	308	12.1	1418	6	028396	028396 equus caball
25	308	12.1	1487	6	077753	077753 canis famill
26	307.5	12.1	1160	4	014046	014046 homo sapien
27	307.5	12.1	1487	4	014047	014047 homo sapien
28	307	12.1	1420	13	090W37	090w37 gallus galli
29	306.5	12.1	1447	13	091B91	091b91 xenopus lae
30	305	12.0	1453	11	063079	063079 rattus norv
31	300.5	11.8	1486	13	091717	091717 xenopus lae
32	299	11.8	1840	11	09J103	09j103 rattus norv
33	298.5	11.8	809	13	093485	093485 oncorhynch
34	298.5	11.8	888	13	090796	090796 gallus galli
35	298.5	11.8	1449	13	0910C0	0910c0 oncorhynch
36	298	11.7	1745	4	09N2Q6	09n2q6 homo sapien
37	297	11.7	1549	11	060444	060444 cricetus
38	296	11.7	684	5	P90679	P90679 arenicola m
39	295.5	11.6	589	11	099JL6	099j16 mus musculi
40	295.5	11.6	730	5	026052	026052 mus musculi
41	295.5	11.6	922	5	044367	044367 mytilus edu
42	295	11.6	2944	11	063870	063870 mus musculi
43	294	11.6	1352	13	090YX0	090yx0 brachydanio
44	294	11.6	1840	11	060467	060467 cricetus
45	293	11.5	1418	13	09W7R9	09w7r9 cynops pyrr

## ALIGNMENTS

### RESULT 1

ID	08R002	PRELIMINARY:	PRT:	243 AA.
AC	08R002			
DT	01-JUN-2002 (TEMBLrel. 21, Created)			
DT	01-JUN-2002 (TEMBLrel. 21, Last sequence update)			
DE	01-JUN-2002 (TEMBLrel. 21, Last annotation update)			
OS	Similar to DKFZP586B0621 protein (Hypothetical 25.4 kDa protein).			
OC	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;			
OX	NCBI_TaxID=10090;			
RN	[1]			
RA	SEQUENCE FROM N.A.			
RA	Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; BC023068; AAH23068.1; -			
DR	EMBL; BC025174; AAH25174.1; -			
KW	Hypothetical protein.			
SQ	SEQUENCE 243 AA; 25420 MW; 498129CD051DB97B CRC64;			



Db	449	-----				-----	GGACCTCGAGGGA	462
Oy	449	-----				-----	GGACCTCGAGGGA	462
Db	475	oProglyProAlaGlyIleAlaThrLysGlyLeuAsnGlyProThrglyProProGlyIpr				-----	GGACCTCGAGGGA	495
Oy	463	CCCGCGGGCGGAGAGAGAGCGG-----				-----	GGACCTCGAGGGA	504
Db	495	oProGlyProIlyGlyHisAlaGlyIleGlyLeuProGlyLeuProGlyProProGlyIpr				-----	GGACCTCGAGGGA	515
Oy	505	GCGTCCGGGGGAGTCTCGGCTGCTCCG-----				-----	GGACCTCGAGGGA	540
Db	515	yProProGlyIpr-----AlaValIprProGlyIprGlyIprGlyIprGlyIprGlyIpr				-----	GGACCTCGAGGGA	554
Oy	541	CTTCAGCGCCAGCGCTCCGAGAGCGGGTGCCT-----				-----	GGACCTCGAGGGA	574
Db	534	eValSerAlaAsnGlyIprValThrGlyMetProValSerAlaPheThrValIleLeuSe				-----	GGACCTCGAGGGA	554
Oy	575	-----CCGCGCTGAGCGACACCTTCCGCTTCGACCGCGGCTGAGAGCA				-----	GGACCTCGAGGGA	624
Db	554	rLysAlaIlyrProAlaIleGlyAlaProIleProPheAspIlyIleLeuIlyrAsnGlyI				-----	GGACCTCGAGGGA	574
Oy	625	GGGACATTACAGCGCGCTCACCGGAGAGTACACGTCGCGGCGGCTGATACATT				-----	GGACCTCGAGGGA	684
Db	574	nglnHisIlyrAspProIlyrStnGlyIlePheThrIlyrAspArgIleProGlyIlyrIpr				-----	GGACCTCGAGGGA	594
Oy	685	CGCGCTCCATGCGCACCGCTTACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG				-----	GGACCTCGAGGGA	744
Db	594	eSerIlyrHisIleHisValIlyrGlyIlyrHisAlaIprValIlyrLeuIlyrLysAsnGly				-----	GGACCTCGAGGGA	614
Oy	745	ATCCATTGCGC---TCCTTCTTCACGATTTTCGGGGGCGGCGGCGGCGGCGGCTC				-----	GGACCTCGAGGGA	801
Db	614	rProValMetIlyrThrIlyrAspGlyIlyrValIlyrGlyIlyrLeuAspGlnAla----				-----	GGACCTCGAGGGA	632
Oy	802	GGGGGGGGCGCATGCTGAGGCTGGAGACCTGAGACCAAGTGTGGGTCCAGTGGTGG				-----	GGACCTCGAGGGA	861
Db	632	rGlySerAlaIleLeuAspLeuThrAspAsnAspGlnValIlyrPheGlnLeuProAsnAl				-----	GGACCTCGAGGGA	652
Oy	862	TGACTACATTTGGGACATCTATGCGCAGCATCAAGACAGACAGCACACCTTCGATTTGG				-----	GGACCTCGAGGGA	921
Db	652	aglYserAsnGlyLeuIlyrSerSerGlyIlyrValHisSerSerPheSerGlyPheLeuVa				-----	GGACCTCGAGGGA	672
Oy	922	G 922				-----	GGACCTCGAGGGA	922
Db	672	1 672				-----	GGACCTCGAGGGA	672

RESULT 3

0921K4	PRELIMINARY:	PRT:	295 AA.
AC	0921K4:		
DT	01-MAY-1999 (TREMBLrel. 10, Created)		
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)		
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)		
DE	Collagen alpha 1 type X (Fragment).		
GN	COL10A1.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY;		
RX	MEDLINE=20310874; PubMed=10853827;		
RA	Marx S.A., Lundmark C., Christensen C., Wirtz T., Odgren P.R.,		
RT	Seifert M.F., Mackay C.A., Mason-Savas A., Popoff S.E.;		
RT	"Endochondral bone formation in toothless (osteopetrotic) rats:		
RL	failures of chondrocyte patterning and type x collagen expression."		
DR	Int. J. Dev. Biol. 44:309-316(2000).		
DR	EMBL: AJ131848; CAA10518.1; -		
DR	InterPro: IPR001073; C1q.		
DR	InterPro: IPR000087; Collagen.		
DR	Pfam: PF00386; C1q; 1.		





```

QY 251 CTCCTGGGCGTGGCGGGCTGGCGGGCCCTGAGCAGACACAGATCCCGAGCTTGC 310
    ||||| ||| |||||
Db 27 LeuLeuProLeuProLySgLYala-----Cys 35
QY 311 CCGGGGCAACCCCGGCTTTCAGGCAAGCCGGGCAACATGGCAGCCAGGCGTTCGGGCG 370
    ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 36 Thrlyl-----TrpMetAlaGlyLeuProGlyHisProGlyHisAlaGlyValProGly 53
QY 371 CGCGATGGCGCGGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 430
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 54 ArgAspGlyArgAsp-----GlyThrProGlyLeuLySgLYala 67
QY 431 GGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 463
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68 GlyAspProGlyLeuIleGlyProLySgLYalaThrlylValThrlylVal 87
QY 464 CCGGGGCGCGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 523
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 88 GluGlyProArgGlyPheProGlyIleGlyGlyArgGlyGlyProGlyGlyGly 107
QY 524 GTGCTCCGCGATCCGCTTTCAGCGCCAGCGGCTCCAGAGCGGCGGCGGCGGCGGCTCT 583
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 108 TyrValTyrArgSerAlaPheSerVal---GlyLeuGlyThrTyrValThrValPro--- 125
QY 584 GACGACCGCTTCCCTGACCGCGCTGCTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 643
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 AsnMetProIleLeuArgPheThrlylSerLeuPheGlyHisAlaMetLeuPheThrTyr 145
QY 644 ACCGGCAAGTTCACCTGCGGAGTGGCTGGGCTGACTACTGCGCGGCTCCAGTCCAGC 703
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 146 ThrGlyLysPheHisCysAsnIleProGlyLeuTyrTyrPheAlaTyrHisIleThrVal 165
QY 704 TACCGGGCGAGCTGATGCTGTAAGATGCGAGATCC---ATGCCCTTTC 760
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 166 TyrMetLysAspValLySgLYalaSerLeuPheLySgLYalaMetLeuPheThrTyr 185
QY 761 TTCGATTTTTCGGGGGCTGGCGGCAAGCGGCTGCTCGGCGGCGGCGGCGGCGGCGG 820
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 AspGlnTyrGlnGlnAsnAsnValAspGlnAla-----SerGlySerValLeuLeuHis 203
QY 821 CTGAGCGCTGAGAGCAAGTGTGGTGCAGGTC---GGTGGGTCGACTACTGTCGATC 877
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 204 LeuGlnValGlyAspGlnValTyrPheGlnValTyrGlyGlyGlyGlyGlyGlyGly 223
QY 878 TATGCGACATCAACAGACAGACAGCTTCCGCGATTTCTGCTACTCCGAC 931
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 224 TyrAlaAspAsnAspAsnAspSerThrPheThrGlyPheLeuLeuTyrHisAsp 241

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## RESULT 6

```

Q9D2V4 PRELIMINARY: PRT: 744 AA.
ID 09D2V4.
AC 09D2V4.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE Procollagen, type VIII, alpha 1.
GN COL8A1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mns.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shlnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Glassl C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Mikalido I., Pesole G., Quackenbush J.,

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RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baladrelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
RA Norone P., Rung B., Schoenbach M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK018742; BAB31383.1; -.
DR MGD: MGI:88463; COL8A1.
DR InterPro: IPR001073; C1q.
DR InterPro: IPR000087; Collagen.
DR Pfam: PF00386; C1q; 1.
DR PRINTS: PR00007; COMPLEMENTC1Q.
DR SMART: SM00110; C1Q; 1.
DR PROSITE: PS01113; C1Q; 1.
SQ SEQUENCE 744 AA; 73581 MW; C659BDCBCD6EB9C CRC64;

Alignment Scores:
Pred. No.: 7,566-18 Length: 744
Score: 418.00 Matches: 124
Percent Similarity: 41.318 Conservative: 40
Best Local Similarity: 31.238 Mismatches: 134
Query Match: 16,468 Indels: 99
DB: 11 Gaps: 12

US-09-944-944-41 (1-1377) x Q9D2V4 (1-744)
QY 22 GGAGAGAGAAAGCGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 81
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Db 350 GlyValGlyLysProGlyPheProGlyProLySgLYalaPargLyIleGlyValPro 369
QY 82 GCGGCGC-----TGGCGGGGAGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
    ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 370 GlyValIleGlyProArgGlyGlyLySgLYalaProIleGlyAlaProIleMetGlyLysPro 389
QY 121 CCA-----ACTGAGAGGTCGAGTACGAGAC-----GCCCGAGAGAGGCGCATCGG 168
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 390 ProGlyGlnProGlyLeuProIleProIleProIleProIleProIleProIleProIle 409
QY 169 GAGCGGGA-----GGGAGACTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 216
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 410 PheProGlyProLySgLYalaGlyValValAla---GlyProGlnGlyProProGlyPro 428
QY 217 TGGCAGCGGTATGAGGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 276
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 429 LysGlyGlnProGlyLeuGlnGlyPheProGlyLysProGlyPheLeuGlyGlyValGly 448
QY 277 CCCACTGAGCAGACAAAGATCCCGAGCT----- 306
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 449 ProProGlyMetArgGlyLeuProIleProIleGlyProLySgLYalaGlyLysHisLys 468
QY 307 ---CTGCCGGGGGAGACCCCGGCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 363
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 469 GlyLeuProGlyLeu---ProGlyValAlaProGlyLeuGlyProLySgLYalaGlyProGly 488
QY 364 GCGGCGCGCGATGGCGCGAGCGGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGAG 423
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Db 488 eProLySgLYalaGlyLeuGlnGlyProProGlyLysProGlyLysValGlyProSerGly 508
QY 424 CGAGGCGGAGAGCGCGGAGCTGCGGAGCTCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 466
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 508 yProIleGlyProProGlyLysProGlyProLySgLYalaGlyLysProGlyLysProPro 528
QY 466 ----- 466
Db 528 -oGlyPheProGlyValGlyLysProGlyValAlaGlyLeuHisGlyProProGlyLysPr 548

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QY 757 TTTTCCAGTTTTCGGGGGGTGGCCCAAGCAGCCTTCGTCGCGGGGGGGCCATGAT 816  
 Db 688 rTyrAspLysIleuTyrLysGlyPheLeuAspGlnAla-----SerGlySerAlaValle 706  
 QY 817 GAGCTGAGACCTGAGACCAAGTGTGGTGCAGGTGGGTGTGACTACATTGGCAT 876  
 Db 706 uLeuLeuArpProGlyAspGlnValPheLeuGlnMetProSerGlnGlnAlaAlaGlyLe 726  
 QY 877 CTATGCCAGCATCAAGACAGACAGCAGCCTTCCTCCGATTTTCGTGCTAC 925  
 Db 726 uTyrAlaGlyLeuTyrValHisSerSerPheSerGlyTyrLeuLeuTyr 742

## RESULT 8

096D07

PRELIMINARY: PRT: 744 AA.

ID 096D07  
 AC 096D07  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Hypothetical 73.4 kDa protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=LUNG;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC013581; AAH13581.1;  
 DR InterPro; IPR001073; C1q.  
 DR InterPro; IPR000087; Collagen.  
 DR Pfam; PF00386; C1q; 1.  
 DR ProDom; PD000007; Collagen; 7.  
 DR ProSite; PS01113; C1Q; UNKNOWM\_1.  
 KW Collagen; Hypothetical protein.  
 SQ SEQUENCE 744 AA; 73364 MW; 2BC1B0955DE2C9A3 CRC64;

## Alignment Scores:

Score: 1.07e-17 Length: 744  
 Percent Similarity: 415.50 Matches: 128  
 Best Local Similarity: 41.46% Conservative: 37  
 Query Match: 16.36% Mismatches: 133  
 DB: 4 Gaps: 100  
 13

US-09-944-944-41 (1-1377) x 096D07 (1-744)

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 Db 349 GlyIleuGlyLysProGlyPheProGlyProLysGlyAspArgGlyMetGlyGlyValPro 368  
 QY 82 GCGCGC-----TGCGCGGAGAGAGCGCGGGGGGTGAGCACCA 120  
 Db 369 GlyAlaLeuGlyProArgGlyGlyLysGlyProIleGlyAlaProGlyIleGlyGlyPro 388  
 QY 121 CCA-----ACTGGAGGTCGCGAGTACGAGC-----GCCCGCAAGAGCGCCATCGG 168  
 Db 389 ProGlyLysProGlyLysProGlyLysProGlyLysProGlyLysProGlyLysProGly 408  
 QY 169 GAGCGGGA-----GGGGGACATGCGAGGAGCGCGCGGCGTCCGGGCTCCGG 216  
 Db 409 PheProGlyProLysGlyGlyGlyLeuVal-----GlyProGlnGlyProProGlyPro 427  
 QY 217 TGCAGCGCTATGAGCGCATCTCCCTGCTGCTGCTGCGGCGCTGCGCGCGCTCC 276  
 Db 428 LysGlyGlyProGlyLysGlyGlyGlyPheProGlyLysProGlyPheLeuGlyGlyValGly 447  
 QY 277 CCCACTGAGCAGCAACAGATCCCGACCT----- 306  
 Db 448 ProProGlyMetArgGlyLysProGlyProIleGlyProLysGlyLysGlyLysGlyLys 467

QY 307 -----CTGCCGGGGGACCCCGGCTT-----CCAGGCAC 336  
 Db 468 GlyValProGlyLysProGlyValProGlyLeuGlyProLysGlyGlyProGly 487  
 QY 337 GCCGGGCAACCATGAGCCAG-----GGCTTGCCGGGCGCGATGCCGCGAGCG 387  
 Db 487 eProLysAspGlnGlyLeuGlnGlyProProGlyLysProGlyLysGlyProSerG 507  
 QY 388 CCGCAGCGGCGCGCGCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 447  
 Db 507 yProIleGlyProProGlyLysProGlyProLysGlyGlyProGlyLysProGlyPro 527  
 QY 448 G----- 448  
 Db 527 oGlyPheProGlyLysGlyLysProGlyValAlaGlyLeuHisGlyProProGlyLys 547  
 QY 449 -----GACCTCGAGGGGAGCCCGCGCGGAGAGAGAGAGAGAGAGAGAGAGAG 498  
 Db 547 oGlyAlaLeuGlyProGlnGlyGlnProGlyLysProGlyProGlyProGlyPro 567  
 QY 499 CACCGGGGCT----- 508  
 Db 567 oProGlyProProAlaValMetProProProProProProGlnGlyLysGlyLysPro 587  
 QY 509 -----GCCGGGAGTGCCTCGCTCCGCGATCCGCTTCAGCGCCAGCGCTCCGA 561  
 Db 587 pMetGlyLeuGlyLysAspGlyValLysProProHisAlaTyrGlyAlaLysGlyGly 607  
 QY 562 GAGCGGGGCT-----CC 576  
 Db 607 sAsnGlyGlyProAlaTyrGlyLysMetProAlaPheThrAlaGlyLeuThrAlaProPhe 627  
 QY 577 GCCGTCTGACGACCTTCGCTTCGACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 636  
 Db 627 oProValGlyAlaProValLysPheAsnLysLeuLysGlyLysGlyLysGlyLys 647  
 QY 637 CGCCGTCAACGAGTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 696  
 Db 647 nProGlnThrGlyIlePheThrCysGlyValProGlyLysGlyLysGlyLysGlyLys 667  
 QY 697 CACCGTCAACGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 754  
 Db 667 HisCysLysGlyGlyLysAsnValTyrValAlaLeuPheLysAsnAsnGlnProValMet 687  
 QY 755 -TCTTCTTCCAGCTTTTCGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 813  
 Db 687 ThrTyrAspGlyLysGlyLysGlyPheLeuAspGlnAla-----SerGlySerAla 705  
 QY 814 GGTGAGGCTGAGGCTGAGGAGCAAGTGTGCTGAGGCTGCTGCTGCTGCTGCTGCTG 873  
 Db 705 lLeuLeuLeuArpProGlyAspArgValPheLeuGlnMetProSerGlnGlnAlaAla 725  
 QY 874 CATCTATGCGACATCAAGACAGACAGACAGCAGCCTTCCTCCGATTTTCGTGCTAC 925  
 Db 725 yLeuTyrAlaGlyLeuTyrValHisSerSerPheSerGlyTyrLeuLeuTyr 742

## RESULT 9

08TEJ5

PRELIMINARY: PRT: 705 AA.

ID 08TEJ5  
 AC 08TEJ5  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE FLJ00201 protein (Fragment).  
 GN FLJ00201.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=SPLEEN;  
 RA Jikuya H., Takano J., Nomura N., Kikuno R., Nagase T., Ohara O.;



Query Match:	15.67%	Indels:	50
DB:	11	Gaps:	7
US-09-944-944-41 (1-1377) x Q9D8U4 (1-294)			











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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 12:24:30 ; Search time 2191 Seconds  
(without alignments)  
10178.542 Million cell updates/sec

Title: US-09-944-944-41

Perfect score: 1377

Sequence: 1 gactagtcctcttgagctc.....aaaaaaaaaaaaaaaaa 1377

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST:  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estlin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mam:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	667	48.4	1093	BM924569
2	647	47.0	1154	BM547549
3	631	45.8	1623	BM926477
4	596	43.3	596	BM893587
5	584	42.4	724	BM1771879
6	578	42.0	578	BM893691

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c	8	560	40.7	596	13	BM544255	AGENCOCURT	BM544255
c	9	551	40.0	801	13	BM190880	BM190880	603031867
c	10	549	38.9	553	12	BF882978	IL3-ET011	BF882978
c	11	532	38.6	532	12	BF724241	bx02e11.y	BF724241
c	12	521	37.8	521	14	BM966810	1j26g10.y	BM966810
c	13	517	37.5	517	14	BM966954	1j26e08.y	BM966954
c	14	508	36.9	630	12	BM706609	602672994	BM706609
c	15	481	34.9	567	13	BM021381	1e76e01.y	BM021381
c	16	480	34.9	846	13	BM458455	603198837	BM458455
c	17	476	34.6	792	13	BM170921	603059737	BM170921
c	18	446	32.4	454	9	AI805087	tu33g05.x	AI805087
c	19	435	31.6	879	13	BM20945	603033989	BM20945
c	20	392	28.5	392	10	BE138819	xw95h11.x	BE138819
c	21	367	26.7	869	13	BM763193	603049929	BM763193
c	22	361	26.2	887	13	BM190062	603031867	BM190062
c	23	359	26.1	410	14	BM707291	UI-E-CR1-	BM707291
c	24	359	26.1	413	9	AI083823	qf18c08.x	AI083823
c	25	356	25.9	408	9	AI085548	qf24c09.x	AI085548
c	26	353	25.6	405	9	AI083824	qf18c09.x	AI083824
c	27	352	25.6	442	14	BM693336	UI-E-CR1-	BM693336
c	28	345	25.1	1045	14	BM920874	AGENCOCURT	BM920874
c	29	343	24.9	445	14	BM673416	UI-E-CR1-	BM673416
c	30	339	23.6	462	10	AM070344	xa10d10.x	AM070344
c	31	320	23.2	322	9	AI393090	tg25g10.x	AI393090
c	32	320	23.2	446	14	W92687	z692f04.s1	W92687
c	33	312	22.7	392	10	AM192716	x150b08.x	AM192716
c	34	310	22.5	372	12	BF764330	RC6-CS007	BF764330
c	35	308	22.4	449	13	BM668611	UI-E-CR1-	BM668611
c	36	302	21.9	361	10	AM172659	xj80g01.x	AM172659
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c	38	294	21.4	702	12	BF055285	7j77g02.x	BF055285
c	39	285	20.7	317	10	AM137263	UI-H-B11-	AM137263
c	40	277	20.1	277	9	AI564511	tg80c04.x	AI564511
c	41	269	19.5	370	9	AA775561	z125h01.s	AA775561
c	42	266	19.3	439	13	BM913487	602811208	BM913487
c	43	263	18.4	253	9	AI924106	w19e07.x	AI924106
c	44	248	18.0	316	14	M91217	HUMRTGEB.S	M91217
c	45	247	17.9	536	9	AI346326	qp50a04.x	AI346326

## ALIGNMENTS

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LOCUS  
DEFINITION  
AGENCOCURT\_6767665 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5760942  
5', mRNA sequence.  
ACCESSION  
BM924569  
VERSION  
BM924569.1 GI:19374948  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 1093)  
NIH-MGC <http://mgc.ncl.nih.gov/>.  
AUTHORS  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL  
Unpublished (1999)  
COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: L1AM12808 row: m column: 07  
High quality sequence stop: 590.  
Location/Qualifiers  
1..1093

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/db_xref="taxon:9606"
/clone="IMAGE:5760942"
/clone_1lb="NIH_MGC_116"
/lab_host="DH10B"
/Note="Organ: pooled colon, kidney, stomach; Vector:
pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon; 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC library."
197 a 359 g 198 t 3 others
BASE COUNT
ORIGIN

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Query Match	48.4%	Score 667	DB 14	Length 1093
Best Local Similarity	100.0%	Pred. No.	1.9e-151	
Matches 667	Conservative 0	Mismatches 0	Indels 0	Gaps 0

**QY**      331 AGGACGCCGGCGGCACCATGGCAGCCAGGCGCTTCCGGGCGGCATGGCGCCGCAAGGCGCG 390  
         |||||  
**Db**        1 AGGACGCCGGCGGCACCATGGCAGCCAGGCGCTTCCGGGCGGCATGGCGCCGCAAGGCGCG 60

DY 391 CGACGCGCCGCCGGGGCTCCGGAGAGAAGCCGAGGGCGGAGGCCCGGATGCCGG 450

DB 61 CGACGCGCGCCCCGGGGCTCCGGAGAGAAGGCCTAAGGGTGGAGACCCCGGATCCCCCT 120

[illegible]

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571 GCCTCGCGCTGACGACACCCCTTGCCCTTGCACCGCGCTGCTGGTGAACGAGCAGGAGCA 630

DB 241GGCTCCGGCTCTGACGCACCCCTGGCCCTTCGACCCGCGCTGCTGGTGAACGAGCAGGGGACA 300  
OY 631 TTACGAGCCCGTACCGGCAAGTTCACTGCCAGGTGCTGGGCTCTACTATTGGCCGT 690

Dd 301TTACGACGCCGTCCACCGGCAAGTTCACTCCACCTGCCACAGTGCCTGGGGTCTACTACTTCGGCGT 360

Dy 691 CCATGCCCAACCGTTCACCGGGCCACGCCCTCAGATTGATCTGTGTAGAAGATGGCGATCCAT 750

Db 361 CCATGCCACCGTATACCGGGCCAGCCTCAGTTTGATCTGTCAGAAATGGCCGATCCAT 420  
 Dy 751 TGCCTCTTTCTTCAGTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCTCGGGGGGGGC 810

Db 421 TGCTCTTCTTCAGTTTTCGGGGGGTGGCCCAAGCAGCCTCGTCTCGGGGGGGGAC 480

Db 481 CATGGTGAAGGCTGAGCCTGAGGACCAAGTGTGGGTGCAAGTGGGTGTGGGTACTACAT 540

Dd 541 TGGCATCTATGCGAGCATCAAGACAGACGACACTTCCGGGATTTCTGGTGTACTCCGA 600

531 CTGGACACAGCTCCCCAGCTCTTCTCTATGCCCCACATGGAAAGTGAGCTCATGCTCTCACT 990  
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 601 CTGGACACAGCTCCCCAGCTCTTCTCTATGCCCCACATGGAAAGTGAGCTCATGCTCTCACT 660

QY	991	CCTAGAA	997
Db	661	CCTAGAA	667

## RESULT 2

LOCUS BMS47549 1154 bp mRNA linear EST 20-FEB-2002  
DEFINITION AGNCOURT.6507694 NIH\_MGC\_125 Homo sapiens CDNA clone IMAGE:5724522  
5'', mRNA sequence.  
ACCESSION BMS47549  
VERSION BMS47549.1 GI:18781410  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1154)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: L16M12713. row: 0 column: 19  
 High quality sequence stop: 591.

FEATURES	Location/Qualifiers
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/organism="Homo sapiens"  
/db_xref="taxon:9606"  
/clone="IMAGE:5724522"  
/clone_1lb="NH_MGC_125"  
/lab_host="DH10B"
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/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site\_1: EcoRV (destroyed); Site\_2: NotI; RNA source: pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

BASE COUNT	178 a	382 c	401 g	193 t
ORIGIN				

Query Match	47.0%	Score 647;	DB 13;	Length 1154;
Best Local Similarity	100.0%	Pred. No. 11e-146;		
Matches 647; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

OY 40 CGCGAGGAGCCGAACCAAGACTGTGGGTATACGGCAGGAGGCAGGGGGGCCCTTGSCCGGAGAGA 99  
| | | | |  
Db 1 CGCGAGGAGCGAACCAGGACTTGGGGGTATACGGCAGGAGGCAGGGGGGCCCTTGSCCGGAGAGA 60  
| | | | |

QY 100 AGCGGGGGCTTGAGACACACCAACTGGAGGCTCCGAGTAGCGAGCGCCCGAAGGAG 159  
61 AGCGGGGGGGCTTGAGACACACCAACTGGAGGCTCCGAGTAGCGAGCGCCCGAAGGAG 120			

QY 160 GCCATCGGGAGACCGGGAGGGGGGACTTCGAGAGAGACCCCGGGCTCCGGGCTCCCGGCTTC 219  
|||||

220 CAGCGCTATGAGGCCACTCCCTGCTGCTGCTGCTGCTGCGGCGCGCGCTGCGCCCC 279

Db 181 CAGCGCTATGAGGCCACTCCCTGCTCTGCTGCTCCTTGCGGCTGGCGCGCGGCTCGGCCCC 240

Qy 280 ACTGAGACACACAGATCCCGACGCTGCCCCGGGACACCCCGGCTTCAGAGGCACGCC 339

Db 241 ACTGGAGCACAACAAGATCCCAAGCTCTGCCCCGGGGACCCCGGCTTCCAGGCACAGCC 300

340 GGGCCACCATGGCAGCGAGGGCTTGGCCGGGCCCGATGGCCGCGAGCGAGCCCGCCGACGGCGC 399

[illegible]

QY 400 GCCCGGGGCTCCGGGAGAGAAAGGCGAGGCGGGGAGCTCCGGGAGCTCGAGG 459  
 Db 361 GCCCGGGGCTCCGGGAGAGAAAGGCGAGGCGGGGAGCTCCGGGAGCTCGAGG 420  
 QY 460 GGACCCCGGGCGCGAGGAGAGGCGGACCCCGGGGCGCACCGGGCTCCGGGAGTG 519  
 Db 421 GGACCCCGGGCGCGAGGAGAGGCGGACCCCGGGGCGCACCGGGCTCCGGGAGTG 480  
 QY 520 CTCGGTGCCTCCGGGAGGATCCGCTTCAGGCGCAAGCGCTCCGAGACCCGGGTCTCCGCC 579  
 Db 481 CTCGGTGCCTCCGGGAGGATCCGCTTCAGGCGCAAGCGCTCCGAGACCCGGGTCTCCGCC 540  
 QY 580 GTCTGACGACACCTTTCGCTTCGACCGCGCTCTGTGTAAGAGAGGACATTACGAGC 639  
 Db 541 GTCTGACGACACCTTTCGCTTCGACCGCGCTCTGTGTAAGAGAGGACATTACGAGC 600  
 QY 640 CGTCACCGGCAAGTTTACCTGCCAGAGTCTCTGGGGTCTACTACTTCG 686  
 Db 601 CGTCACCGGCAAGTTTACCTGCCAGAGTCTCTGGGGTCTACTACTTCG 647

RESULT 3  
 BM926477 1623 bp mRNA linear EST 12-MAR-2002  
 LOCUS AGENCOURT\_6644538 NIH\_MGC\_122 Homo sapiens, CDNA clone IMAGE:5766864  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BM926477  
 VERSION BM926477.1 GI:19376856  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 TITLE 1 (bases 1 to 1623)  
 JOURNAL NIH-MGC http://mgi.nci.nih.gov/  
 COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strussberg, Ph.D.  
 Email: csapbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.lnl.gov

Plate: LLM12824 row: d column: 01  
 High quality sequence stop: 558.  
 Location/Qualifiers

# FEATURES

1..1623  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_image="5766864"  
 /clone\_id="NIH\_MGC\_122"  
 /lab\_host="DH10B"  
 /note="Organ: pooled lung and spleen; Vector: pCMV-Sport6;  
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source  
 anonymous pool of 24 week female lung, 16 week female  
 spleen, and 20-22 week male spleens. Library is oligo-dT  
 primed and directionally cloned (EcoRV site is destroyed  
 upon cloning). Average insert size 1.4 kb, insert size  
 range 1-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 026. Note:  
 this is a NIH\_MGC Library."  
 BASE COUNT 263 a 505 c 550 g 299 t 6 others  
 ORIGIN

Query Match 45.8%; Score 631; DB 14; Length 1623;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-143;  
 Matches 631; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 71 GCAGGGCAGGGGGCGCTGGCGGGGAGAGAGCGGGGGCTGTGAGCACCACCACTGAG 130

Db 1 GCAGGGCAGGGGGCGCTGGCGGGGAGAGAGCGGGGGCTGTGAGCACCACCACTGAG 60  
 QY 131 GGTCCGAGTAGACGACGCCGCCGAAAGAGCCATCTGGGAGACCGGGAGGACTGCGA 190  
 Db 61 GGTCCGAGTAGACGACGCCGCCGAAAGAGCCATCTGGGAGACCGGGAGGACTGCGA 120  
 QY 191 GAGGACCCCGGGGCTCCGGGGCTCCGGGTCCAGGCGCTATGAGGCCATCTCTGCTGCTG 250  
 Db 121 GAGGACCCCGGGGCTCCGGGGCTCCGGGTCCAGGCGCTATGAGGCCATCTCTGCTGCTG 180  
 QY 251 CTCCTGGGCTTGGGGCGCGGCTCGGCCCTCAGTGCAGCAACAAGATCCCAAGCTCTGCG 310  
 Db 181 CTCCTGGGCTTGGGGCGCGGCTCGGCCCTCAGTGCAGCAACAAGATCCCAAGCTCTGCG 240  
 QY 311 CCGGGGCACCCCGGCTTCCAGGACGCGCGGACACATGAGCAGGAGGCTTGGCGGGC 370  
 Db 241 CCGGGGCACCCCGGCTTCCAGGACGCGCGGACACATGAGCAGGAGGCTTGGCGGGC 300  
 QY 371 CGCGATGGCGCGGACGCGCGGAGAGCGCGCGCGGCGCTCCGGGAGAGAGCGAGGAGC 430  
 Db 301 CGCGATGGCGCGGACGCGCGGAGAGCGCGCGCGGCGCTCCGGGAGAGAGCGAGGAGC 360  
 QY 431 GGGAGGCCGGGAGTCCCGGAGCTTCGAGGAGACCCCGGGCGCGAGAGAGCGGAGACC 490  
 Db 361 GGGAGGCCGGGAGTCCCGGAGCTTCGAGGAGACCCCGGGCGCGAGAGAGCGGAGACC 420  
 QY 491 GCGGGGCCACCGGGGCTTCGCGGGAGAGTGTCTCGCTCCGCCATCCGCTTACGCCCC 550  
 Db 421 GCGGGGCCACCGGGGCTTCGCGGGAGAGTGTCTCGCTCCGCCATCCGCTTACGCCCC 480  
 QY 551 AAGCGCTCCGAGAGCGGGGCTCTCCGCGCTGTCAGCAGCCCTTCGAGCGCGCTG 610  
 Db 481 AAGCGCTCCGAGAGCGGGGCTCTCCGCGCTGTCAGCAGCCCTTCGAGCGCGCTG 540  
 QY 611 CTGGTGAACGAGCAGGACATTACGACCGCGCTCAGCAGGCAAGTTTACCTGCCAGTGTGCT 670  
 Db 541 CTGGTGAACGAGCAGGACATTACGACCGCGCTCAGCAGGCAAGTTTACCTGCCAGTGTGCT 600  
 QY 671 GGGGCTCTACTTCTTCCGCTCCATGTCACCG 701  
 Db 601 GGGGCTCTACTTCTTCCGCTCCATGTCACCG 631

RESULT 4  
 BM893587/c 596 bp mRNA linear EST 29-APR-2002  
 LOCUS 112610.x1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens  
 DEFINITION cDNA clone IMAGE:6136122 3' similar to TR:Q9UFY4 Q9UFY4  
 HYPOTHETICAL 22.8 KD PROTEIN ;, mRNA sequence.  
 ACCESSION BM893587  
 VERSION BM893587.1 GI:19349055  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 TITLE 1 (bases 1 to 596)  
 JOURNAL Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,  
 Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,  
 Hillier, L., Marra, M., Pape, D., Wyllie, T., Martin, J., Blaisdell, A.,  
 Schmitt, A., Theising, B., Rittler, E., Ronko, I., Bennett, J., Cardenas,  
 M., Gibbons, M., McCann, R., Cole, R., Tsagaris, R., Williams, T.,  
 Jackson, Y., and Bowers, Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557





REFERENCE 1 (bases 1 to 574)  
 AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scarsdale,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blalstein,A., Schmitt,A., Theising,B., Ritter,E., Runko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarelis,I., Williams,T., Jackson,Y. and Bowers,Y.  
 TITLE Endocrine Pancreas Consortium  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept. of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@molbio.harvard.edu  
 Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: Juliana Brown (brown@fas.harvard.edu) This sequence now available from the IMAGE consortium, for clone orders contact: info@image.llnl.gov  
 High quality sequence stop: 413.

FEATURES  
 source  
 1..574  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5672905"  
 /clone\_1lb="Melton Normalized Human Islet 4 N4-HIS 1"  
 /sex="Both"  
 /issue\_type="Islets of Langerhans"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B"  
 /note="Organ: Pancreas; Vector: pSPORT1; Site:1: Not 1; Site:2: Sal 1; Starting library constructed using SuperScript Plasmid Library kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 128 a 175 c 162 g 109 t  
 ORIGIN

Query Match 41.4%; Score 570; DB 13; Length 574;  
 Best Local Similarity 100.0%; Pred. No. 6.3e-128;  
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 779 TGGCCCAAGCCAGCTCTGCTGGGGGGGCGCATGTGAGCTGAGACCTGAGACCAA 838  
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 DB 574 TGGCCCAAGCCAGCTCTGCTGGGGGGGCGCATGTGAGCTGAGACCTGAGACCAA 515  
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QY 839 GTGTGGGTGAGGGGTGGTGGTGGTACTACATTGGCATGTGATGCGACGATCAAGACAG 898  
 |||||||  
 DB 514 GTGTGGGTGAGGGGTGGTGGTGGTACTACATTGGCATGTGATGCGACGATCAAGACAG 455  
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QY 899 AGCAGCTTCCGAGATTTCTGATGCTCCGATGCGACAGCTCCCGAGCTTTGGCTTAG 958  
 |||||||  
 DB 454 AGCAGCTTCCGAGATTTCTGATGCTCCGATGCGACAGCTCCCGAGCTTTGGCTTAG 395  
 |||||||

QY 959 TGGCCACTGCAAGTGAAGTCAATGCTCTACTCTTAGAAGAGGGGTGAGCTGACAC 1018  
 |||||||  
 DB 394 TGGCCACTGCAAGTGAAGTCAATGCTCTACTCTTAGAAGAGGGGTGAGCTGACAC 335  
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QY 1019 CAGGTATCCAGAGAGGGGTGGCCCGCTGGAATATTGTGAATACATAGAGAGGTGGGGTA 1078  
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 DB 334 CAGGTATCCAGAGAGGGGTGGCCCGCTGGAATATTGTGAATACATAGAGAGGTGGGGTA 275  
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QY 1079 GAGCAGCTTCCGCTCTGCTGCTGCGCAAGATGGAGAACAGTGTCTGCGATCAGGTC 1138  
 |||||||  
 DB 274 GAGCAGCTTCCGCTCTGCTGCTGCGCAAGATGGAGAACAGTGTCTGCGATCAGGTC 215  
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QY 1139 TGGCAGCATGGGGGCGATGGCTGTGATTTCTGCCCAAGACACAGAGAGTGTGCTGCGC 1198  
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 DB 214 TGGCAGCATGGGGGCGATGGCTGTGATTTCTGCCCAAGACACAGAGAGTGTGCTGCGC 155  
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QY 1199 AAGGTAAAGTCCCGCATTTGCTGTGTCAGAGACCCACAGGTGGGGTGTCTTCTCGTG 1258  
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 DB 154 AAGGTAAAGTCCCGCATTTGCTGTGTCAGAGACCCACAGGTGGGGTGTCTTCTCGTG 95  
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QY 1259 TCCCTGCTTCTGTGATGCTCCCGACCCCTCTGCTGCGGGCGGCGCTTTCTCTCA 1318  
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 DB 94 TCCCTGCTTCTGTGATGCTCCCGACCCCTCTGCTGCGGGCGGCGCTTTCTCTCA 35  
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QY 1319 GAGATCACTCAATTAACCTTAAGAACCTCA 1348  
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 DB 34 GAGATCACTCAATTAACCTTAAGAACCTCA 5  
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RESULT 8  
 BM544255  
 LOCUS  
 DEFINITION  
 AGENCOURT\_6490655 NIH\_MGC\_125 Homo sapiens cDNA clone IMAGE:5587759  
 5', mRNA sequence.  
 ACCESSION  
 BM544255  
 VERSION  
 BM544255.1 GI:18775356  
 KEYWORDS  
 EST.  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NIH-MGC http://mgi.ncl.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@gs-femail.nih.gov  
 Tissue Procurement: Invitrogen  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:  
 http://image.llnl.gov  
 Plate: LAM12357 row: m column: 08  
 High quality sequence stop: 595.

FEATURES  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5587759"  
 /clone\_1lb="NIH\_MGC\_125"  
 /lab\_host="DH10B"  
 /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6; Site:1: EcoRV (destroyed); Site:2: NotI; RNA source pool of three ovaries, from females ranging in age from 38 to 49 yo. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb, insert size range 1-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 036."

BASE COUNT 138 a 158 c 172 g 127 t 1 others  
 ORIGIN

Query Match 40.7%; Score 560; DB 13; Length 596;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-125;  
 Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 789 CAGCTCTGCTCTGCGGGGGGCGCATGTGAGCTGAGCCTGAGACCAAGTGTGGGTGC 848  
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```

Db      1 CAGCCTCCGCTCGGGGGGGCCATGTGAGCTGAGGCTGAGGACCAAGTGTGGTGC 60
QY      849 AGTGGGCTGTGGGTGACTACATTTGGCATTTATGCCAGCATCAAGACAGACACTTCT 908
Db      61 AGTGGGCTGTGGGTGACTACATTTGGCATTTATGCCAGCATCAAGACAGACACTTCT 120
QY      909 CCGGATTTCTGTGTACTCCGACAGTCCAGCTCCCACTTTTGTGTGTGTGTGTGTGTGT 968
Db      121 CCGGATTTCTGTGTACTCCGACAGTCCAGCTCCCACTTTTGTGTGTGTGTGTGTGT 180
QY      969 AAAGTAGCTCATGTCTCTCATCTCTAAGAAGAGGGGTGTAGAGCTGACCAACAGTCTATCC 1028
Db      181 AAAGTAGCTCATGTCTCTCATCTCTAAGAAGAGGGGTGTAGAGCTGACCAACAGTCTATCC 240
QY      1029 AGGAGGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1088
Db      241 AGGAGGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 300
QY      1089 CGTCTGTCTGTGTGCAAGAAATGGAACAGTGGCTGTGTGCAATGCTGTGTGTGTGTGTGT 1148
Db      301 CGTCTGTCTGTGTGCAAGAAATGGAACAGTGGCTGTGTGCAATGCTGTGTGTGTGTGTGT 360
QY      1149 GGGCAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1208
Db      361 GGGCAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY      1209 CCCCCAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1268
Db      421 CCCCCAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
QY      1269 CTCTGGATCTCTCCCAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1328
Db      481 CTCTGGATCTCTCCCAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 540
QY      1329 AATTAACCTTAAGACCTCA 1348
Db      541 AATTAACCTTAAGACCTCA 560

RESULT 9
LOCUS   B1490880/c 801 bp mRNA linear EST 28-AUG-2001
DEFINITION 603031867r1 NIH_MGC.115 Homo sapiens cDNA clone IMAGE:5172880 3',
ACCESSION B1490880
VERSION   B1490880.1 GI:15330108
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
AUTHORS   1 (bases 1 to 801)
           National Institutes of Health, Mammalian Gene Collection (MGC)
           Unpublished (1999)
           Contact: Robert Strausberg, Ph.D.
           Email: cgaabs-remail.nih.gov
           Tissue Procurement: Life Technologies, Inc.
           cDNA Library Preparation: Life Technologies, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLM11430 row: f column: 17
           High quality sequence start: 8
           High quality sequence stop: 738
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               /organism="Homo sapiens"
               /db_xref="taxon:9606"
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/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
/notes="Organ: pooled brain, lung, testis; Vector:
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source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dr primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."

BASE COUNT      180 a      251 c      237 g      133 t

Query Match      40.0%; Score 551; DB 13; Length 801;
Best Local Similarity 100.0%; Pred. No. 1.7e-123;
Matches 551; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      730 GGTGAAGATGGGGAATCCATTCCTCTTCCAGTTTTCGGGGGGTGGCCAAAGCC 789
Db      580 GGTGAAGATGGGGAATCCATTCCTCTTTCCTTCAGTTTTCGGGGGGTGGCCAAAGCC 521
QY      790 AGCCTGCTCTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 849
Db      520 AGCCTGCTCTCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 461
QY      850 GGTGGGTGGGTGGGTGACTATATGGCATATGCGACATCAAGACAGACAGACCTTCTC 909
Db      460 GGTGGGTGGGTGGGTGACTATATGGCATATGCGACATCAAGACAGACAGACCTTCTC 401
QY      910 CGGATTTCTGGGTGACTCTGACCTGACAGCTGCCAGCTCCAGCTTGTGTGTGTGTGTGTGT 969
Db      400 CGGATTTCTGGGTGACTCTGACCTGACAGCTGCCAGCTGCCAGCTTGTGTGTGTGTGTGT 341
QY      970 AAGTAGCTCATGTCTCTCACTCTCTAGAGAGAGGGGTGTAGGCTGACACACAGTCAATCCA 1029
Db      340 AAGTAGCTCATGTCTCTCACTCTCTAGAGAGAGGGGTGTAGGCTGACACACAGTCAATCCA 281
QY      1030 GGAGGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 1089
Db      280 GGAGGGCTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 221
QY      1090 GTCTGTGCTCTGTGGCAAGAAATGGAACAGTGGCTGTGTGCAATGCTGTGCAAGATGG 1149
Db      220 GTCTGTGCTCTGTGGCAAGAAATGGAACAGTGGCTGTGTGCAATGCTGTGCAAGATGG 161
QY      1150 GGCAGTGGCTGTGATTTCTGCCCCAAGACAGAGAGAGTGTGTGTGTGTGTGTGTGT 1209
Db      160 GGCAGTGGCTGTGATTTCTGCCCCAAGACAGAGAGAGTGTGTGTGTGTGTGTGTGT 101
QY      1210 CCCCAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1269
Db      100 CCCCAGTGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 41
QY      1270 TCTGTGATCTCTC 1280
Db      40 TCTGTGATCTCTC 30

RESULT 10
LOCUS   BF882978/c 553 bp mRNA linear EST 17-JAN-2001
DEFINITION IL3-ET0113-061200-374-Cl01 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF882978
VERSION   BF882978.1 GI:12273104
KEYWORDS EST.
SOURCE   human.
ORGANISM Homo sapiens
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE Dias Neto, F., Garcia Correa, R., Verjovski-Almeida, S., Bionesi, M.R.,
           1 (bases 1 to 553)

```

TITLE  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags

JOURNAL  
MEDLINE  
COMMENT  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rue Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&ct=IL3-ET0113-  
061200-374-C10&ct3=2000-12-06&ct4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 553.

FEATURES  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_id="ET0113"  
/dev\_stage="Adult"  
/note="Organ: Lung; tumor: Vector: puc18; Site: 1: Sma1;  
Site: 2: Sma1; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."

BASE COUNT  
ORIGIN  
131 a 176 c 152 g 94 t

Query Match 39.9%; Score 549; DB 12; Length 553;  
Best Local Similarity 100.0%; Pred. No. 7.1e-123;  
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

749 ATTGCGCTCTTCTTCGAGTTTTCGGGGGGGCCCAAGCCAGCTGCTCTGGGGGGG 808  
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553 ATTGCGCTCTTCTTCGAGTTTTCGGGGGGGCCCAAGCCAGCTGCTCTGGGGGGG 494  
|||||  
809 GCCATGCTGAGCGTGGAGCGTGGAGCAAGTGTGGGTGAGCGTGGGTGGGTGACTAC 868  
|||||  
493 GCCATGCTGAGCGTGGAGCGTGGAGCAAGTGTGGGTGAGCGTGGGTGGGTGACTAC 434  
|||||  
869 ATTGCGATCTATGCGACATCAAGACAGACAGACACTTTCGCGATTTCGTGCTACTCC 928  
|||||  
433 ATTGCGATCTATGCGACATCAAGACAGACAGACACTTTCGCGATTTCGTGCTACTCC 374  
|||||  
929 GACTGGCAGACGCTCCCAAGCTCTTTCGTTAGTCCCACTGCAAAAGTCAAGCTCA 988  
|||||  
373 GACTGGCAGACGCTCCCAAGCTCTTTCGTTAGTCCCACTGCAAAAGTCAAGCTCA 314  
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989 CTCTAGAGAGAGGTGTGAGGCTGACACAGAGTCAATCCAGAGAGGCTGGCCCCCTGG 1048  
|||||  
313 CTCTAGAGAGAGGTGTGAGGCTGACACAGAGTCAATCCAGAGAGGCTGGCCCCCTGG 254  
|||||  
1049 AATATTGTGATGACTAGAGAGGTGTGAGGCTGACACAGTCTCCGTCCTGCTGGCAAGGA 1108  
|||||  
253 AATATTGTGATGACTAGAGAGGTGTGAGGCTGACACAGTCTCCGTCCTGCTGGCAAGGA 194  
|||||  
1109 ATGGGAACAGTGGCTGTCTCCGATCAGAGTCTGGCAGCAGTGGGCGAGTGGGATTTCTG 1168  
|||||  
193 ATGGGAACAGTGGCTGTCTCCGATCAGAGTCTGGCAGCAGTGGGCGAGTGGGATTTCTG 134  
|||||  
1169 CCCAAGCCAGAGAGTGTCTGTGCTGGCAGAGTGAAGTCCCGCACTGCTGCTGCCA 1228  
|||||

Db 133 CCCAAGCCAGAGAGTGTCTGTGCTGGCAGTGAAGTACCCCAAGTCTGTGTCCA 74  
Oy 1229 GGAGCCACAGGTGGGGGCTCTCTCCGTCGTCCTGTCGTGATCCGCCACCCC 1288  
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Db 73 GGAGCCACAGGTGGGGGCTCTCTCTCCGTCGTCCTGTCGTGATCCGCCACCCC 14  
Oy 1289 CTCCTGCTC 1297  
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Db 13 CTCCTGCTC 5

RESULT 11  
BF724241 532 bp mRNA linear EST 05-JAN-2001  
LOCUS BF724241  
DEFINITION bx02ell.y1 Human Iris cDNA (Un-normalized, unamplified): BX Homo  
sapiens cDNA clone bx02ell 5', mRNA sequence.  
ACCESSION BF724241  
VERSION BF724241.1 GI:12040150  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 532)  
Wistow G.J., Bernstein S., Behal A. and Smith D.  
NEIBANK: EST analysis and bioinformatics for ocular genomics  
Invest. Ophthalmol. Vis. Sci. 41, (2000) In press  
Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: gwaemehel@nei.nih.gov  
Plate: 02 row: e column: 11  
Seq primer: M13Rpl reverse primer (ABI).  
Location/Qualifiers  
1. 532  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/clone\_id="Human Iris cDNA (Un-normalized, unamplified):  
BX"  
/tissue\_type="Iris"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem Iris  
tissue was pooled from 10 individuals ranging in age from  
4-80 years and RNA was extracted. From this pooled sample  
an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A  
directionally cloned cDNA library in the pCMVSPORT6 vector  
was constructed at Life Technologies, essentially  
following the protocols of the Superscript Plasmid System  
full details of which are contained in the manufacturer's  
instruction manual (http://www.lifetech.com/). First  
strand synthesis was carried out using a Not I  
primer-adaptor (5'-pgactagctcagatccgacgagccgccc(t)15-3'  
). Not I blunt end inserts were cloned into the Not I/EcoR  
V sites in the vector. EST analysis was performed on the  
unamplified library at the NIH Intramural Sequencing  
Center (NISC)."

BASE COUNT  
ORIGIN  
77 a 186 c 223 g 46 t

Query Match 38.6%; Score 532; DB 12; Length 532;  
Best Local Similarity 100.0%; Pred. No. 8.8e-119;  
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 39 CCGGAGGAGGAGCAACAGAGTGGGTGAGCGCAGGAGGCGGCGCTGGCGGGAG 98  
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Db 1 CCGGAGGAGGAGCAACAGAGTGGGTGAGCGCAGGAGGCGGCGCTGGCGGGAG 60  
|||||  
Oy 99 AACGGGGGGGCTGAGCACCACCACTGAGAGGTCCGAGTAGCAGAGGCCCGCAAGGA 158  
|||||



SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 517)  
AUTHORS Melton, D., Brown, J., Kenly, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scaear, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Bilstain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelshvili, R., Williams, T., Jackson, Y., and Bowers, Y.  
TITLE Endocrine Pancreas Consortium  
JOURNAL Unpublished (2000)  
COMMENT Other-ESTs: 1j28e08.x1  
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@hdp.harvard.edu  
Library was constructed by Dr. Douglas Melton DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Juliana Brown  
(Brown@fas.harvard.edu)  
Seq primer: -40NP from Glibco  
High quality sequence stop: 456.  
Location/Qualifiers  
1. 517  
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/db\_xref="taxon:9606"  
/clone="IMAGE:6136046"  
/clone\_lib="Melton Normalized Human Islet 4 N4-HIS 1"  
/sex="Both"  
/tissue\_type="Islets of Langerhans"  
/dev\_stage="Adult"  
/lab\_host="DH10B"  
/note="Organ: Pancreas; Vector: pSPORT1, Site\_1: Not 1; Site\_2: Sal 1; Starting library constructed using Superscript Plasmid Library Kit (Life Technologies). cDNA made by oligo-dT priming. Size-selected by column fractionation; average insert size 1.08 kb. Library was amplified once on solid support and plasmid DNA from library was prepared. The library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded library plasmid DNA was mixed with 5 micrograms PCR product representing library inserts and hybridized to an EcoT of 20. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."

BASE COUNT 94 a 138 c 166 g 119 t  
ORIGIN

Query Match 37.5%; Score 517; DB 14; Length 517;  
Best Local Similarity 100.0%; Pred. No. 3.6e-115;  
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 657 CTTGCCAGTGTCTGGGCTACTACTTCGCTCCATCGCACCGTACCGGCGCCGCC 716  
Db 1 CCGGCCAGTGTCTGGGCTACTACTTCGCTCCATCGCACCGTACCGGCGCCGCC 60  
QY 717 TCGAGTTTGTCTGGGCTACTACTTCGCTCCATCGCACCGTACCGGCGCCGCC 776  
Db 61 TCGAGTTTGTCTGGGCTACTACTTCGCTCCATCGCACCGTACCGGCGCCGCC 120  
QY 777 GGTGGCCCAAGCAGCTCGCTCGGGGGGGGCCATGGTGGAGCTGGAGCC 836  
Db 121 GGTGGCCCAAGCAGCTCGCTCGGGGGGGGCCATGGTGGAGCTGGAGCC 180  
QY 837 AAGTGTGGTGCAGTGGGTGGGTGACTACATTTGGCATTTGCGAGCATCAAGCAG 896  
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Db 181 AAGTGTGGTGCAGTGGGTGGGTGACTACATTTGGCATTTGCGAGCATCAAGCAG 240  
QY 897 ACAGACCTTCTCCGGAATTTCTGTGTACTCCGACGTGCACAGCTCCCGAGCTTGTCTT 956  
Db 241 ACAGACCTTCTCCGGAATTTCTGTGTACTCCGACGTGCACAGCTCCCGAGCTTGTCTT 300  
QY 957 AGTCCCAAGTCAAGTGTAGTGTCTGTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 1016  
Db 301 AGTCCCAAGTCAAGTGTAGTGTCTGTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 360  
QY 1017 ACCAGTGTATTCAG 1076  
Db 361 ACCAGTGTATTCAG 420  
QY 1077 TAGAGACTCTCCGCTCTGCTGTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1136  
Db 421 TAGAGACTCTCCGCTCTGCTGTGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480  
QY 1137 TCTGGCAGCATGGGGCAGTGGCTGGATTTGCCCCAA 1173  
Db 481 TCTGGCAGCATGGGGCAGTGGCTGGATTTGCCCCAA 517

RESULT 14  
Bg706609  
LOCUS 630 bp mRNA linear EST 07-MAY-2001  
DEFINITION 602672994F1 NIH\_MGC\_96 Homo sapiens cDNA clone IMAGE:4795558 5', mRNA sequence.  
ACCESSION Bg706609  
VERSION Bg706609.1 GI:13982121  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 630)  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: L1AM10678 row: 1 column: 23  
High quality sequence stop: 630.  
Location/Qualifiers  
1. 630  
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/db\_xref="taxon:9606"  
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/clone\_lib="NIH\_MGC\_96"  
/tissue\_type="hypothalamus"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site\_1: BamHI, Site\_2: SalI-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTATTTTAA-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT 93 a 215 c 257 g 65 t  
ORIGIN

Query Match 36.9%; Score 508; DB 12; Length 630;  
Best Local Similarity 99.7%; Pred. No. 4.3e-113;



OY 919 G 919  
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Db 567 G 567

Search completed: June 21, 2003, 14:32:36  
Job time : 2196 secs











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Db      71 AGCGGGGGGCTGGAGCACACCAACCTGAGGGGTCGGAGTAGAGGAGGCCCGAAGAG 130
Qy      160 GCCATCGGGGAGACCGGGAGGGGAGCTCGAGAGAGACCCGGCGTCCGGGCTCCCGGTGC 219
Db      131 GCCATCGGGGAGACCGGGAGGGGAGCTCGAGAGAGACCCGGCGTCCGGGCTCCCGGTGC 190
Qy      220 CAGGCTATGAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 279
Db      191 CAGGCTATGAGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 250
Qy      280 ACTGGAGACACAACAGATCCCGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 339
Db      251 ACTGGAGACACAACAGATCCCGAGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
Qy      340 GGGCCACCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 399
Db      311 GGGCCACCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 370
Qy      400 GCGCGGGGCTCGGGGAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 459
Db      371 GCGCGGGGCTCGGGGAGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 430
Qy      460 GGACCCCGGGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 519
Db      431 GGACCCCGGGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 490
Qy      520 CTCGGTGCCTCGGGATCCGCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 579
Db      491 CTCGGTGCCTCGGGATCCGCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 550
Qy      580 GTCGACGACACCTTGGCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 639
Db      551 GTCGACGACACCTTGGCTTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 610
Qy      640 GTCGACGAGCAATTCACCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 699
Db      611 GTCGACGAGCAATTCACCTGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 670
Qy      700 GCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 759
Db      671 GCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 730
Qy      760 CTCGACGATTTTTCGGGGGGTGGGCCAAGCCGCTCGGAGGAGGAGGAGGAGGAGGAGGAG 819
Db      731 CTCGACGATTTTTCGGGGGGTGGGCCAAGCCGCTCGGAGGAGGAGGAGGAGGAGGAGGAG 790
Qy      820 GCTGAGGCTTACAGCAAGTGTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 879
Db      791 GCTGAGGCTTACAGCAAGTGTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 850
Qy      880 TGGCAGGATCAAGACAGACACCTTCCGGATTTTGTGGTACTCCGACTGACAG 939
Db      851 TGGCAGGATCAAGACAGACACCTTCCGGATTTTGTGGTACTCCGACTGACAG 910
Qy      940 CTCGCCAGCTTTTGTGTTAGTCCGACCTCAAAAGTGTGAGTCACTCACTCTGAAGG 999
Db      911 CTCGCCAGCTTTTGTGTTAGTCCGACCTCAAAAGTGTGAGTCACTCACTCTGAAGG 970
Qy      1000 AGGGTGTAGGCTGACAAACAGGTATCCAGAGGGGCTGGCCCCCTGGAATTTGTGA 1059
Db      971 AGGGTGTAGGCTGACAAACAGGTATCCAGAGGGGCTGGCCCCCTGGAATTTGTGA 1030
Qy      1060 TGACTAGGAGGAGTGGGGTAGAGCACTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1119
Db      1031 TGACTAGGAGGAGTGGGGTAGAGCACTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1090
Qy      1120 GGGCTGTGCGATCAGTCTGCGACATGGGCAATGGCTGATTTTGTCCCAAGACAG 1179
Db      1091 GGGCTGTGCGATCAGTCTGCGACATGGGCAATGGCTGATTTTGTCCCAAGACAG 1150
Qy      1180 AGGAGTGTGCTGTGCTGCAAGTGTAACTCCCGCAAGTGTCTGCTGCTGCTGCTGCTGCTGCT 1239

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Db      1151 AGGAGTGTGCTGTGCTGCAAGTGAAGTCCCGCAGTGTGCTGTGCTGCTGCTGCTGCT 1210
Qy      1240 TGGGCTGCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1299
Db      1211 TGGGCTGCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1270
Qy      1300 GGGGCGGCGCTTTTCTGAGAGTCACTCAATTAACCTAAGAACCTGATTAATAAAAAA 1359
Db      1271 GGGGCGGCGCTTTTCTGAGAGTCACTCAATTAACCTAAGAACCTGATTAATAAAAAA 1330
Qy      1360 AAAAAA 1366
Db      1331 AAAAAA 1337

RESULT 5
HSM800923      1068 bp      mRNA      linear      PRI 18-FEB-2000
LOCUS          Homo sapiens mRNA, cDNA DKF2p586B0621 (from clone DKF2p586B0621).
DEFINITION
ACCESSION      AL110261
VERSION        AL110261.1 GI:5817222
KEYWORDS
SOURCE
ORGANISM       Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1068)
Ottewill, B., Obermayer, B., Mewes, H.W., Gassenhuber, J. and
Wiemann, S.
Direct Submission
Submitted (15-AUG-1999) MIPS, Am Klopferplatz 18a, D-82152
Martinsried, GERMANY
COMMENT
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
sequenced by MedGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. This clone
(DKF2p586B0621) is available at the RZPD in Berlin. Please contact
the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.

FEATURES
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/clone_lib="586 (synonym: hute1). Vector pSport1; host
DH10B; sites NotI + SalI/MluI"
/dev_stage="adult"
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RVLVNDSQHYDAVNGKPTGCVGVYFVAVHATVYKASLOFDLVKNGESIASPFQFEG
WPKRASLSGGMVRLPEPDQWVGVGVGVDYIGIVASIKTDSFSLVYSDMHSPPV
A"

polyA_signal
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ORIGIN
Query Match      77.3%; Score 1064.4; DB 9; Length 1068;
Best Local Similarity 99.9%; Pred. No. 9.2e-174;
Matches 1065; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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D 1 |
D 1 CCCAGCTCTGCCCCGGGACACCCGGCTTCCAGGACGCCGGGACCATGACACCCAG 60
QY 359 GGCATTGCGGGGCGGATGGCGCGGAGCGCGGACCGCGCGCGCGCGCGCGCGCGGAG 418
D 61 GGCATTGCGGGGCGGATGGCGCGGAGCGCGGACCGCGCGCGCGCGCGCGCGCGGAG 120
QY 419 AAGAGCGAGGCGGGAGGCGCGGAGCTCCGCGGACCTCGAGGAGGAGCCCGGCGCGGAG 478
D 121 AAGAGCGAGGCGGGAGGCGCGGAGCTCCGCGGACCTCGAGGAGGAGCCCGGCGCGGAG 180
QY 479 GAGCGGGGACCCCGGGGCGCGGAGCGCGGCTCCGCGGAGTCTCGTGGCTCCCGGATCC 538
D 181 GAGCGGGGACCCCGGGGCGCGGAGCGCGGCTCCGCGGAGTCTCGTGGCTCCCGGATCC 240
QY 539 GCTTTCAGCGCGCAGCGCTCCGAGAGCGCGGCTGCTCGCGGCTCGAGCGACCCCTTGCC 598
D 241 GCTTTCAGCGCGCAGCGCTCCGAGAGCGCGGCTGCTCGCGGCTCGAGCGACCCCTTGCC 300
QY 599 TTCGACCGCGTGTGTGAACGAGCAGGACATTACGACGCGCTACCGCGCACTTCCACC 658
D 301 TTCGACCGCGTGTGTGAACGAGCAGGACATTACGACGCGCTACCGCGCACTTCCACC 360
QY 659 TGGCAGGTGCTGGGGTCTACTTCTGCGCGCTCATCGCCGCTCTACCGGCGCACTG 718
D 361 TGGCAGGTGCTGGGGTCTACTTCTGCGCGCTCATCGCCGCTCTACCGGCGCACTG 420
QY 719 CAGTTGATCTGTGAGAAATGAGCAATGCGCAATGCTCTTCTTCCAGTTTTCGGGGGG 778
D 421 CAGTTGATCTGTGAGAAATGAGCAATGCGCAATGCTCTTCTTCCAGTTTTCGGGGGG 480
QY 779 TGGCCCAAGCCAGCTCTGCTCGGGGGGGGCCATGTGTGAGGCTGAGACCTGAGACCAA 838
D 481 TGGCCCAAGCCAGCTCTGCTCGGGGGGGGCCATGTGTGAGGCTGAGACCTGAGACCAA 540
QY 839 GTGGGGGTGAGGGGTGGTGGTGTGATGATGCGATGCGATGCGATGCGATGCGATGCGAT 898
D 541 GTGGGGGTGAGGGGTGGTGGTGTGATGATGCGATGCGATGCGATGCGATGCGATGCGAT 600
QY 899 AGCACCCTTCCCGGATTTCTGTGTACTCGGACTGGCAGACGCTCCGAGCTTCTGCTAG 958
D 601 AGCACCCTTCCCGGATTTCTGTGTACTCGGACTGGCAGACGCTCCGAGCTTCTGCTAG 660
QY 959 TGGCCACTGCAAGTGTGCTATGCTCTACTCTCTAGAGAGGGGTGTGAGGCTGACAC 1018
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QY 1019 CAGGTCTCCAGAGGAGGCTGGCCCGCTGGAAATTTGTGAATGATGAGGAGGTGGGTA 1078
D 721 CAGGTCTCCAGAGGAGGCTGGCCCGCTGGAAATTTGTGAATGATGAGGAGGTGGGTA 780
QY 1079 GAGCACTCTCCGCTGCTGCTGCGCAAGAGATGGGAACAGTGGCTGTCTGCGATCAGT 1138
D 781 GAGCACTCTCCGCTGCTGCTGCGCAAGAGATGGGAACAGTGGCTGTCTGCGATCAGT 840
QY 1139 TGGCAGCATGGGCAATGGCTGATTTCTGCGCAAGACGAGAGAGTGTGCTGTGCTG 1198
D 841 TGGCAGCATGGGCAATGGCTGATTTCTGCGCAAGACGAGAGAGTGTGCTGTGCTG 900
QY 1199 AAGGTGAATGCCCGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1258
D 901 AAGGTGAATGCCCGAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
QY 1259 TCCCTGCTTCTCTGATCTCTCCACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1318
D 961 TCCCTGCTTCTCTGATCTCTCCACCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
QY 1319 GAGATCACTCAATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAA 1364
D 1021 GAGATCACTCAATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAA 1066
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RESULT 6
AP003396/c 191362 bp DNA linear PRI 25-APR-2002
LOCUS Homo sapiens genomic DNA, chromosome 11q clone:RP11-334B6, complete
DEFINITION
ACCESSION AP003396
VERSION AP003396.1 GI:20302607
KEYWORDS HTG.
SOURCE Homo sapiens DNA, clone:RP11-334B6.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published only in Database (2002)
REFERENCE 2 (bases 1 to 191362)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2001) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsr.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
This work was done in collaboration with Aral, Y., Kubo, T. and
Ohki, M.
COMMENT National Cancer Center Research Institute
Cancer Genomic Division
5-1-1, Tsukiji, Chuo-ku, Tokyo, JAPAN
zip: 104-0045
phone: 81-3-3542-2511 ex 4752, fax: 81-3-3542-0688 e-mail:
yara@ncrc.go.jp.
FEATURES
SOURCE location/Qualifiers
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BASE COUNT 46535 a 45977 c 46722 g 50128 t
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Query Match 66.1% Score 909.8; DB 9; Length 191362;
Best Local Similarity 99.8%; Pred. No. 2.6e-147;
Matches 911; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 438 CGGAGCTCCGGGACCTCGAGGAGACCCCGGCGCGGAGAGAGCGCGGAGCGG 497
D 6384 CAGAGCTGCGGGACCTCGAGGAGACCCCGGCGCGGAGAGAGCGCGGAGCGG 6325
QY 498 CCAACCGGCGCTGCGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 557
D 6324 CCAACCGGCGCTGCGGGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6265
QY 558 CCGAGAGCCGGGTGCTCGCGCTGAGCGACACCTTGCCTTGACCGCGTGTGTA 617
D 6264 CCGAGAGCCGGGTGCTCGCGCTGAGCGACACCTTGCCTTGACCGCGTGTGTA 6205
QY 618 ACAGAGGAGCAATTAGAGAGCGCTGACCGGCAAGTTACCTGCGAGAGTGTGCTG 677
D 6204 ACAGAGGAGCAATTAGAGAGCGCTGACCGGCAAGTTACCTGCGAGAGTGTGCTG 6145
QY 678 ACTACTTCCGCGCTCATGACACGCTACCGGCGCAAGCTGCAATTTGATGTGTGAAGA 737
D 6144 ACTACTTCCGCGCTCATGACACGCTACCGGCGCAAGCTGCAATTTGATGTGTGAAGA 6085
QY 738 ATGGCGAATTCATTTGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 797
D 6084 ATGGCGAATTCATTTGCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 6025
QY 798 TCTCGGGGGGGGCGCATGTGTGAGCTGAGGCTGAGAGCAAGTGTGGGTGAGGTGG 857
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VERSION	AP002956.1	GI:22255355	
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AUTHORS	1 Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Tokoki,Y., Watanabe,H. and Sakaki,Y.		
TITLE	Homo sapiens 219,574 genomic DNA of 11q		
JOURNAL	Published Only in Database (2002)		
REFERENCE	2 (bases 1 to 219574)		
AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Tokoki,Y., Watanabe,H. and Sakaki,Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (24-NOV-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Saito-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: hattori@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)		
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	Additional author information				
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	National Cancer Center Research Institute				
	Cancer Genomics Division				
	5-1-1, Tsukiji, Chuo-ku, Tokyo, JAPAN				
	zip: 104-0045				
	phone: +81-3-3542-2511 ex4752, fax: +81-3-3542-0688 e-mail:				
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ACCESSION AF469650
VERSION AF469650.1 GI:22023766
KEYWORDS   Mus musculus.
SOURCE      Mus musculus.
ORGANISM   Mus musculus.
REFERENCE 1 (bases 1 to 4220)
AUTHORS   Kameya,S., Hawes,N.L., Chang,B., Heckenlively,J.R., Nagert,J.K. and Nishina,P.M.
TITLE      Mfrp, a gene encoding a frizzled related protein, is mutated in the mouse retinal degeneration 6
JOURNAL   Hum. Mol. Genet. 11 (16), 1879-1886 (2002)
PUBMED   12140190
AUTHORS   Kameya,S., Nagert,J.K. and Nishina,P.M.
TITLE      Direct Submission
JOURNAL   Submitted (17-JAN-2002) The Jackson Laboratory, 600 Main Street, Bar Harbor, ME 04609, USA
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 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
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 JOURNAL Published Only in Database (2000)  
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 Direct Submission  
 TITLE  
 JOURNAL Submitted (05-JAN-2000) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);



## COMMENT

Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,  
Japan (E-mail: hattori@gsc.riken.go.jp,  
URL: http://hgp.gsc.riken.go.jp/, Tel: 81-42-778-9923,  
Fax: 81-42-778-9924)  
On May 31, 2000 this sequence version replaced g1:6997762.

## Genome Center

Center: RIKEN Genomic Sciences Center (GSC)

Center code: RIKEN

Web site: http://hgp.gsc.riken.go.jp/

Contact: hattori@gsc.riken.go.jp

Project Information

Center project name: HumDraT11

Center clone name: Rp11-680C5

Sequencing vector: PCR products

Chemistry: Dye-terminator ET-amersham; 100% of reads

Assembly program: Phrap, version 0.990329

Consensus quality: 149676 bases at least Q40

Consensus quality: 160868 bases at least Q30

Consensus quality: 167161 bases at least Q20

Insert size: 170338; sum-of-contigs

Quality coverage: 4.33x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs 'N', but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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Sequence updated (26-May-2000).

NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of 'N', but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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33790      33789: gap of 100 bp
47432      47432: contig of 13643 bp in length
47533      47532: gap of 100 bp

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## FEATURES

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* 47533      63392: contig of 15860 bp in length
* 63393      63492: gap of 100 bp
* 63493      74234: contig of 10742 bp in length
* 74235      74334: gap of 100 bp
* 74335      85357: contig of 11023 bp in length
* 85358      85457: gap of 100 bp
* 85458      93597: contig of 8140 bp in length
* 93598      93697: gap of 100 bp
* 93698      101983: contig of 8286 bp in length
* 101984      102083: gap of 100 bp
* 102084      110022: contig of 7939 bp in length
* 110023      110122: gap of 100 bp
* 110123      118116: contig of 7994 bp in length
* 118117      118216: gap of 100 bp
* 118217      126464: contig of 8248 bp in length
* 126465      126564: gap of 100 bp
* 126565      132136: contig of 5572 bp in length
* 132137      132236: gap of 100 bp
* 132237      135290: contig of 3054 bp in length
* 135291      135390: gap of 100 bp
* 135391      140229: contig of 4839 bp in length
* 140230      140328: gap of 100 bp
* 140330      143896: contig of 3567 bp in length
* 143897      143996: gap of 100 bp
* 143997      147572: contig of 3576 bp in length
* 147573      147672: gap of 100 bp
* 147673      150446: contig of 2774 bp in length
* 150447      150546: gap of 100 bp
* 150547      153715: contig of 3169 bp in length
* 153716      153815: gap of 100 bp
* 153816      157273: contig of 3458 bp in length
* 157274      157373: gap of 100 bp
* 157374      159817: contig of 2444 bp in length
* 159818      159917: gap of 100 bp
* 159918      161743: contig of 1826 bp in length
* 161744      161843: gap of 100 bp
* 161844      163684: contig of 1441 bp in length
* 163685      163784: gap of 100 bp
* 163785      165216: contig of 1432 bp in length
* 165217      165316: gap of 100 bp
* 165317      166557: contig of 1441 bp in length
* 166558      166757: gap of 100 bp
* 166758      168307: contig of 1550 bp in length
* 168308      168407: gap of 100 bp
* 168408      170030: contig of 1623 bp in length
* 170031      170130: gap of 100 bp
* 170131      171725: contig of 1995 bp in length
* 171726      171825: gap of 100 bp
* 171826      173038: contig of 1213 bp in length.
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*     /db_xref="taxon:9606"
*     /chromosome="11"
*     /map="11q23"
*     /clone="Rp11-680C5"
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 Matches 741; Conservative 0; Mismatches 5; Indels 4; Gaps 4;

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QY 664 GGTGGCTGGGCTCTACTACTTCCGCCATGCCACCGTGTACCGGGCCAGCTGGCAGTT 723
DB 166817 GGTGGCTGGGCTCTACTACTTCCGCCATGCCACCGTGTACCGGGCCAGCTGGCAGTT 166876
QY 724 TGAATCTGTGAAGATGCGAATCCATTCCTCTTTTCCAGTTTTC-GGGGGGTGGC 782
DB 166877 TGAATCTGTGAAGATGCGAATCCATTCCTCTTTTCCAGTTTTCGGGGGGGTGGC 166936
QY 783 CCAAGCCAGCCTCGCTCTCGGGGGGGGCGCATGTGAGCGTGAAGCCTGAGACCAACTGT 842
DB 166937 CCAAGCCAGCCTCGCTCTCGGGGGGGGCGCATGTGAGCGTGAAGCCTGAGACCAACTGT 166996
QY 843 GGGTGAAGGTGGGTGGGTGACTACTATGGCATCTATGGCAGCATTAAGACAGACAGCA 902
DB 166997 GGGTGAAGGTGGGTGGGTGACTACTATGGCATCTATGGCAGCATTAAGACAGACAGCA 167056
QY 903 CTTTTCGCGATTTCTGTACTCTGACATGCGACAGCTCCCGAGTCTTTGCTTAGTGGC 962
DB 167057 CTTTTCGCGATTTCTGTACTCTGACATGCGACAGCTCCCGAGTCTTTGCTTAGTGGC 167116
QY 963 CACTGCAAGTGAAGTCACTCTCACTCTAGAAGAGAGGTGTGAGGCTGACAAACAGG 1022
DB 167117 CACTGCAAGTGAAGTCACTCTCACTCTAGAAGAGAGGTGTGAGGCTGACAAACAGG 167176
QY 1023 TCAAT-CCAGAGAGGCTGGCCCCC-TGGAATATTGTGATGACTAGGAGAGTGGGTAGA 1080
DB 167177 TCAATCCAGAGAGGCTGGCCCCC-TGGAATATTGTGATGACTAGGAGAGTGGGTAGA 167236
QY 1081 GCACTCTCGCTCTGCTGCTGCGAAGGAATGGGAACAGTGGCTGTCGGCATCAGGCTG 1140
DB 167237 GCACTCTCGCTCTGCTGCTGCGAAGGAATGGGAACAGTGGCTGTCGGCATCAGGCTG 167296

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QY 1141 GCAGCATGGGAGAGTGGCTGATTTCTGCCAAGACAGAGAGTGTGCTGTGCGCAA 1200
DB 167297 GCAGCATGGGAGAGTGGCTGATTTCTGCCAAGACAGAGAGTGTGCTGTGCGCAA 167356
QY 1201 GTGTAGTCCCGCAGTTGCTGTGTGTCAGAGACCCAGCGTGGTGTCTTCTGTGTC 1260
DB 167357 GTGTAGTCCCGCAGTTGCTGTGTGTCAGAGACCCAGCGTGGTGTCTTCTGTGTC 167416
QY 1261 CTCGTCTTCTGTGATCTCCCGACCCCTCTGCTGCTGGGGCCGCTTTTCTGAGA 1320
DB 167417 CTCGTCTTCTGTGATCTCCCGACCCCTCTGCTGCTGGGGCCGCTTTTCTGAGA 167476
QY 1321 GATCAGTCATTAACCTAAGAACCTGATA 1350
DB 167477 GATCAGTCATTAACCTAAGAACCTGATA 167506

RESULT 11
BC025174 1234 bp mRNA linear ROD 07-AUG-2002
LOCUS BC025174 Mus musculus, clone MGC:36714 IMAGE:3978387, mRNA, complete cds.
DEFINITION BC025174
ACCESSION BC025174
VERSION BC025174.1 GI:19263583
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclerognath; Muridae; Murinae; Mus.
1 (bases 1 to 1234)
REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (05-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
USA
NHI-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-help@nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
Sequencing Center
Center code: BCM-MGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnar, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowals, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Series: IRAC Plate: 61 Row: f Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis.

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RASLPDLVKNQOSIASPFOYEGGMPKRAISGSGAMRLBEEEDQVWVGVDYIGIT
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ORIGIN

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Query Match      50.4%; Score 693.6; DB 10; Length 1234;
Best Local Similarity 77.9%; Pred. No. 7e-110;
Matches 919; Conservative 0; Mismatches 239; Indels 22; Gaps 6;

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369 GCCCGGATGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 428
429 GCGGAGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 488
314 GCGGAGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 373
489 CCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 548
374 CCATGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 433
549 CCAAGCGCTCGGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 608
434 CCAAGCGATCCGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 493
609 TGCGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 668
494 TGCGGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 553
669 CTGGGCGCTACTACTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 728
554 CTGGCGTCTACTACTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 613
729 TGGTGAAGATGCGGAATCATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 788
614 TTGTCAAAAAGGCGCGAGTCATCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 673
789 CAGCGCTGCTCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 848
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849 AGGTGGGCGTGGGAGTACTACTACTACTACTACTACTACTACTACTACTACTACT 908
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909 CCGGATTTCTGCTGCTACTCTGCGAGTGCACAGCTCCCAAGTCTTGTGCTTGTG 968
794 CTGATTTCTGCTGCTACTCTGCGAGTGCACAGCTCCCAAGTCTTGTGCTTGTG 853
969 AAAGTGAAGTCTGCTGCTACTCTGCGAGTGCACAGCTCCCAAGTCTTGTGCTT 1028
854 ACCCGAGCTGCGCACTTGTCTCTCTGAGTGCAGGAGTGCACAGTCCCAAGTCT 913
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1149 GGGCGTGGCGCGGATTTCTGCGCGAGAGAGAGAGTGTGCTGCTGGCAAGTAAAGT 1208
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1209 CCCCCAGTGGCTGCTGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1265
1086 C-----CTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1134
1266 CTCTCTGATCTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1325
1135 CTTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1194
1326 CTGATTAAGCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1365
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RESULT 12
BC023068
LOCUS
DEFINITION Mus musculus, similar to Dkfpz586B0621 protein, clone MGC:38635
ACCESSION BC023068
VERSION BC023068.1 GI:18605993
KEYWORDS MGC.
SOURCE house mouse.
ORGANISM Mus musculus.

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REFERENCE
AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1271)
TITLE Direct Submission
JOURNAL

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REMARK
COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunsaratne, P.H., Garcia, A.M., Lu, X., Huylk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNLI at: <http://image.llnl.gov>  
 Series: IRAX Plate: 54 Row: b Column: 4  
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

#### FEATURES

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/clone_lib="NCI_CGAP_Mam6"
/lab_host="DH10B"
/Note="Vector: pCMV-SPORT6"
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CDS

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BASE COUNT      258 a      375 c      378 g      260 t
ORIGIN

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Best Local Similarity	77.9%	Pred. No. 1.8e-109		
Matches 916	Conservative 0	Mismatches 236	Indels 22	Gaps 6

OY	189	GAGAGGACCCCGGGCTCCGGGTCCGGATGAGGCCACTCCTCGCTGC	248
Db	115	GAGAGTTCCTCGAGTCTGAACCTCCGGGGGTCAACACCATGAGGCCACTTCTGCCCTTC	174
OY	249	TGCTTCGGGGCTTGCGGGCTCGCCCCACTGAGACAGACAAGAATCCCAGCTCT	308
Db	175	TGCTTCGGGGCTGTGTACAGGCTCTCTCTGTGGAGAAAMAAGATCCCGACCTGT	234
OY	309	GCCCGGGGACCCCGGCTTCCAGAGCACAGCGGGGCCAACATGGCAGCGAGGCTTGGCGG	368
Db	235	GTCCCGGGCAGACC GGCGCTTCCAGAGCACACAGGTTACACATGGCAGCCAGCGCTGCTG	294
OY	369	GCCGCGATTGGCCGCGAGCGCCGAGCGCGCCCGGGCTCCGGGAGAGAAAGCAGAG	428
Db	295	GCCCTGACGGCCGTGATGTGCGCGCACAGGTGACCCCGGAGCTCCGGGAGAGAAAGCAGG	354
OY	429	GCGGAGGCGCGGAGCTGCGGGGACCTTGAGGGGAGACCCGGGGCCCGAGAGAGGCGGGAC	488
Db	355	GCGGAGAACCGGGACTACTGCGCCACGTGGGGAGCCCGGGCCCGTGGAGAGGCAAGGC	414
OY	489	CCGCGGGGCCACCGGGGCTGCGCGGGAGTGTGTGTCCTCCGACATCCGCTTTCAGCG	548
Db	415	CCATGGGGGCTATCGGGCTGCGGGGGAGTGTCTGTGTACCCCAAGATAGACCTTTCAGTG	474
OY	549	CCAAGGCTCTCGAAGCGCGGGTGCTCCGCCGTGTAGACGACACTTGTCCCTTGCAGCCGG	608
Db	475	CCAAGGCATCCGAAGCGGGGTACTTCGCGCGGACGACACACCCCTTCTTTCACCCGTG	534
OY	609	TGCTGTGAACGAGCAGGACATTACGACGCGCTCACCGGCAATTACCTGCCAGGTGC	668
Db	535	TGCTGTGAATGAGCAGGCGCATTTTCACACCCCACTACTGGCMASTTCACTGCCAAGTGC	594
OY	669	CTGGGGTCTACTTACTTTCGCGGTCCATGCCACCGTCAACCGGGCCAGGCTCGAGTTTATC	728
Db	595	CTGGCGTCTACTTACTTGTGTGTGCAACCCCACTGTCTACCGGGCCAGCTTCAGTTTATC	654
OY	729	TGGTAGAAGTAATGGGAAATTCATCCCTTTCCTTCCAGTTTTTGGGGGGGGGCCCAAGC	788
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Db	715	CAGCCTGCTCTCAGGGGGTGCAGTGGTAAAGGCTAGAAACCTGAGGACCAAGTGTGGGTGC	774
OY	849	AGTGGGTGTGGTGACTACATTGGCATTTATGCGACAGATCAGACAGACAGCACTTCT	908
Db	775	AGTGGGGCTGGGTGATTACATTGGCATTTATGCGACAGATCAGACAGAGATCTTCT	834
OY	909	CCGATTTCTGGTCTACTCCGAGTGGGAGCAAGCTCCCGAGCTTGTAGTGCCCACTGC	968
Db	835	CTGATTTCTCTCTATTCTGACTGGCAGCAAGCTCCCGAGTCTTGCCTTAAACACAGTGA	894
OY	969	AAAATGAGCTCATGCTCTCACTCCTAGAGAGAGGGTGTGAGGCTGACACACAGGTCATCC	1028
Db	895	ACCGGAGTGTGGCACTGCTCTCAGTAGAGGAGGTGTACACTAACCCGGCAGGCACTAC	954
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DB		955	CAGAGA	GCGCTGCGCCCTCGGAATTTGTGGATGACTTAGAAGAGAGGAG-CCACTTCC	1013
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DB		1014	GGTGCCCACTGCTGGCAATGATGAGAGACA--GGCTGTCTTAAGGTCA----	1067	
OY		1149	GGGAGAGGCGGTGAATTTCGTGGCCAAGACCAGAGAGTGTCTGTGGTGGCAAGTMAGT	1208	
DB		1068	GAGCAGTGGCTGGTTTTCTGTGCCAGGACTTTTA-GAATGCAGTAGTGGCTGACACTGTGGGT	1126	
OY		1209	CCCCAGTGTGCTGTGATCAGAGAGCCCACAGGTGGGTGCTCTCTTGTGGTCTGTG--	1265	
DB		1127	C-----CTGGCCACAGACTCCAGAGTGGAGTGTCTCATCTTACTCTGTGGCC	1175	
OY		1266	CTTCTCTGAGTCCCTCCCAACCCCTCTGCTCTCTGGGGGGGGCCCTTTTCAGAGATCA	1325	
DB		1176	CCTTAGTGTCCCTGACATCTCTGTGCTCCAGGAGGCCCTTTTCTTCAGAGGTCA	1235	
OY		1326	CTCAATAAACCTAAGAACCTCATMAAAAAAAAAAAAAA	1361	
DB		1236	CTTAATAAACCTAATAATCTTCAAAAAAA	1271	
RESULT_13					
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LOCUS		Homo sapiens chromosome 11 clone RP11-657A24 map 11q23, WORKING			
DEFINITION		DRAFT SEQUENCE, 42 unordered pieces.			
ACCESSION		AP001156			
VERSION		AP001156.2 GI:8118724			
KEYWORDS		HTG; HTGS_PHASE1; HTGS_DRAFT.			
SOURCE		Homo sapiens DNA, clone:RP11-657A24.			
ORGANISM		Homo sapiens			
REFERENCE		Eumalariota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE		1 (bases 1 to 198902)			
JOURNAL		Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,			
REFERENCE		Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.			
AUTHORS		Published Only In Database (2000)			
TITLE		2 (bases 1 to 198902)			
JOURNAL		Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,			
REFERENCE		Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.			
AUTHORS		Direct Submission			
TITLE		Submitted (10-FEB-2000) Masahira Hattori, The Institute of Physical			
JOURNAL		and Chemical Research (RIKEN), Genomic Sciences Center (GSC);			
REFERENCE		Kitaaso Univ., 1-15-1 Kitaaso, Sagamihara, Kanagawa 228-8555,			
AUTHORS		Japan (E-mail:hattori@gscc.riken.go.jp,			
TITLE		URI:http://hgsc.riken.go.jp/, Tel:81-42-778-9923,			
JOURNAL		Fax:81-42-778-9924)			
COMMENT		On May 31, 2000 this sequence version replaced gi:6597842.			
		----- Genome Center			
		Center: RIKEN Genomic Sciences Center(GSC)			
		Center code: RIKEN			
		Web site: http://hgsc.riken.go.jp/			
		Contact: hattori@gscc.riken.go.jp			
		----- Project Information			
		Center project name: Humdrat11			
		Center Clone name: RP11-657A24			
		----- Summary Statistics			
		Sequencing vector: PCR products; 100% of reads			
		Assembly program: Phrap; version 0.990329			
		Consensus quality: 171788 bases at least Q40			
		Consensus quality: 184443 bases at least Q30			
		Consensus quality: 191295 bases at least Q20			
		Insert size: 194802; sum-of-contigs			
		Quality coverage: 4.12x in Q20 bases; sum-of-contigs			
		----- NOTE: This is a 'working draft' sequence. It currently consists of			
		42 contigs. The true order of the pieces is not known and their			
		order in this sequence record is arbitrary. Gaps between the			
		contigs are represented as runs N, but the exact sizes of the gaps			



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Best Local Similarity 99.7%; Pred. No. 3.8e-96;
Matches 614; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 735 AGAATGGCGAATCCATTCCTCTTCTTCCAGTTTTCGGGGGGTGGCCCAAGCCACT 794
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Db 194389 AGAATGGCGAATCCATTCCTCTTCTTCCAGTTTTCGGGGGGTGGCCCAAGCCACT 194448

QY 795 CGCTCTGGGGGGGGCCATGGTGGAGCTGGAGCCTGGAGACCAAGTGTGGTGCAGGTG 854
    |||||||
Db 194449 CGCTCTGGGGGGGGCCATGGTGGAGCTGGAGCCTGGAGACCAAGTGTGGTGCAGGTG 194508

QY 855 GTGTGGGTACTACATTTGGCATCTATGCGCAGCATCAAGACAGACAGACCTTCTCGGAT 914
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QY 1335 CCTAAGAACCTCATTA 1350
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RESULT 14
AC112557 173657 bp DNA linear HTG 14-JUL-2002
LOCUS Rattus norvegicus clone CH230-904, *** SEQUENCING IN PROGRESS ***,
DEFINITION 72 unordered pieces.
ACCESSION AC112557
VERSION AC112557.2 GI:21735369
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
          Rattus.
REFERENCE 1 (bases 1 to 173657)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
        Alshrooks,S.L., Amaralunga,H.C., Are,J.R., Ayele,M., Banks,T.,
        Barberia,J., Benton,J., Bimge,K., Blankenburg,K., Bonnin,D.,

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Wang,S., Ward-Moore,S., Warren,R., Washington,C., Wellington,S.,
Williams,G., Williamson,A., Wleceyk,R., Wooden,S., Worley,K.,
Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 173657)
Worley,K.C.
Submitted (22-FEB-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 173657)
Worley,K.C.
Direct Submission
Submitted (14-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jul 12, 2002 this sequence version replaced gi:18860143.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GKAB
Center clone name: CH230-904
----- Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 105614 bases at least Q40
Consensus quality: 111210 bases at least Q30
Consensus quality: 115587 bases at least Q20
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* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank/draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 72 contigs. The true order of the pieces
* is not known and their order in this sequence record is

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RESULT 15  
LOCUS ARI38195 729 bp DNA linear PAT 16-JUN-2001

DEFINITION Sequence 10 from patent US 6197930.

ACCESSION ARI38195

VERSION ARI38195.1 GI:14479704

KEYWORDS

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 729)

AUTHORS Sheppard,P.O. and Humes,J.M.

TITLE Adipocyte-specific protein homologs

JOURNAL Patent: US 6197930-A 10 06-MAR-2001;

FEATURES

source location/Qualifiers

1..729 /organism="unknown"

BASE COUNT 77 a 101 c 160 g 81 t 310 others

ORIGIN

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Query Match          36.6%; Score 504; DB 6; Length 729;
Best Local Similarity 57.6%; Prod. No. 3 4e-77;
Matches 419; Conservative 145; Mismatches 164; Indels 0; Gaps 0;
OY      227 ATGAGGCGACCTCTCTGCTGCTGCTGCTCTGCTCTGAGGCGGTGGCGGCGGCTCGCCCGACATGAGC 286
Dd      1   ATGMGNCCNNTYNTNGNTNTYNTNTYNTNGNYTNMGNCNGMNCNGMNSNCNCNCTNTNGAY 60

OY      287 GACAAACAAGATCCCCAGACCTCTGTCCCGGGGGCACCCCGCGCTTCTCAGGCAACGGCGGGGCAC 346
Dd      61 GATAAAYAAATHCCCMNSNNTYTNTGYCCNGGCAACCCGNGNYTNCCNCGNACNCCNGSNCAAY 120

OY      347 CATGGACGACGAGGCTTTGGCCGGCGCCGAGATGCGCGGACGCGGCGGACGCGGCGCGCGG 406
Dd      121 CAVGGMNSNCARGSNNTTNCNCGNMNGAYGGMNGMNGAYGMMNGMNGAYGSMNGMNGMNCNCGN 180

OY      407 GCTCCGGGAGAGAAAGGCGAGGGCGGAGGCGGAGCTCCCGGAGCTTCGAGGGAGACCC 466

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QY	647	GGCAAGTTCACCGCGCAGGTGGCGGTCTACTACTCGCGGNCATCGCACCGGTAC	706
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QY	947	GCTCTTCG 954	
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Job time : 3729 secs








GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 03:38:34 ; Search time 368 Seconds

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Title: US-09-944-944-41

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Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0  
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Listing first 45 summaries

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1377	100.0	1377	21	AAD01241
4	1377	100.0	1377	21	AAA6907
5	1377	100.0	1377	21	AAA9560
6	1377	100.0	1377	22	AA521424
7	1375.4	99.9	1377	21	AAC58626
8	1322.2	96.0	1347	20	AAK24684
9	1296.6	94.2	1338	22	AAK44970

10	1295	94.0	1338	22	AAK44998	Human secreted pro
11	1295	94.0	1338	22	AAK44999	Human secreted pro
12	1295	94.0	1338	22	AAK45000	Human secreted pro
13	1295	94.0	1338	22	AAK45001	Human secreted pro
14	1084.8	78.8	3248	24	AAK39624	Human secreted pro
15	923.6	67.1	1082	23	AAK76911	DNA encoding novel
16	763	55.4	764	24	AAK62228	CDNA sequence #15
17	717	52.1	728	22	AAK49971	Human TANGO 253 OR
18	717	52.1	728	22	AAK44997	Human secreted pro
19	715.4	52.0	728	22	AAK44994	Human secreted pro
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21	715.4	52.0	728	22	AAK44996	Human secreted pro
22	692.8	50.3	1263	22	AAK4972	Murine TANGO 253 O
23	691.2	50.2	1263	22	AAK45006	Murine secreted pr
24	691.2	50.2	1263	22	AAK45007	Murine secreted pr
25	691.2	50.2	1263	22	AAK45008	Murine secreted pr
26	691.2	50.2	1263	22	AAK45009	Murine secreted pr
27	606	44.0	1001	21	AAK61745	CDNA encoding rat
28	606	44.0	1001	22	AAK96678	SKIN cell CDNA, SE
29	606	44.0	1001	24	ABL34830	Rat CDNA isolated
30	606	44.0	1015	21	AAK61635	CDNA encoding rat
31	606	44.0	1015	22	AAK99568	SKIN cell CDNA, SE
32	606	44.0	1015	24	ABL34720	Rat CDNA isolated
33	596	43.3	602	22	AAK33447	Human colon cancer
34	564.2	41.0	729	22	AAK44973	Murine TANGO 253 c
35	562.6	40.9	729	22	AAK45038	Murine secreted pr
36	562.6	40.9	729	22	AAK45039	Murine secreted pr
37	562.6	40.9	729	22	AAK45040	Murine secreted pr
38	562.6	40.9	729	22	AAK45041	Murine secreted pr
39	504	36.6	729	20	AAK24685	Degenerate DNA enc
40	347	25.2	502	21	AAZ98154	Rat TANGO 253 codi
41	257.8	18.7	601	22	AAK44991	DNA encoding novel
42	247.4	18.0	536	23	AAK76910	CDNA encoding rat
43	149.6	10.9	393	21	AAK61631	SKIN cell CDNA, SE
44	149.6	10.9	393	22	AAK99564	Rat CDNA isolated
45	149.6	10.9	393	24	ABL34716	

ALIGNMENTS

RESULT 1		AAK87258		standard; CDNA; 1377 BP.	
AAK87258;		27-SEP-1999 (first entry)		CDNA clone encoding human PRO344, amplified in tumour cells.	
XX		XX		PRO344; UNQ0303; cancer; tumour; diagnosis; therapy; human; ss.	
XX		XX		Homo sapiens.	
XX		XX		Key	
XX		XX		CDS	
XX		XX		sig_peptide	
XX		XX		mat_peptide	
XX		XX		Location/Qualifiers	
XX		XX		W09935170-A2.	
XX		XX		15-JUL-1999.	
XX		XX		05-JAN-1999;	
XX		XX		99WO-US00106.	
XX		XX		20-NOV-1998;	
XX		XX		05-JAN-1998;	
XX		XX		29-APR-1998;	
XX		XX		22-MAY-1998;	

10-JUN-1998: 98US-0088742.  
10-NOV-1998: 98US-0107783.  
(GETH ) GENENTECH INC.  
Botstein D, Goddard A, Gurney AT, Hillan KJ, Lawrence DA;  
Roy MA, Wood WI;  
WPI: 1999-430385/36.  
P-PSDB; AAY06481.  
Antibody against proteins expressed in neoplastic cells, useful for  
tumor diagnosis and treatment  
Example 1; Fig 9; 162pp; English.  
This is the nucleotide sequence of cDNA clone DNA40592 (ATCC 209492  
coding for human PRO34 (UM303) (see AAY06481). The clone was  
isolated from a foetal kidney library. Amplification of DNA40592  
was observed in primary lung tumours and in primary colon tumours,  
suggesting an association with tumour formation or growth.  
Antagonists (e.g. antibodies) directed against PRO34 may have  
utility in cancer therapy. The invention identifies 14 genes (see  
AAH87254-67) that are amplified in the genome of tumour cells. Such  
amplification is expected to be associated with overexpression of  
the gene product and to contribute to tumorigenesis. The encoded  
proteins (see AAY06477-90) may be useful targets for the diagnosis  
and/or treatment (including prevention) of certain cancers, and may  
act as predictors of the prognosis of tumour treatment.  
Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;

Query Match	100.0%	Score 1377	DB 20	Length 1377
Best Local Similarity	100.0%	Pred. No. 1.7e-24		
Matches 1377	Conservative 0	Mismatches 0	Indels 0	Gaps 0
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QY	121	CCAACGTGAGGGGTCCGGAGTAGCGAGCCGCCGGAAGAGAGGCATATGGGGAGCCGGGAGAG	180	
Db	121	CCAACGTGAGGGGTCCGGAGTAGCGAGCCGCCGGAAGAGAGGCATATGGGGAGCCGGGAGAG	180	
QY	181	GGGAGCTGCGAGAGAACCCCGGCGTTCGGGGCTCCGGGTCCAGACGCTATGAGGCCACTCT	240	
Db	181	GGGAGCTGCGAGAGAACCCCGGCGTTCGGGGCTCCGGGTCCAGACGCTATGAGGCCACTCT	240	
QY	241	CGTCTCGTGTCTCTCGGGGCTGGGGGCGGGGCGTCCGCCACTGAGCGACACAAATATCC	300	
Db	241	CGTCTCGTGTCTCTCGGGGCTGGGGGCGGGGCGTCCGCCACTGAGCGACACAAATATCC	300	
QY	301	CAGCCTCTGACCAGGGGACCCCGGCGCTTCCAGGCAAGCGCCGGGACCAATGAGCGACAGAG	360	
Db	301	CAGCCTCTGACCAGGGGACCCCGGCGCTTCCAGGCAAGCGCCGGGACCAATGAGCGACAGAG	360	
QY	361	CTTTCGCGGGCCGCAATGAGCGCGGACGCGCGGACGCGCCCGGGGCTCCGGGAGAGAA	420	
Db	361	CTTTCGCGGGCCGCAATGAGCGCGGACGCGCGGACGCGCCCGGGGCTCCGGGAGAGAA	420	
QY	421	AGGGAGGGGGCGGAGGCGCGGAGACATCGCGGGAGACATCCCGGGGCGCGGAGGAGA	480	
Db	421	AGGGAGGGGGCGGAGGCGCGGAGACATCGCGGGAGACATCCCGGGGCGCGGAGGAGA	480	
QY	481	GGCGGAGACCCCGGAGGCCACCGGAGCTGCGCGGGAGATGCTCGGAGTATCCG	540	
Db	481	GGCGGAGACCCCGGAGGCCACCGGAGCTGCGCGGGAGATGCTCGGAGTATCCG	540	
QY	541	CTTTCAGCGCCAGCGCTCCGAGAGCCGGGCTCTCCGCCGTGACGACCATTTGACCTT	600	

Db	541	CTTCAGCGCAGGAGCGCTCCGAGAGCGCGGGTGGCTCCGCGCTGTGAGACGACCCCTTGGCCCTT	600
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QY	781	GCCCCAAGCAGCCTGGCTCTCGGGGGGGGCCAATGGTAGCGGTGGAGCCGTAAGACCAAT	840
Db	781	GCCCCAAGCAGCCTGGCTCTCGGGGGGGGCCAATGGTAGCGGTGGAGCCGTAAGACCAAT	840
QY	841	GTTGGGTGAGGTGGGTGTGGGTGAGTACATTGGCATCTATTGCGAGCATCAACAGACAG	900
Db	841	GTTGGGTGAGGTGGGTGTGGGTGAGTACATTGGCATCTATTGCGAGCATCAACAGACAG	900
QY	901	CACCTTCTCCGGAATTTCTGGTGTACTCCGACTGCGACAGCTCCCAAGTCTTTGCTTAACTG	960
Db	901	CACCTTCTCCGGAATTTCTGGTGTACTCCGACTGCGACAGCTCCCAAGTCTTTGCTTAACTG	960
QY	961	CCCACTGCAAAAGTAGAGCTCATGCTCTACCTCTAGAAGAGAGGGGTGAGGCTGACACCA	1020
Db	961	CCCACTGCAAAAGTAGAGCTCATGCTCTACCTCTAGAAGAGAGGGGTGAGGCTGACACCA	1020
QY	1021	GGTCAATCAGAGAGGCGCTGGCCCCCTGGAAATTTGTGAATGACTAGGAGGTGGGGGTAGA	1080
Db	1021	GGTCAATCAGAGAGGCGCTGGCCCCCTGGAAATTTGTGAATGACTAGGAGGTGGGGGTAGA	1080
QY	1081	GCACGCTCCGCTCTGCTGGTGGCAAGAAATGGGAACAGTGGCTGTGATCAGAGCTG	1140
Db	1081	GCACGCTCCGCTCTGCTGGTGGCAAGAAATGGGAACAGTGGCTGTGATCAGAGCTG	1140
QY	1141	GCAGCATGGGGCAGTGGGTGTGATTTCTGCGCAAGACACGAGAGTGTGCTGTGTCGCA	1200
Db	1141	GCAGCATGGGGCAGTGGGTGTGATTTCTGCGCAAGACACGAGAGTGTGCTGTGTCGCA	1200
QY	1201	GTTGAATGTCGCCCAATTTGCTGTGGTCCAGAGACCCAGCGTGGGGGTCTCTTCCGTGTC	1260
Db	1201	GTTGAATGTCGCCCAATTTGCTGTGGTCCAGAGACCCAGCGTGGGGGTCTCTTCCGTGTC	1260
QY	1261	CTCTGCTTCTGTGATTCCTCCACACCCCTCTGCTGCTCGGGGGCGGCGCTTTTTCACAA	1320
Db	1261	CTCTGCTTCTGTGATTCCTCCACACCCCTCTGCTGCTCGGGGGCGGCGCTTTTTCACAA	1320
QY	1321	GATCACTCAATTAACCTTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAAA	1377
Db	1321	GATCACTCAATTAACCTTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAAA	1377
RESULT 2			
AAK80052			
ID	AAK80052	standard: cDNA, 1377 BP.	
XX	AAK80052;		
XX	AC		
XX	DT	12-AUG-1999 (first entry)	
XX	DE		
XX	XX	Human PRO344 nucleotide sequence.	
XX	XX	Human; PRO protein; tumour necrosis factor family; TNF; cytokine;	
XX	XX	secreted protein; transmembrane protein; inflammation disorder; ss.	
XX	XX	Homo sapiens.	
XX	XX	FN	WO928462-A2.



DT 08-NOV-2000 (first entry)  
 XX Human PRO344 protein encoding cDNA clone, DNA0592-1242.  
 DE  
 XX PRO344: DNA0592-1242; human: ATCC No: 209492; antiproliferative;  
 KW neoplastic cell growth inhibitor; cytostatic; treatment; cancer; tumour;  
 KW breast; prostate; colon; lung; renal; ovarian; central nervous system;  
 KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; secreted protein;  
 KW extracellular domain; ECD; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 227..958  
 FT /\*tag= a  
 FT /product= "Human PRO344 protein"  
 FT /note= "Derived from clone DNA0592-1242"  
 FT sig\_peptide 227..271  
 FT /\*tag= b  
 FT mat\_peptide 272..955  
 FT /\*tag= c  
 FT /product= "Mature human PRO344 protein"  
 XX  
 PN W0200032778-A2.  
 XX  
 PD 08-JUN-2000.  
 XX  
 PF 30-NOV-1999; 99WO-US28409.  
 XX  
 PR 01-DEC-1998; 98MO-US25108.  
 PR 16-DEC-1998; 98US-0112850.  
 PR 22-DEC-1998; 98US-0113296.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 XX  
 XX (GENTH ) GENENTECH INC.  
 PA  
 PI Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;  
 XX  
 DR WPI; 2000-412325/35.  
 DR P-PSDB; AAY71468.  
 XX  
 PT New composition useful for inhibiting neoplastic cell growth and for  
 PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or  
 PT their antagonists  
 XX  
 PS Claim 20; Fig 5; 108bp; English.  
 XX  
 CC The present sequence is the cDNA clone, designated as DNA0592-1242,  
 CC encoding the human PRO344 polypeptide. It is isolated from human foetal  
 CC lung tissue cDNA library, identified using probes based on a consensus  
 CC sequence DNA34398, derived from secreted protein extracellular domain  
 CC (ECD). Expressed Sequence Tag (EST). This clone is assigned ATCC deposit  
 CC No: 209492. PRO344 functions as a neoplastic cell growth inhibitor and  
 CC is used for treating tumors, using an effective amount of PRO655, PRO364  
 CC and PRO344. This composition is especially useful for treatment of human  
 CC cancers such as breast, prostate, colon, lung, renal, ovarian and CNS,  
 CC leukemia and melanoma.  
 CC  
 XX  
 SQ Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;

QY 121 CCAACTGAGAGGTCGGAGTAGAGGAGCGCCCGGAAGAGAGGAGCCATCGGGAGCCGGAGAGG 180  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 121 CCAACTGAGAGGTCGGAGTAGAGGAGCGCCCGGAAGAGAGGAGCCATCGGGAGCCGGAGAGG 180  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 181 GGGAGCTGGAGAGAGACCCCGGCGCTCCCGGGTCCCGGCTATGAGCCATCTCT 240  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 181 GGGAGCTGGAGAGAGACCCCGGCGCTCCCGGGTCCCGGCTATGAGCCATCTCT 240  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 241 CGTCTGCTGCTCTCTGGGCGCTGGGCGCGGCGGCTCCCGCACTGGAGCAGCAAGATCCC 300  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 241 CGTCTGCTGCTCTCTGGGCGCTGGGCGCGGCGGCTCCCGCACTGGAGCAGCAAGATCCC 300  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 301 CAGCCTTGCCCGGGGAGACCCCGGCTCTTCAGGACGCGGGGCCACCATGGCAGCCAGG 360  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 301 CAGCCTTGCCCGGGGAGACCCCGGCTCTTCAGGACGCGGGGCCACCATGGCAGCCAGG 360  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 361 CTTGCGGGCGCGGATGCGCGGAGCGCGGCGGAGCGGCGCGCGGCGCGCGGAGGAA 420  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 361 CTTGCGGGCGCGGATGCGCGGAGCGCGGCGGAGCGGCGCGCGGCGCGGAGGAA 420  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 421 AGCGAGGCGGAGAGCGCGGAGCTGCGGAGCTGAGAGGAGACCCCGGCGGAGAGA 480  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 421 AGCGAGGCGGAGAGCGCGGAGCTGCGGAGCTGAGAGGAGACCCCGGCGGAGAGA 480  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 481 GCGGAGACCGCGGGGCCACCGGGCTGCGGGGAGTCTGCTGCTCCGCGATCCG 540  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 481 GCGGAGACCGCGGGGCCACCGGGCTGCGGGGAGTCTGCTGCTCCGCGATCCG 540  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 541 CTTGAGGCGCAAGGCTCCGAGAGACCGGGTCCCGCGCTGCTGCTGCTGCTGCTGCTGCT 600  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 541 CTTGAGGCGCAAGGCTCCGAGAGACCGGGTCCCGCGCTGCTGCTGCTGCTGCTGCTGCT 600  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 601 CGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 601 CGACCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 661 CGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 661 CGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 721 GTTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 721 GTTGTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 781 GCCCAACCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 781 GCCCAACCGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 841 GTGGGTGAGAGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 900  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 841 GTGGGTGAGAGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGT 900  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 901 CACCTTCCGAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 901 CACCTTCCGAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 961 CCCACTGCAAGTGAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 961 CCCACTGCAAGTGAAGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1021 GGTGATCAGAGAGGCTGGGCGCCCGCTGGAATATTGTGAATGACTAGGAGAGTGGGTAGA 1080  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1021 GGTGATCAGAGAGGCTGGGCGCCCGCTGGAATATTGTGAATGACTAGGAGAGTGGGTAGA 1080  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1081 GCACTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1081 GCACTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1141 GCAAGATGAGGAGAGTGGCTGATTTTCTGCCAAGACCAAGAGAGTGTGCTGTGGCAA 1200  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1141 GCAAGATGAGGAGAGTGGCTGATTTTCTGCCAAGACCAAGAGAGTGTGCTGTGGCAA 1200  
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1201 GTGTAAAGTCCCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260

Db 1201 GTGTAAATCCCAATGCTCTGCTCAGAGACCAGGTGGGGTCTCTCTGCTC 1260  
 QY 1261 CTGTGCTCTCTGATGCTCCCAACCCCTCTCTCTGCTGAGGCGGCGCTTTCTCAGA 1320  
 Db 1261 CTGTGCTCTCTGATGCTCCCAACCCCTCTCTCTGCTGAGGCGGCGCTTTCTCAGA 1320  
 QY 1321 GATCAGTCAATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAAA 1377  
 Db 1321 GATCAGTCAATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAAA 1377  
 RESULT 4  
 ID AAA46907 standard; CDNA: 1377 BP.  
 AC AAA46907;  
 DE 03-OCT-2000 (first entry)  
 DE CDNA encoding novel polypeptide PRO344.  
 KM PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357;  
 KM PRO1715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;  
 KM tumorigenesis; cancer; neoplastic cell growth; cell proliferation; ss.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 227..958  
 FT /\*tag= a  
 PN MO20037640-A2.  
 PD 29-JUN-2000.  
 PF 16-DEC-1999; 99WO-US30095.  
 PR 22-DEC-1998; 98US-0113296.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 02-DEC-1999; 99WO-US28565.  
 PA (GETH ) GENENTECH INC.  
 PI Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;  
 PI Wood WT;  
 DR WPI: 2000-452188/39.  
 DR P-PSDB: AAY93688.  
 PT New anti-polypeptide antibody useful in the treatment and diagnosis of  
 PT neoplastic cell growth and proliferation -  
 PS Claim 50; Fig 9; 220pp; English.  
 CC The present sequence encodes a novel human polypeptide. The  
 CC specification describes novel polypeptides designated PRO201, PRO292,  
 CC PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO1017,  
 CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in  
 CC to tumorigenesis. The polypeptides are useful target for the  
 CC identification of certain cancers, and may act as predictors of the  
 CC prognosis of tumour treatment. Antibodies against these polypeptides  
 CC are useful in the treatment and diagnosis of neoplastic cell growth  
 CC and proliferation in mammals.  
 XX Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;

Query Match 100.0%; Score 1377; DB 21; Length 1377;  
 Best Local Similarity 100.0%; Pred. No. 1,7e-244;  
 Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGAGCCGGCAGAGAGCGAAGCAGAGC 60  
 Db 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAGAAAGCGAGCCGGCAGAGAGCGAAGCAGAGC 60  
 QY 61 TGGGTGACGGCAGGGGCGCTGGCCGGGGAGAGAGCGGGGGCTGGAGCACCA 120  
 Db 61 TGGGTGACGGCAGGGGCGCTGGCCGGGGAGAGAGCGGGGGCTGGAGCACCA 120  
 QY 121 CCAACTGAGGGTCCGGAGTACGAGCCGCCGGAAGAGGCGCATCGGGGAGCGGGAGG 180  
 Db 121 CCAACTGAGGGTCCGGAGTACGAGCCGCCGGAAGAGGCGCATCGGGGAGCGGGAGG 180  
 QY 181 GGGAGTGGAGAGACCCCGGCTCCGGGTCCAGCGCTATGAGGCCACTCT 240  
 Db 181 GGGAGTGGAGAGACCCCGGCTCCGGGTCCAGCGCTATGAGGCCACTCT 240  
 QY 241 GGTCTGTCTCTCTGGGCTTGGGGCGGCTCGCCCTCCAGTGGACACACAGATCCC 300  
 Db 241 GGTCTGTCTCTCTGGGCTTGGGGCGGCTCGCCCTCCAGTGGACACACAGATCCC 300  
 QY 301 CAGCTTGGCCGGGGGACCCCGGCTTCCAGGCGCGGGGGGACATGGCAGCCAGG 360  
 Db 301 CAGCTTGGCCGGGGGACCCCGGCTTCCAGGCGCGGGGGGACATGGCAGCCAGG 360  
 QY 361 CTGTGCGGGCGCGATGGCGGCGAGCGCGGCGCGCGCGCGCGCGCGCGAGAGA 420  
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 QY 421 AGCGAGGGCGGGAGGCGGAGCTGCGGAGCTTGAGAGGAGACCCGGGGCGAGAGA 480  
 Db 421 AGCGAGGGCGGGAGGCGGAGCTGCGGAGCTTGAGAGGAGACCCGGGGCGAGAGA 480  
 QY 481 GGGGGGACCCGGGGGCGACCGGGGCGGGGGAGTGTGCTTCGGCGATTCGCG 540  
 Db 481 GGGGGGACCCGGGGGCGACCGGGGCGGGGGAGTGTGCTTCGGCGATTCGCG 540  
 QY 541 CTTCAGCGCCAAAGCGCTCCAGAGAGCGGGTCCCTCCGCTGAGACACCTTCGCT 600  
 Db 541 CTTCAGCGCCAAAGCGCTCCAGAGAGCGGGTCCCTCCGCTGAGACACCTTCGCT 600  
 QY 601 CGACCGCTGCTGTGTAAGAGAGAGGACATTTAGAGCGCCGTCACCGCAAGTTCCTG 660  
 Db 601 CGACCGCTGCTGTGTAAGAGAGAGGACATTTAGAGCGCCGTCACCGCAAGTTCCTG 660  
 QY 661 CGAGTGTGCTGTGTAAGAGAGGACATTTAGAGCGCGGTCATGCGGGGCGAGCTGCA 720  
 Db 661 CGAGTGTGCTGTGTAAGAGAGGACATTTAGAGCGCGGTCATGCGGGGCGAGCTGCA 720  
 QY 721 GTTGTATCTGTGTAAGAGAGGACATTTAGAGCGCTTCTTCCAGTTTTCGGGGGTG 780  
 Db 721 GTTGTATCTGTGTAAGAGAGGACATTTAGAGCGCTTCTTCCAGTTTTCGGGGGTG 780  
 QY 781 GCCCAAGCCAGCTCTGCTGCGGGGGGCGCATGTGAGGTGAGGCTGAGAGCAAGT 840  
 Db 781 GCCCAAGCCAGCTCTGCTGCGGGGGGCGCATGTGAGGTGAGGCTGAGAGCAAGT 840  
 QY 841 GTGGGTGAGGGGTGGGTGGGTGAGTACATTTAGAGCGATTCGACATCAAGAGAGAG 900  
 Db 841 GTGGGTGAGGGGTGGGTGGGTGAGTACATTTAGAGCGATTCGACATCAAGAGAGAG 900  
 QY 901 CACCTTCCCGGATTTCTGTACTCCGAGTGGACAGCTCCCGAGCTTGTGTTAGTG 960  
 Db 901 CACCTTCCCGGATTTCTGTACTCCGAGTGGACAGCTCCCGAGCTTGTGTTAGTG 960  
 QY 961 CCCACTGCAAGAGTGTCTACTCTCTAGAGAGAGGAGGTGAGGCTGACACCA 1020  
 Db 961 CCCACTGCAAGAGTGTCTACTCTCTAGAGAGAGGAGGTGAGGCTGACACCA 1020





|||||  
Db 241 CGTCTGCTCTCTGGGCTTGCGGCGCGCTCCGCCCCCTGAGACGACAACAAGATCCC 300  
Qy 301 CAGCCTTGCCCGGGGACCCCGGCTTCCAGAGACCGCGGGCCACCATGGACGCGAGG 360  
Db 301 CAGCCTTGCCCGGGGACCCCGGCTTCCAGAGACCGCGGGCCACCATGGACGCGAGG 360  
Qy 361 CTTGCCGGGCCGATGGCCGACGCGCGGACGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
Db 361 CTTGCCGGGCCGATGGCCGACGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420  
Qy 421 AGGCGAGGCGCGGAGCGCGGACCTGCGGAGCTTCGAGGGAGACCCCGGCGCGAGAGA 480  
Db 421 AGGCGAGGCGCGGAGCGCGGAGCTGCGGAGCTTCGAGGGAGACCCCGGCGCGAGAGA 480  
Qy 481 GGGCGAGCCCGCGGGGCGCACCGGAGCCCGCGGGAGTGCCTGGGCTCCGCGATCCG 540  
Db 481 GGGCGAGCCCGCGGGGCGCACCGGAGCCCGCGGGAGTGCCTGGGCTCCGCGATCCG 540  
Qy 541 CTTGAGGCGCAAGCGCTCCAGAGACCGGAGCTCCGCGCTCTGACGCAACCTTGCCCTT 600  
Db 541 CTTGAGGCGCAAGCGCTCCAGAGACCGGAGCTCCGCGCTCTGACGCAACCTTGCCCTT 600  
Qy 601 CGACCGGCTGCTGTAACGAGACGACGACATTCAGACGCGCTCACCGGCAAGTTACCTG 660  
Db 601 CGACCGGCTGCTGTAACGAGACGAGCATTCAGACGCGCTCACCGGCAAGTTACCTG 660  
Qy 661 CCAGTGGCTGGGCTCTACTCTCGGCGCATGCCGCTCACGGGGGCGACGCTGCA 720  
Db 661 CCAGTGGCTGGGCTCTACTCTCGGCGCATGCCGCTCACGGGGGCGACGCTGCA 720  
Qy 721 GTTTGATCTGTGTAAGATGGCGAATCCATTCCTTTCTTCCAGTTTTCGGGGGGTG 780  
Db 721 GTTTGATCTGTGTAAGATGGCGAATCCATTCCTTTCTTCCAGTTTTCGGGGGGTG 780  
Qy 781 GCGCAAGCGACCCCTGCTCTCGGGGGGGGGCCATGTGAGGCTGAGAGCTGAGACCAAGT 840  
Db 781 GCGCAAGCGACCCCTGCTCTCGGGGGGGGGCCATGTGAGGCTGAGAGCTGAGACCAAGT 840  
Qy 841 GTGGTGCAGGTGGGTGAGTGCATACATTCGATGATCCAGCATCAAGACAGACAG 900  
Db 841 GTGGTGCAGGTGGGTGAGTGCATACATTCGATGATCCAGCATCAAGACAGACAG 900  
Qy 901 CACCTTCTCGGATTTCTGTGTACTCGACTGGCAGACGCTCCCAAGTCTTTGCTAGTG 960  
Db 901 CACCTTCTCGGATTTCTGTGTACTCGACTGGCAGACGCTCCCAAGTCTTTGCTAGTG 960  
Qy 961 CCCACTGCAAGAGTCACTGCTCTCACTCTGAAAGAGAGGCTGAGGCTGACAACCA 1020  
Db 961 CCCACTGCAAGAGTCACTGCTCTCACTCTGAAAGAGAGGCTGAGGCTGACAACCA 1020  
Qy 1021 GGTCTATCCAGAGAGGCTGGCCCCCTTGGAATATTGTGAATAGTACAGGAGGTGGGTA 1080  
Db 1021 GGTCTATCCAGAGAGGCTGGCCCCCTTGGAATATTGTGAATAGTACAGGAGGTGGGTA 1080  
Qy 1081 GCACTCTCCGCTCTGCTGCTGGAAGAAGTGAAGAGTGGCTCTGCGATTCAGGCTG 1140  
Db 1081 GCACTCTCCGCTCTGCTGCTGGAAGAAGTGAAGAGTGGCTCTGCGATTCAGGCTG 1140  
Qy 1141 GCACGATGGGCAATGGCTGGATTCTGCCCCAACAACAGAGAGATGCTGTGCTGCGCAA 1200  
Db 1141 GCACGATGGGCAATGGCTGGATTCTGCCCCAACAACAGAGATGCTGTGCTGCGCAA 1200  
Qy 1201 GTGTAAGTCCCGCAGTTGCTGTGCTCAGAGACCGCAGGTTGGCTCTCTTCTCTGTC 1260  
Db 1201 GTGTAAGTCCCGCAGTTGCTGTGCTCAGAGACCGCAGGTTGGCTCTCTTCTCTGTC 1260  
Qy 1261 CTTGCTCTCTGATCTCTCCCAACCCCTCTCTGCTCTGCGGCGCGCGCTTTCTCAGA 1320  
Db 1261 CTTGCTCTCTGATCTCTCCCAACCCCTCTCTGCTCTGCGGCGCGCGCTTTCTCAGA 1320  
Qy 1321 GATGACTCAATTAACCTTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAAA 1377  
Db 1321 GATGACTCAATTAACCTTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAAA 1377

Db 1321 GATGACTCAATTAACCTTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAAA 1377  
RESULT 7  
ID AAC58626 standard; CDNA: 1377 BP.  
AAC58626;  
29-JAN-2001 (first entry)  
Human PRO344 protein UNQ303 encoding cDNA SEQ ID NO:240.  
Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
dermatological; antihypertic; antirheumatic; immunosuppressive;  
haemostatic; antithyroid; antidiabetic; noctropic; neuroprotective;  
antianemic; hepatotropic; vitruclide; antiporiatic; antiallergic;  
antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;  
osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
autoimmune thrombocytopaenia; immune-mediated renal disease;  
demyelinating disease; hepatobiliary disease; Whipple's disease;  
inflammatory bowel disease; gluten-sensitive enteropathy;  
autoimmune disease; immune-mediated skin disease; allergic disease;  
immunological disease; transplantation associated disease;  
graft rejection; graft-versus-host-disease; ss.  
Homo sapiens.  
WO200053758-A2.  
14-SEP-2000.  
02-MAR-2000; 2000WO-US05841.  
08-MAR-1999; 99WO-US05028.  
10-MAR-1999; 99US-0123618.  
12-MAR-1999; 99US-0123957.  
23-MAR-1999; 99US-0125775.  
12-APR-1999; 99US-0128849.  
20-APR-1999; 99WO-US08615.  
28-APR-1999; 99US-0131445.  
04-MAY-1999; 99US-0132371.  
14-MAY-1999; 99US-0134287.  
02-JUN-1999; 99WO-US12252.  
23-JUN-1999; 99US-0141037.  
20-JUL-1999; 99US-0144758.  
26-JUL-1999; 99US-0145698.  
28-JUL-1999; 99US-0146222.  
01-SEP-1999; 99WO-US20111.  
08-SEP-1999; 99WO-US20594.  
13-SEP-1999; 99WO-US20944.  
15-SEP-1999; 99WO-US21090.  
26-SEP-1999; 99WO-US21547.  
05-SEP-1999; 99WO-US23089.  
29-OCT-1999; 99US-0162506.  
29-NOV-1999; 99US-US28214.  
30-NOV-1999; 99WO-US28313.  
30-NOV-1999; 99WO-US28409.  
01-DEC-1999; 99WO-US28301.  
01-DEC-1999; 99WO-US28634.  
02-DEC-1999; 99WO-US28551.  
02-DEC-1999; 99WO-US28564.  
02-DEC-1999; 99WO-US28565.  
16-DEC-1999; 99WO-US30995.  
20-DEC-1999; 99WO-US30999.  
30-DEC-1999; 99WO-US31274.  
05-JAN-2000; 2000WO-US00219.  
06-JAN-2000; 2000WO-US00277.  
06-JAN-2000; 2000WO-US00376.  
11-FEB-2000; 2000WO-US03565.  
18-FEB-2000; 2000WO-US04341.



PR 18-FEB-2000; 2000MO-US04342.  
 XX 22-FEB-2000; 2000MO-US04414.  
 PA (GENE) GENENTECH INC.  
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kalkbrenner RC, Lu Y, Pan J, Penhale D, Shelton DL, Smith V;  
 PI Stewart RA, Tumas D, Watanabe CK, Wood WT, Yan M;  
 XX MPI: 2000-572271/53.  
 DR P-PSDB: AAB33461.  
 XX Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PR immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PR arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX  
 PS Claim 23; Fig 95; 309pp; English.  
 XX  
 CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune hemolytic  
 CC anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC83937 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC8642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 CC  
 XX  
 XX Sequence 1377 BP; 251 A; 423 C; 471 G; 232 T; 0 other;

Query Match 99.9%; Score 1375.4; DB 21; Length 1377;  
 Best Local Similarity 99.9%; Pred. No. 3.3e-244;  
 Matches 1376; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGAGCCGAGAGGAGCGAACCAGGAC 60  
 DB 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAGAAAGCGAGCCGAGAGGAGCGAACCAGGAC 60  
 QY 61 TGGGCTGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
 DB 61 TGGGCTGAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
 QY 121 CCAACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
 DB 121 CCAACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
 QY 181 GGGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240  
 DB 181 GGGAGTGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 240  
 QY 241 GGTGCTGCTGCTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
 DB 241 GGTGCTGCTGCTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
 QY 301 CAGCTCTGCTGCTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 DB 301 CAGCTCTGCTGCTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
 QY 361 CTGGCGGGGCGGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
 DB 361 CTGGCGGGGCGGAGTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
 QY 421 AGGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480

DB 421 AGGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
 QY 481 GGGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
 DB 481 GGGCGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
 QY 541 CTTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
 DB 541 CTTGAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600  
 QY 601 CGAGCGGCTGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
 DB 601 CGAGCGGCTGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
 QY 661 CGAGTGGCTGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
 DB 661 CGAGTGGCTGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
 QY 721 GTTATGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
 DB 721 GTTATGCTGTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780  
 QY 781 GCGCAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
 DB 781 GCGCAAGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
 QY 841 GTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
 DB 841 GTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900  
 QY 901 CACCTTCTCCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
 DB 901 CACCTTCTCCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960  
 QY 961 CCCACTGCAAGAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 DB 961 CCCACTGCAAGAGTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
 QY 1021 GGTATCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
 DB 1021 GGTATCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
 QY 1081 GCACATCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
 DB 1081 GCACATCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140  
 QY 1141 GCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200  
 DB 1141 GCAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200  
 QY 1201 GTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260  
 DB 1201 GTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260  
 QY 1261 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
 DB 1261 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
 QY 1321 GATCAGTCAATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1377  
 DB 1321 GATCAGTCAATTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1377  
 RESULT 8  
 AAX24684  
 ID AAX24684 standard; cDNA; 1347 BP.  
 XX  
 AC AAX24684;  
 XX  
 DT 21-JUN-1999 (first entry)  
 XX  
 DE Human adipocyte-specific protein zs1g39 cDNA.



[illegible]

Dd		195	CACCTCCTGCTCTGTGCTCTCTGGAGCCTTGGGCGCGGCTCCGCCCTTGCACATGGACANACA	254
OY		294	AGATCCCAGCCTCTGCCCGGGGAGCACCCCGGCTTCAGAGCACGCCGGGGCACCATGGCA	353
Dd		255	AGATCCCCAGCCTTGCCCGGGGGACACCOCGGCTTCAGAGGACAGCGGGGCCACCATGGCA	314
OY		354	GCCAGGCTTCCCGGGGCCGATGAGCGCGACAGCGCCGAGCGGGCGCCGGGGCTCCGG	413
Dd		315	GCCAGGCTTCCCGGGGCCGATGAGCGCGACAGCGCCGAGCGGGCGCCGGGGCTCCGG	374
OY		414	GAGAAAGGAGGGGCGGAGGCGGGAGCGGAGACTGCGGGAGCTCGAGGGGACCCGGGGCGC	473
Dd		375	GAGAAAGGCGAGGGCGGGAGG-CGGGACTGCGGGAGCTCGAGGGGACCCCGGGCGC	433
OY		474	GAGGAGAGCGCGGAGCCCGCGGGGCGCACCGGGGCTCCCGGGGAGTGCCTGGCTCCGC	533
Dd		434	GAGGAGAGGGGAGACCCGCGGGGCGCACCGGGGCTCCCGGGGAGTGCCTGGCTCCGC	493
OY		534	GATCGCGCTTAGAGCGCCAGAGCGCTCCAGAGACCGGGTCTCCGCGCTCTACGCACCT	593
Dd		494	GATCGCGCTTAGAGCGCCAGAGCGCTCCAGAGACCGGGTCTCCGCGCTCTACGCACCT	553
OY		594	TGCGCTTGAGCGGGTGTGGTTGAACGAGCGGAGCAATTAGAGCGCGTCACGGGCAAGT	653
Dd		554	TGCGCTTGAGCGGGTGTGGTTGAACGAGCGGAGCAATTAGAGCGCGTCACGGGCAAGT	613
OY		654	TCACCTGCGCAGGTGCTGGGGTCTACTACTTTCGCGCTCATGCCACCGCTTACCGGGCCA	713
Dd		614	TCACCTGCGCAGGTGCTGGGGTCTACTACTTTCGCGCTCATGCCACCGCTTACCGGGCCA	673
OY		714	GCTGCGACTTGTGATCTGGTTGAAGAATGGCGAATCCATTCCTCTTCCAGTTTTTCG	773
Dd		674	GCTGCGACTTGTGATCTGGTTGAAGAATGGCGAATCCATTCCTCTTCCAGTTTTTCG	733
OY		774	GGGGTGGCCCAACCCACCTCCGCTTCGCGGGGGGGCCATGGTAGAGCTGGAGGCTGAGG	833
Dd		734	GGGGTGGCCCAACCCACCTCCGCTTCGCGGGGGGGCCATGGTAGAGCTGGAGGCTGAGG	793
OY		834	ACCAAGTGTGGGTGACAGTGGGTGGGTGGTGACTACATTGGCATGTATCCAGCATCAGA	893
Dd		794	ACCAAGTGTGGGTGACAGTGGGTGGGTGGTGACTACATTGGCATGTATCCAGCATCAGA	853
OY		894	CAGACGACACTTCTCGGATTTCTGTGTACTCCGACTGGCACAGCTCCCCAGCTCTTTCG	953
Dd		854	CAGACGACACTTCTCGGATTTCTGTGTACTCCGACTGGCACAGCTCCCCAGCTCTTTCG	913
OY		954	CTTAGTGGCCCACTGCAAAAGTAGCTCATGCTCTCACTCTTAGAAGGAGGGTGTAGAGCTG	1013
Dd		914	CTTAGTGGCCCACTGCAAAAGTAGCTCATGCTCTCACTCTTAGAAGGAGGGTGTAGAGCTG	973
OY		1014	ACAACGAGGTATCCAGGAGGGGCTGGCCCCCTGGAAATATTGTAAATGACTAGGAGAGTGT	1073
Dd		974	ACAACGAGGTATCCAGGAGGGGCTGGCCCCCTGGAAATATTGTAAATGACTAGGAGAGTGT	1033
OY		1074	GGGTAGAGCACTTCGCTCTGTGCTGGTGGCAAGGAATGGGAACAGTGGCTGTCTGCATC	1133
Dd		1034	GGGTAGAGCACTTCGCTCTGTGCTGGTGGCAAGGAATGGGAACAGTGGCTGTCTGCATC	1093
OY		1134	AGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCGCCAACAGACAGAGAGATGTGCTGTG	1193
Dd		1094	AGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCGCCAACAGACAGAGAGATGTGCTGTG	1153
OY		1194	CTGGCAGTGTAAATTCGCCAGGTGGTCTGGTCCAGAGACCCAGAGTGGGTGTCTCTT	1253
Dd		1154	CTGGCAGTGTAAATTCGCCAGGTGGTCTGGTCCAGAGACCCAGAGTGGGTGTCTCTT	1213
OY		1254	CCTGTCCTCTGCTTCTGTGATCTCTCCACACCCCTCTCTGCTCTGAGGGCGGGCCCTTT	1313
Dd		1214	CCTGTCCTCTGCTTCTGTGATCTCTCCACACCCCTCTCTGCTCTGAGGGCGGGCCCTTT	1273
OY		1314	TTCTGAGATCTCATTAATAACTTAAGAACCTTCATAAAAAAAAAAAAAAAAAAAAA	1368

DB		1274	TCTCAGAGATGTCACGTAAATAAACCTAAGAACCCTCCAAAAA	1328
RESULT	10			
ID	AAF44998			
XX	AAF44998 standard; cDNA; 1338 BP.			
AC				
XX	AAF44998;			
XX				
DT	28-MAR-2001 (first entry)			
XX				
DE	Human secreted protein related coding sequence SEQ ID NO: 103.			
XX				
KM	Human; mouse: secreted protein; TANGO253; TANGO 257; TANGO 281;			
KM	INTERCEPT 258; coronary disorder; olfactory disorder;			
KM	neurological disorder; pulmonary disorder; immunological disorder;			
KM	developmental disorder; kidney disorder; ss.			
OS	Homo sapiens.			
XX				
PN	WO200078808-A1.			
XX				
PD	28-DEC-2000.			
XX				
PF	19-JUN-2000; 2000WO-US16883.			
XX				
PR	18-JUN-1999; 99US-0336536.			
XX				
PA	(MILL-) MILLENNIUM PHARM INC.			
PI	Leidy KR, McKay C, Bossone S;			
XX				
DR	WPI; 2001-050109/06.			
XX				
PT	New nucleic acids for treating diseases and disorders, e.g.			
PT	atherosclerosis, infection, autoimmune diseases, obesity, ear			
PT	disorders, brain disorders, tumors, diabetes, arthritis, multiple			
PS	sclerotics and asthma -			
XX				
PS	Disclosure; Page 271, 332pp: English.			
XX				
CC	The present invention provides the protein and coding sequences of the			
CC	human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,			
CC	TANGO 281 and INTERCEPT 258. These are useful in the treatment of			
CC	coronary, pulmonary, olfactory, immunological, neurological,			
CC	developmental and kidney disorders.			
XX				
SO	Sequence 1338 BP; 229 A; 422 C; 460 G; 227 T; 0 other;			
Query Match	94.0%; Score 1295; DB 22; Length 1338;			
Best Local Similarity	99.5%; Pred. No. 2e-229;			
Matches 1309; Conservative	.0; Mismatches 5; Indels 1; Gaps 1			
OY				
DB	54 CCAGAGCTGGGGTGAAGCGGAGGGGGGCCCTGGCCGGGAGAGAGCGGGGGCTGG 113			
15	CCGGGACTGGGGTGACGGAGGGGCGCCTGGGCCGGGGAGAGCGGGGGCTGG 74			
OY	114 AGACACCAACTGAGGGGTCGCGAGTAGCGAGCGCCCCGGAAGAGGCCCATCGGGGAGCC 173			
DB	75 AGACACCACTGAGGGGTCGCGAGTAGCGAGCGCCCCGGAAGAGGCCCATCGGGGAGCC 134			
OY	174 GGGAGGGGGGACTGCGAAGAGAGACCCCGCGCTCCGGGGCTCCGGTGCACGCTATTAGAGCC 233			
DB	135 GGGAGGGGGGACTGCGAAGAGAGACCCCGCGCTCCGGGGCTCCGGTGCACGCTATTAGAGCC 194			
OY	234 CACTCTGCTCTGTGTCCTGTCCTGGGGCTGGGGCGGGGCGGCCGCCCACTGAGACGAACA 293			
DB	195 CACTCTGCTCTGTGTCCTGTCCTGGGGCTGGGGCGGGGCGGCCGCCCACTGAGACGAACA 254			
OY	294 AGATCCCAGGCTCTGCCCCGGGGGACCCCGGCGCTTCAAGAGCACGCCGGGGCACCATGGA 353			
DB	255 AGATCCCAGGCTCTGCCCCGGGGGACCCCGGCGCTTCAAGAGCACGCCGGGGCACCATGGA 314			

QY	354	GCACAGGCGCTTGCCTGGGGCCCGCATATGGCCGCGACGGCCGACAGGGCCGCGCCCGGGGCTCCGG	413
Db	315	GCCAGGGGCTTGCCTGGGGCCCGCATATGGCCGCGACGGCCGACAGGGCTGCGCCCGGGGCTCCGG	374
QY	414	GAGAGAAAGCCGAGGGCGGGAGCGCGGAGCTGCCGGGACCTCGAGGGGAGACCCGGGCGCG	473
Db	375	GAGAGAAAGCCGAGGGCGGGAGAG - CGGGAGCTCCGGGACCTCGAGGGGAGACCCGGGCGCG	433
QY	474	GAGGAGAGGGCGGGAGCCCGGGGGGCCACCGGGCGTCCGGGGAGTCTGGTGCCTCCCG	533
Db	434	GAGGAGAGGGCGGGAGCCCGGGGGGCCACCGGGCGTCCGGGGAGTCTGGTGCCTCCCG	493
QY	534	GATCCGCGCTTCAGCGCCAGCGCTCCGAGAGCGCGGGTGCCTCCGCGCTCTGACGACACCT	593
Db	494	GATCCGCGCTTCAGCGCCAGCGCTCCGAGAGCGCGGGTGCCTCCGCGCTCTGACGACACCT	553
QY	594	TGCCCTTGCAGCCGCGTGCCTGGTGAACGACAGGAGACATTACGAGCGCGTCCACCGGACAT	653
Db	554	TGCCCTTGCAGCCGCGTGCCTGGTGAACGACAGGAGACATTACGAGCGCGTCCACCGGAGAT	613
QY	654	TCACCTGCAGAGTGCCTGGGGGTCTACTACTATTGCGCGCTCCATGCGACACCGTCAACCGGACCA	713
Db	614	TCACCTGCAGAGTGCCTGGGGGTCTACTACTATTGCGCGCTCCATGCGACACCGTCAACCGGACCA	673
QY	714	GCCTGCAGTTTATCTGGTGAAGATGGCGAATCCATTGCCCTTTCTTCCAGTTTTCG	773
Db	674	GCCTGCAGTTTATCTGGTGAAGATGGCGAATCCATTGCCCTTTCTTCCAGTTTTCG	733
QY	774	GGGGGTGGGCCCAAGCCAGCGCTCGCTCCGGGGGGGCCAATGGAGAGGCTGAGACCTGAGG	833
Db	734	GGGGGTGGGCCCAAGCCAGCGCTCGCTCCGGGGGGGCCAATGGAGAGGCTGAGACCTGAGG	793
QY	834	ACCAAGTGTGGGTGACAGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCATCAAG	893
Db	794	ACCAAGTGTGGGTGACAGTGGGTGTGGGTGACTACATTGGCATCTATGCCAGCATCAAG	853
QY	894	CAGACAGACCTTCCTCCGATTTTCGGGTGTACTCCGACGTGGGACACCTCCCGACGTTCG	953
Db	854	CAGACAGACCTTCCTCCGATTTTCGGGTGTACTCCGACGTGGGACACCTCCCGACGTTCG	913
QY	954	CTTAGTGCCCACTGCAAAAGTGAAGCTCATGCTCTCACTCTAGAGAGGAGGTGTGAGACTG	1013
Db	914	CTTAGTGCCCACTGCAAAAGTGAAGCTCATGCTCTCACTCTAGAGAGGAGGTGTGAGACTG	973
QY	1014	ACAACACAGGTCAATCCAGAGAGGCTGGCCCCCTCGGAATTTGTGAATTACTAGAGAGGTG	1073
Db	974	ACAACCTGGTCAATCCAGAGAGGCTGGCCCCCTCGGAATTTGTGAATTACTAGAGAGGTG	1033
QY	1074	GGGTAGAGACATCTCCGTCTCTGCTGCTGCGCAAGAAATGGGAACAGTGGCTGTCTGAGATC	1133
Db	1034	GGGTAGAGACATCTCCGTCTCTGCTGCTGCGCAAGAAATGGGAACAGTGGCTGTCTGAGATC	1093
QY	1134	AGGTGTGGACAGCATGGGGCAGTGGCTGGAATTTCTGCCCCAAGACAGAGCAGTGTGCTGTG	1193
Db	1094	AGGTGTGGACAGCATGGGGCAGTGGCTGGAATTTCTGCCCCAAGACAGAGCAGTGTGCTGTG	1153
QY	1194	CTGGAGAAGTAAAGTCCCCCAGTTGGCTGGTGCACAGAGACCCACAGGTGGGGTGTCTCTTT	1253
Db	1154	CTGGAGAAGTAAAGTCCCCCAGTTGGCTGGTGCACAGAGACCCACAGGTGGGGTGTCTCTTT	1213
QY	1254	CCTGTCTCTCTGCTTCTGTGATCTCTCCACCCCTCTCTGCTCTGGGGCCGGGCGCTT	1313
Db	1214	CCTGTCTCTCTGCTTCTGTGATCTCTCCACCCCTCTCTGCTCTGGGGCCGGGCGCTT	1273
QY	1314	TCTCAGAGATCACTCAATTAACCTAAGAACCTCAATTAACCTAAGAACCTCAATTAACCTAAGAACCT	1368
Db	1274	TCTCAGAGATCACTCAATTAACCTAAGAACCTCAATTAACCTAAGAACCTCAATTAACCTAAGAACCT	1328

[illegible]

QY	474	GAGAGAGAGGGAGGACCCGGGGGGGGCCACACGGGGGGCCCGCGGGGAGAGTGGCTGGCTCCGC	533
Db	434	GAGGAGAGGGGGAGACCGGGGGGGCCACCGGGGGCTGTGGGGAGAGTGGCTGGCTCCGC	493
QY	534	GATCGCGCTTACAGGGCCAAAGCGCTCCAGAGACCGGGGTGCTCCCGCGCTGTACGACACCT	593
Db	494	GATCGCGCTTACAGGGCCAAAGCGCTCCAGAGACCGGGGTGCTCCCGCGCTGTACGACACCT	553
QY	594	TGCCCCCTTGACCCGGGTGCTGTTGAACGACGAGGAGCAATTACGACCGGTCAACGGCAAGT	653
Db	554	TGCCCCCTTGACCCGGGTGCTGTTGAACGAGAGGAGCAATTACGACCGGTCAACGGCAAGT	613
QY	654	TCACCTGCGAGGTGGCTGGGGTCTACTACTTGGCGGTCCATGGCCACCGCTCACGGGGGCA	713
Db	614	TCACCTGCGAGGTGGCTGGGGTCTACTACTTGGCGGTCCATGGCCACCGCTCACGGGGGCA	673
QY	714	GCTGTCAGATTGATCTGGTGAAGAATGAGCGAATCCATTCGCTCTTCTCCAGTTTTTCG	773
Db	674	GCTGTCAGATTGATCTGGTGAAGAATGAGCGAATCCATTCGCTCTTCTCCAGTTTTTCG	733
QY	774	GGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCCATGGTAGAGCTGAGCCTGAGG	833
Db	734	GGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGGGGGCCCATGGTAGAGCTGAGCCTGAGG	793
QY	834	ACCAAGTGTGGGTGCAGGTGGGGTGGGGTGACTCAATTGGCATCTATGCGCAGCATCAAGA	893
Db	794	ACCAAGTGTGGGTGCAGGTGGGGTGGGGTGACTCAATTGGCATCTATGCGCAGCATCAAGA	853
QY	894	CAGACAGCACCTTCTCCGGATTCTTGGTGATCTCACTCCGACTGGACAGCTCCCCAGCTTTG	953
Db	854	CAGACAGCACCTTCTCCGGATTCTTGGTGATCTCACTCCGACTGGACAGCTCCCCAGCTTTG	913
QY	954	CTTAGTGGCCACTGCAAAAGTAGCTCATGCTCTCACTCTTGAAAGAGAGGTGTAGAGCTG	1013
Db	914	CTTAGTGGCCACTGCAAAAGTAGCTCATGCTCTCACTCTTGAAAGAGAGGTGTAGAGCTG	973
QY	1014	ACAACACAGTATCCAGAGAGGGGGCGCCGCCCTGGAAATATGTGAATACTAGGAGAGGTG	1073
Db	974	ACAACCTGTGATCCAGAGAGGGGGCGCCGCCCTGGAAATATGTGAATACTAGGAGAGGTG	1033
QY	1074	GGGTAGAGCACTCCGCTCGTCTGCTGGCAGGAATGGGAACAGTGGCTGTGCGATC	1133
Db	1034	GGGTAGAGCACTCCGCTCGTCTGCTGGCAGGAATGGGAACAGTGGCTGTGCGATC	1093
QY	1134	AGGTCTGGCACATGGGGCAGTGGCTGGATTTCGTGCCAAGACAGAGAGATGTGCTGTG	1193
Db	1094	AGGTCTGGCACATGGGGCAGTGGCTGGATTTCGTGCCAAGACAGAGAGATGTGCTGTG	1153
QY	1194	CTGGCAAGTGAAGTCCCGCCAGTTGCTGTGTCAGAGAGCCACAGGTTGGGTGCTCTCTT	1253
Db	1154	CTGGCAAGTGAAGTCCCGCCAGTTGCTGTGTCAGAGAGCCACAGGTTGGGTGCTCTCTT	1213
QY	1254	CTGTGCTCTGCTTCTGTGTGATCCCTCCACCCCTCTGCTCTGTGGGGCGGGCCCTTT	1313
Db	1214	CTGTGCTCTGCTTCTGTGTGATCCCTCCACCCCTCTGCTCTGTGGGGCGGGCCCTTT	1273
QY	1314	TCTCAGAGATACATCAATAAACCTTAAGAACCCTCATATAAAAAAAAAAAAAAAAAAAAA	1368
Db	1274	TCTCAGAGATACATCAATAAACCTTAAGAACCCTCATATAAAAAAAAAAAAAAAAAAAAA	1328
RESULT 12			
AAAF45000			
ID AAF45000 standard; cDNA: 1338 BP.			
AAAF45000;			
28-MAR-2001 (first entry)			
Human secreted protein related coding sequence SEQ ID NO: 107.			
Human; mouse;secreted protein; TANGO253; TANGO 257; TANGO 281;			

Query Match	94.0%: Score 1295; DB 22; Length 1338;	Best Local Similarity 99.5%: Pred. No. 2e-229;	Matches 1309; Conservative 0; Mismatches 5; Indels 1; Gaps 1
XX	INTERCEPT 258; coronary disorder; olfactory disorder;		
KW	neurological disorder; pulmonary disorder; immunological disorder;		
KW	developmental disorder; kidney disorder; ss.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200078808-A1.		
XX			
XX	28-DEC-2000.		
XX			
XX	19-JUN-2000; 2000WO-US16883.		
PF			
XX			
PR	18-JUN-1999; 99US-0336536.		
XX			
XX	(MILL-) MILLENNIUM PHARM INC.		
PA			
XX			
PI	Leiby KR, McKay C, Bossone S;		
XX			
DR	WPI; 2001-050109/06.		
XX			
PT	New nucleic acids for treating diseases and disorders, e.g.,		
PT	atherosclerosis, infection, autoimmune diseases, obesity, ear		
PT	disorders, brain disorders, tumors, diabetes, arthritis, multiple		
PT	sclerosis and asthma -		
XX			
PS	Disclosure; Page 273; 332pp; English.		
XX			
CC	The present invention provides the protein and coding sequences of the		
CC	human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,		
CC	TANGO 281 and INTERCEPT 258. These are useful in the treatment of		
CC	coronary, pulmonary, olfactory, immunological, neurological,		
CC	developmental and kidney disorders.		
XX			
SQ	Sequence 1338 BP; 229 A; 424 C; 460 G; 225 T; 0 other;		
QY	Query Match		
Db	Best Local Similarity 99.5%: Pred. No. 2e-229;		
Db	Matches 1309; Conservative 0; Mismatches 5; Indels 1; Gaps 1		
QY	54 CCAGACTCGGGTGACGCGCAGGGGCGCCTTGCCCGGGAAGAGCGCGGGGCTGG 113		
Db	15 CCGGACTCGGGGTGACGGCAGGGGCGCCTTGCGCGGAGAGAGCGCGGGGCTGG 74		
QY	114 AGCACCACCACTGGAGGGGTCCGAGTAGCGAGGGGCCCGAGAGAGGCCATCGGGGAGGC 173		
Db	75 AGCACCAACCACTGGAGGGGTCCGAGTAGCGAGGGGCCCGAGAGAGGCCATCGGGGAGGC 134		
QY	174 GGGAGGGGGGACTGCGAGAGAGACCCCGGCGTCCGGGCTCCAGCGCTATGAGGC 233		
Db	135 GGGAGGGGGGACTGCGAGAGAGACCCCGGCGTCCGGGCTCCAGCGCTATGAGGC 194		
QY	234 CACTCTCTGCTGCTGCTCTCTGGGCGCTGGCGGCGCGGCTGCCCTCTGAGCAGCAACA 293		
Db	195 CACTCTCTGCTGCTGCTCTCTGGGCGCTGGCGGCGCGGCTGCCCTCTGAGCAGCAACA 254		
QY	294 AGATTCCTCAGCTCTGCCCCGGGGGACCCCGGCTTCAGAGGACGCCGGGACCACTGAGCA 353		
Db	255 AGATTCCTCAGCTCTGCCCCGGGGGACCCCGGCTTCAGAGGACGCCGGGACCACTGAGCA 314		
QY	354 GCCAGGGGTTGCGCGGGGCGCGATGCGCGAGAGGGCGGAGGGGCGCGCGGGGGCTCCGG 413		
Db	315 GCCAGGGGTTGCGCGGGGCGCGATGCGCGAGAGGGCGGAGGGGCGCGCGGGGGCTCCGG 374		
QY	414 GAGAGAAAGCGGAGGCGCGGAGAGCGCGGAGTCCCGGAGCTTCGAGAGGAGACCCCGGCGGC 473		
Db	375 GAGAGAAAGCGGAGGCGCGGAGAG -CGGAGACTTCGCGGAGACTTCGAGAGGAGACCCCGGCGGC 433		
QY	474 GAGAGAGAGCGGAGACCCCGGGGGCCCACTGGGGCTGCGGGGAGTGTCTGCTGCTCCGC 533		
Db	434 GAGGAGAGAGCGGAGACCCCGGGGGCCCACTGGGGCTGCGGGGAGTGTCTGCTGCTCCGC 493		
QY	534 GATCGCGCTTGAAGCGCCAAAGGCTTCGAGAGACCGGGGTCTCTCCGCTCTAGCGACCT 593		

Db	494	GATCGCGCTTACAGGCGCAAGGCGCTCGAGAGCGCGGGTGCTCCTCCGCGCTGTGACGCAACCT	553
QY	554	TGCCCTTGCACCCGCGCTGCTGGTGAACGACGACGAGCATTTACGAGCGCGTCAACGGCAAGT	653
Db	554	TGCCCTTGCACCCGCGCTGCTGGCGAAGCAGACGAGGACATTTAGACGCGCGTCAACGGCAAGT	613
QY	654	TCACCTGCGAGGTGCGTGGGGCTCTACTTCTGCGCGCTCATGCGCCACCGCTTACCGGGGCA	713
Db	614	TCACCTGCGAGGTGCGTGGGGCTCTACTTCTGCGCGCTCATGCGCCACCGCTTACCGGGGCA	673
QY	714	GCCITGCATTTGATCTGGTGAAGATGCGAATCCATTGCTCTTTCTTCAGTTTTTCG	773
Db	674	GCCITGCATTTGATCTGGTGAAGATGCGAATCCATTGCTCTTTCTTCAGTTTTTCG	733
QY	774	GGGGGTGCCCAAGCAGCAGCTTCTCTCTGGGGGGGGCCATGTGTAGGCTGGAGCTGAGG	833
Db	734	GGGGGTGCCCCAAGCAGCAGCTTCTCTCTGGGGGGGGCCATGTGTAGGCTGGAGCTGAGG	793
QY	834	ACCAAGTGTGGGTGCGAGGTGGGTGGGTGACTACATTGGCATCTATGCCAGCATCAAGA	893
Db	794	ACCAAGTGTGGGTGCGAGGTGGGTGGGTGACTACATTGGCATCTATGCCAGCATCAAGA	853
QY	894	CAGACAGCAGCTTCTCCGGAATTTTCGTGTACTCCGAGCTGGCAGCAGCTCCCGAGCTTTG	953
Db	854	CAGACAGCAGCTTCTCCGGAATTTTCGTGTACTCCGAGCTGGCAGCAGCTCCCGAGCTTTG	913
QY	954	CTTAGTGGCCCACTGCAAAAGTGAAGTCACTGCTCTCACTCTTAGAAGAGAGGTGTAGGCTG	1013
Db	914	CTTAGTGGCCCACTGCAAAAGTGAAGTCACTGCTCTCACTCTTAGAAGAGAGGTGTAGGCTG	973
QY	1014	ACAACGAGTATCCAGAGAGGGGCTGCGCCCGCTGGAAATATTGTGAATCACTAGAGGAGGTG	1073
Db	974	ACAACGAGTATCCAGAGAGGGGCTGCGCCCGCTGGAAATATTGTGAATCACTAGAGGAGGTG	1033
QY	1074	GGGTAGAGCAGCTTCCGCTCTGCTGCTGGCAGAGAAATGGGAACAGTGGCTGTCCGATC	1133
Db	1034	GGGTAGAGCAGCTTCCGCTCTGCTGCTGGCAGAGAAATGGGAACAGTGGCTGTCCGATC	1093
QY	1134	AGGCTGCGCAGCATGAGGGGCACTGGCTGGATTTCTGCCCCAAGACGAGAGATGTCTGTG	1193
Db	1094	AGGCTGCGCAGCATGAGGGGCACTGGCTGGATTTCTGCCCCAAGACGAGAGATGTCTGTG	1153
QY	1194	CTGGCAATGTAAAGTCCGCCAGTTGCTCTGGTGCAGAGACCCAGAGGTTGGGTGCTCTCTT	1253
Db	1154	CTGGCAATGTAAAGTCCGCCAGTTGCTCTGGTGCAGAGACCCAGAGGTTGGGTGCTCTCTT	1213
QY	1254	CCTGGTCTCTGCTTCTCTGAGATCTTCCCAACCCCTCTGCTCTCTGCGGCGCGCCCTTT	1313
Db	1214	CCTGGTCTCTGCTTCTCTGAGATCTTCCCAACCCCTCTGCTCTCTGCGGCGCGCCCTTT	1273
QY	1314	TCTCAGAGATCACTCAATAAACTTAAGAACCCCTCATTAATAAAAAAAAAAAAAA	1368
Db	1274	TCTCAGAGATCACTCAATAAACTTAAGAACCCCTCATTAATAAAAAAAAAAAAAA	1328
RESULT 13			
ID	AAAF45001	standard; cDNA; 1338 BP.	
XX	AAF45001:		
DT	28-MAR-2001	(first entry)	
DE	Human secreted protein related coding sequence SEQ ID NO: 109.		
KW	Human; mouse; secreted protein; TANGO25; TANGO 257; TANGO 281;		
KW	INTERCEPT 258; coronary disorder; olfactory disorder;		
KW	neurological disorder; pulmonary disorder; immunological disorder;		
KW	developmental disorder; kidney disorder; ss.		
OS	Homo sapiens.		
PN	WO200078808-A1.		

XX	28-DEC-2000.	
-PD		
XX	19-JUN-2000; 2000WO-US16883.	
XX		
PF	18-JUN-1999; 99US-0336536.	
XX		
PR	(MILL-) MILLENNIUM PHARM INC.	
XX		
PA	Leibyl KR, McKay C, Bossone S;	
XX		
PI	WPI; 2001-050109/06.	
DR		
XX		
PT	New nucleic acids for treating diseases and disorders, e.g.	
XX	atherosclerosis, infection, autoimmune diseases, obesity, ear	
PT	disorders, brain disorders, tumors, diabetes, arthritis, multiple	
PT	sclerosis and asthma -	
XX		
PS	Disclosure; Page 274-275; 332pp; English.	
XX		
CC	The present invention provides the protein and coding sequences of the	
CC	human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,	
CC	TANGO 281 and INTERCEPT 258. These are useful in the treatment of	
CC	coronary, pulmonary, olfactory, immunological, neurological,	
CC	developmental and kidney disorders.	
XX		
XX	Sequence 1338 BP; 228 A; 424 C; 460 G; 226 T; 0 other;	

Query Match	94.0%;	Score 1295;	DB 22;	Length 1338;
Best Local Similarity	99.5%;	Pred. No. 2e-229;		
Matches 1309;	Conservative	0;	Mismatches 5;	Indels 1;
			Gaps	1

OY	54	CCAGGACTGGGGGTGACGGCAGGGGCGCCCTGGGGCGGGAGAAACGCGGGGGCTGG	113
Db	15	CCGGGACTGGGGGTGACGGCAGGGGCGCCCTGGGGCGGGAGAAACGCGGGGGCTGG	74
OY	114	AGCACCAACTGGAGGGGTCCGGAGTAGCGAGCGCCCCGAAGAGGCCATCGGGGAGCC	173
Db	75	AGCACCACAACTGGAGGGGTCCGGAGTAGCGAGCGCCCCGAAGAGGGCCATCGGGGAGCC	134
OY	174	GGGAGGGGGGACTGGAGAGGACCCCGGCGTCCGGGGGTCGCCGGTCCACAGCGCTATAGAGGC	233
Db	135	GGGAGGGGGGACTGGAGAGGACCCCGGCGTCCGGGGGTCGCCGGTCCACAGCGCTATAGAGGC	194
OY	234	CACCTCTGCTGCTGCTCTCTGGGCTTGCGGCGCCGCGCTGCGCCCACTGGACGACAACA	293
Db	195	CACCTCTGCTGCTGCTCTCTGGGCTTGCGGCGCCGCGCTGCGCCCACTGGACGACAACA	254
OY	294	AGATCCCCAGCCTCTGCCCCGGGGGCAACCCCGCCTTCCAGGCAACGCCGGGGCCACCATATGGCA	353
Db	255	AGATCCCCAGCCTCTGCCCCGGGGGCAACCCCGCCTTCCAGGCAACGCCGGGGCCACCATATGGCA	314
OY	354	GCCAGGGGCTTCCCGGGGCGGCATGGCCCGCAGAGGCGCGAGCGACGCGCCCGGGGCTTCGGG	413
Db	315	GCCAGGGGCTTCCCGGGGCGGCATGGCCCGCAGAGGCGCGAGCGACGCGCCCGGGGCTTCGGG	374
OY	414	GAGAGAAAGCGGAGGGCGGGGAGGCCCGGGACTTCGCGGGACCTTCGAGGGGAAACCCGGGCGCG	473
Db	375	GAGAGAAAGCGGAGGGCGGGGAGGCCCGGGACTTCGCGGGACCTTCGAGGGGAAACCCGGGCGCG	433
OY	474	GAGAGAGAGCGGGAACCCCGGGGCGCCACCGGGGCTGCGGGGAGTAGTCTCGGTCCTCCGC	533
Db	434	GAGAGAGAGCGGGAACCCCGGGGCGCCACCGGGGCTGCGGGGAGTAGTCTCGGTCCTCCGC	493
OY	534	GATCGGCTTCAGCGCCCAAGCGCTTCGAGAGCGCGGGGTGCTCCGCGCTGTGACGACCTT	593
Db	494	GATCGGCTTCAGCGCCCAAGCGCTTCGAGAGCGCGGGGTGCTCCGCGCTGTGACGACCTT	553
OY	594	TGCGCTTGGACCGGGTGTCTGGTGAACGAGCGAGGACATTATGAGCGCCGTCACCGGCAAGT	653
Db	554	TGCGCTTGGACCGGGTGTCTGGTGAACGAGCGAGGACATTATGAGCGCCGTCACCGGCAAGT	613
OY	654	TCACCTGGCAGGTGCTGGGGGTCTACTACTTTCGCGGTCCGATCCACCGTCTACCGGGCCA	713

Db	614	TCACCTTCCAGAGTGCCTGGGGGTCTACTCTGCGCCTCCATGCCACCGCTTACCGGGGCCA	673
QY	714	GCCTCAGTTTGAATCTGGTGAGAAATGCGCATCCATTCCTCTTCTTCCAGTTTTCG	773
Db	674	GCCTGCAGTTTGAATCTGGTGAGAAATGCGCATCCCTTGGCTCTTCTTCCAGTTTTCG	733
QY	774	GGGGGTGGCCCAAGCCACGCTGCTCTCGGGGGGGGGGCANATGGTAGGGCTGAGACCCGAGG	833
Db	734	GGGGGTGGCCCAAGCCACGCTGCTCTCGGGGGGGGGGCANATGGTAGGGCTGAGACCCGAGG	793
QY	834	ACCAAGTGTGGGTGACAGTGTGGGTGGGTGACATACATTTGGCATCTATGCGAGATCAAGA	893
Db	794	ACCAAGTGTGGGTGACAGTGTGGGTGGGTGACATACATTTGGCATCTATGCGAGATCAAGA	853
QY	894	CAGACAGCACCTTCTCCGGATTCTGGTGTACTCCGACTGCGACAGCTCCCACTCTTTG	953
Db	854	CAGACAGCACCTTCTCCGGATTCTGGTGTACTCCGACTGCGACAGCTCCCACTCTTTG	913
QY	954	CTTAGTCCCACTGCAAAAGTAGCTATGCTCAGCTCCAGAGAAGGAGGTGAGAGCTG	1013
Db	914	CTTAGTCCCACTGCAAAAGTAGCTATGCTCAGCTCCAGAGAAGGAGGTGAGAGCTG	973
QY	1014	ACAACCAAGTTCATCCAGAGAGGGCTGCCCCCTGGAAATATTGTGAATGACTAGGAGGTG	1073
Db	974	ACAACCAAGTTCATCCAGAGAGGGCTGCCCCCTGGAAATATTGTGAATGACTAGGAGAGTG	1033
QY	1074	GGGTAGAGCACTCCGCTCGCTGGTGGGCAAGAAATGGAGACAGTGGCTGTGCGATC	1133
Db	1034	GGGTAGAGCACTCCGCTCGCTGGTGGGCAAGAAATGGAGACAGTGGCTGTGCGATC	1093
QY	1134	AGGCTTGGGCAGCATGGGGGCAGTGGCTGGATTTCTTGCCCAAGACAGAGAGTGTGCTGTG	1193
Db	1094	AGGCTTGGGCAGCATGGGGGCAGTGGCTGGATTTCTTGCCCAAGACAGAGAGTGTGCTGTG	1153
QY	1194	CTGGCAAGTGAATGATCCCGCCAGTGGCTGTGTGTCCAGAGGCCACAGGTGGGTCTCTCTT	1253
Db	1154	CTGGCAAGTGAATGATCCCGCCAGTGGCTGTGTGTCCAGAGGCCACAGGTGGGTCTCTCTT	1213
QY	1254	CTGTGTCCTGTGCTCTGTGATCTCCACCACCCTCCCTGCTCTGTGAGGGCCGACCCTTT	1313
Db	1214	CTGTGTCCTGTGCTCTGTGATCTCCACCACCCTCCCTGCTCTGTGAGGGCCGACCCTTT	1273
QY	1314	TCTCAGAGATCACTCAATAAAGCTAAGAACCTTCATTAATAAAAAAAAAAAAAA	1368
Db	1274	TCTCAGAGATCACTCAATAAAGCTAAGAACCTTCATTAATAAAAAAAAAAAAAA	1328

RESULT 14

AAI39624

ID AAI39624 standard; DNA: 3248 BP.

XX

XX AAI39624:

XX

XX 05-SEP-2002 (first entry)

XX

XX Human secreted protein DNA SEQ ID No 68.

XX

XX Antiarteriosclerotic; cytostatic; HIV; antiallergic; antihaemic;

XX antiasthmatic; cardiatic; vasotropic; neuroprotective; nootropic; SECP;

XX anticonvulsant; antiparkinsonian; cerebroprotective; antinflammatory;

XX immunosuppressive; human secreted protein; cell proliferative disorder;

XX arteriosclerosis; cancer; autoimmune; inflammatory disorder; AIDS;

XX allergy; anaemia; asthma; cardiovascular disease; developmental disorder;

XX ischaemic heart disease; congestive heart failure; neurological disorder;

XX renal tubular acidosis; hypothyroidism; Alzheimer's disease; dementia;

XX Parkinson's disease; epilepsy; stroke; knockin humanised animal;

XX transgenic animal; gene therapy; gene; ds.

XX

XX Homo sapiens.

XX

XX W0200238602-A2.

XX

QY	1134	AGGCTGTGGCAGCANNNGGGGCAAGTGGCTGGATTCTTGGCCCAAGACCAAGAGAGTGGCTGG	1193
Db	1094	AGGCTGTGGCAGCANNNGGGGCAAGTGGCTGGATTCTTGGCCCAAGACCAAGAGAGTGGCTGG	1153
QY	1194	CTGGCAGAGTGAATGAATCCCAAGTGGCTGTGGTCCAGAGAGCCCAAGGTGGGCTCTCTT	1253
Db	1154	CTGGCAGAGTGAATGAATCCCAAGTGGCTGTGGTCCAGAGAGCCCAAGGTGGGCTCTCTT	1213
QY	1254	CTGGTGCCTGTGGCTGTCTGTGGATCTCTCCCAACCCCTCTCTGCTCTGAGGCGGACCCTTT	1313
Db	1214	CTGGTGCCTGTGGCTGTCTGTGGATCTCTCCCAACCCCTCTCTGCTCTGAGGCGGACCCTTT	1273
QY	1314	TCTCAGAGATCACTCAATAAAGCTAAGAACCCCTCATPAAAAAAAAAAAAAAAAAAAAA	1368
Db	1274	TCTCAGAGATCACTCAATAAAGCTAAGAACCCCTCAAAAAAAAAAAAAAAAAAAAAA	1328

RESULT 14  
 AAL39624  
 ID AAL39624 standard; DNA; 3248 BP.  
 XX  
 AC  
 XX  
 DT 05-SEP-2002 (first entry)  
 XX  
 DE Human secreted protein DNA SEQ ID No 68.  
 KW Antiartherosclerotic; cytostatic; HIV; anti allergic; anti anaemic;  
 KW antiasthmatic; cardiac; vasotropic; neuroprotective; nootropic; SECP;  
 KW anticonvulsant; antiparkinsonian; cerebroprotective; antiinflammatory;  
 KW immunosuppressive; human secreted protein; cell proliferative disorder;  
 KW arteriosclerotic; cancer; autoimmune; inflammatory disorder; AIDS;  
 KW allergy; anaemia; asthma; cardiovascular disease; developmental disorder;  
 KW ischaemic heart disease; congestive heart failure; neurological disorder;  
 KW renal tubular acidosis; hypothyroidism; Alzheimer's disease; dementia;  
 KW Parkinson's disease; epilepsy; stroke; knockin humanised animal;  
 KW transgenic animal; gene therapy; gene; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200238602-A2.  
 XX



PD 16-MAY-2002.  
 XX 08-NOV-2001; 2001MO-US47420.  
 XX 08-NOV-2000; 2000US-247505P.  
 PR 09-NOV-2000; 2000US-248642P.  
 PR 16-NOV-2000; 2000US-248824P.  
 PR 21-NOV-2000; 2000US-252824P.  
 PR 08-DEC-2000; 2000US-254305P.  
 PR 18-DEC-2000; 2000US-256448P.  
 XX  
 PA (INCYTE GENOMICS INC.  
 XX Yue H, Yao MG, Gandhi AR, Baughn MR, Swarnakar A, Walla NR,  
 PI Sanjwalwa M, Thornton M, Elliott VS, Lu Y, Gietzen KJ, Burford N;  
 PI Ding L, Hafalia AJA, Tang YT, Bandman O, Warren BA, Honchell CD;  
 PI Lu DAM, Thangavelu K, Lee S, Xu Y, Yang J, Lal PG, Tran B;  
 PI Ison CH, Duggan BM, Saperstein SK;  
 XX  
 DR WPI: 2002-519296/55.  
 DR P-PSDB: AA021653.  
 XX  
 PT Human secreted proteins and polynucleotides for diagnosing, treating or  
 PT preventing disorders of cell proliferative, cardiovascular,  
 PT developmental, neurological and autoimmune/inflammatory disorders -  
 PS  
 PS Claim 5; Page 194-195; 229pp; English.  
 XX  
 CC The invention relates to an isolated human secreted protein (SECP)  
 CC polypeptide from 63 fully defined protein sequences given in the  
 CC specification. The polypeptide is useful for the diagnosing/treating of a  
 CC disease with decreased/overexpression of SECP. Examples of disorders  
 CC associated with abnormal expression of SECP include a cell proliferative  
 CC disorder e.g. arteriosclerosis, cancers; autoimmune/inflammatory  
 CC disorder, AIDS, allergies, anaemia, asthma; cardiovascular disease e.g.  
 CC congestive heart failure, ischaemic heart disease; developmental disorder  
 CC e.g. renal tubular acidosis, hypothyroidism; neurological disorder e.g.  
 CC Alzheimer's disease, dementia, Parkinson's disease, epilepsy or stroke.  
 CC The SECP polynucleotide and polypeptide are further useful for analysing  
 CC the proteome of a tissue or a cell type. The polynucleotide is useful for  
 CC creating knockin humanised animals (pigs) or transgenic animals (mice or  
 CC rats) to model human disease, and for somatic or germ-line gene therapy,  
 CC and further for generating hybridisation probes useful in mapping the  
 CC naturally occurring genomic sequence. This polynucleotide sequence  
 CC represents the DNA of a human secreted protein of the invention.  
 CC  
 XX  
 SQ Sequence 3248 BP; 565 A; 1058 C; 946 G; 679 T; 0 other;  
 Query Match 78.88; Score 1084.8; DB 24; Length 3248;  
 Best Local Similarity 90.58; Pred. No. 1.le-190;  
 Matches 1222; Conservative 0; Mismatches 2; Indels 126; Gaps 1;  
 QY 7 TTCCTCTGAGTCTGGAGAGAGAAAGCGAGCGGAGGAGGAGCAACAGAGTGGGT 66  
 Db 2025 TCCCTCTGAGTCTGGAGAGAGAAAGCGAGCGGAGGAGGAGCAACAGAGTGGGT 2084  
 QY 67 GAGGCGAGGCGAGGCGGCGCTGGCGGGGAGAAAGCGGCGGCTGGAGCAACCAACT 126  
 Db 2085 GAGGCGAGGCGAGGCGGCGCTGGCGGGGAGAAAGCGGCGGCTGGAGCAACCAACT 2144  
 QY 127 GGAGGCTCGGAGTACGAGGAGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGT 186  
 Db 2145 GGAGGCTCGGAGTACGAGGAGCGGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGT 2204  
 QY 187 GCGAGAGAGAGCGGCGGCGTCCGGGCTCCGGTGCAGAGGCTATGAGGCGACGCTCGTCC 246  
 Db 2205 GCGAGAGAGAGCGGCGGCGTCCGGGCTCCGGTGCAGAGGCTATGAGGCGACGCTCGTCC 2264  
 QY 247 GCTGCTCTCTGGGCTGGGCGGCGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 306  
 Db 2265 GCTGCTCTCTGGGCTGGGCGGCGGCGGCTCGGCGGCGGCGGCGGCGGCGGCGGCGG 2234  
 QY 307 CTGCGCGGCGGCGGCGGCGCTTCAGAGCAAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 366

Db 2325  
 QY 367  
 Db 2329  
 QY 427  
 Db 2329  
 QY 487  
 Db 2379  
 QY 547  
 Db 2439  
 QY 607  
 Db 2499  
 QY 667  
 Db 2559  
 QY 727  
 Db 2619  
 QY 787  
 Db 2679  
 QY 847  
 Db 2739  
 QY 907  
 Db 2799  
 QY 967  
 Db 2859  
 QY 1027  
 Db 2919  
 QY 1087  
 Db 2979  
 QY 1147  
 Db 3039  
 QY 1207  
 Db 3099  
 QY 1267  
 Db 3159  
 QY 1327  
 Db 3219  
 RESULT 15



AA576911  
ID AAS76911 standard; cDNA; 1082 BP.  
XX  
AC AAS76911;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #12715.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW Food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US08631.  
XX  
PR 31-MAR-2000; 2000US-0540217.  
PR 23-AUG-2000; 2000US-0649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
PI WPI: 2001-639362/73.  
XX  
DR P-PSDB; AB612724.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity  
XX  
PS Claim 1; SEQ ID NO 12715; 103bp; English.  
XX  
CC The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human  
CC diagnostic coding sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 1082 BP; 193 A; 334 C; 353 G; 202 T; 0 other;

Query Match 67.1%; Score 923.6; DB 23; Length 1082;  
Best Local Similarity 96.5%; Pred. No. 4,4e-161;  
Matches 1042; Conservative 0; Mismatches 24; Indels 14; Gaps 9;

QY 299 CCCAGCCTCTGCCCGGGGACCCCGGCTTCCAGGACGACCGGCGCCACCATGAGACCCAG 358  
DB 1 CCCAGCCTCTGCCCGGGGACCCCGGCTTCCAGGACGACCGGCGCCACCATGAGACCCAG 60

QY 359 GGGTGGCGGGCGGGGATGGCGGCGGACGCGGACGCGGCGCGGGGCTCCGGGAGAG 418  
DB 61 GGGTGGCGGGCGGGGATGGCGGCGGACGCGGACGCGGCGCGGGGCTCCGGGAGAG 120

QY 419 AAAGCGAGGGCGGGGAGGCGGAGCTGCCGGGACCTCGAGGGGACCCCGGCGGAGGA 478  
DB 121 AAAGCGAGGGCGGGGAGGCGGAGCTGCCGGGACCTCGAGGGGACCCCGGCGGAGGA 180

QY 479 GAGGCGGAGCCCGCGGGGCGCCACCGGGCTGCGGGGAGTGTCTGGTCTCCGCGATCC 538  
DB 181 GAGGCGGAGCCCGCGGGGCGCCACCGGGCTGCGGGGAGTGTCTGGTCTCCGCGATCC 240

QY 539 GCGTTACGCGCCCAAGCGCTCCGAGAGCCGGGTGCTCCGGCGCTGACGACCCCTTGCC 598  
DB 241 GCGTTACGCGCCCAAGCGCTCCGAGAGCCGGGTGCTCCGGCGCTGACGACCCCTTGCC 300

QY 599 TTCGACCGCGGTGCTGTAAGGAGGAGGACATTAACGAGCGGTCACCGGCAAGTCCACC 658  
DB 301 TTCGACCGCGGTGCTGTAAGGAGGAGGACATTAACGAGCGGTCACCGGCAAGTCCACC 360

QY 659 TGCAGAGTCTGGGGTCTACTACTTCCGCGTCATGCCACCGCTACCGGGCGACCCCTG 718  
DB 361 TGCAGAGTCTGGGGTCTACTACTTCCGCGTCATGCCACCGCTACCGGGCGACCCCTG 420

QY 719 CAGTTTGAATCTGTGAAGAATGCGCAATTCATTTGCTCTTCTTCTCGAGTTTTCGGGGG 778  
DB 421 CAGTTTGAATCTGTGAAGAATGCGCAATTCATTTGCTCTTCTTCTCGAGTTTTCGGGGG 480

QY 779 TGGCCCAAGCCAGCCCTCGCTTCGGGGGGGGGCGCATGTAGGCTGAGGCTGAGACCAA 838  
DB 481 TGGCCCAAGCCAGCCCTCGCTTCGGGGGGGGGCGCATGTAGGCTGAGGCTGAGACCAA 540

QY 839 GTGTGGGTCCAGGTGGGTGGGTGATCTATTCATTTGGCATTCAGCATCAAGACAGAC 898  
DB 541 GTGTGGGTCCAGGTGGGTGGGTGATCTATTCATTTGGCATTCAGCATCAAGACAGAC 600

QY 899 AGCAGCTTCTCCGGATTTTGTGTGTACTCCGACTGG--CAGAGCTCCCACTTTTGTGT 955  
DB 601 AGCAGCTTCTCCGGATTTTGTGTGTACTCCGACTGGCATCTCCCACTTTTGTGT 660

QY 956 TAGTGCC--ACTGCAAGTGAAGCATCTCTC--ACTCTGAAGAGAGGTGTAGAGCT 1012  
DB 661 TAGTGCCCAAGTGAAGCATCTCTCTCTCAACTCTGAAGAGAGGTGTAGAGCT 720

QY 1013 GACAAACAGATATCC-AGGAGGGGTGGCCCGCTGGAATTTGTGAATGACTAGGAGG 1071  
DB 721 GACAAACAGATATCCAAAGAGGGGTGGCCCGCTGGAATTTGTGAATGACTAGGAGG 780

QY 1072 T--GGGGTAGACACTCTCC--GTCTGCTGCTGGCAAGGAAT--GGGAAGAGGCTCTCT 1127  
DB 781 TTTGGGGTAGACACTCTCTCAGTCTGCTGCTGGCAAGGAATGGGAACAGTGGCTCTCT 840

QY 1128 GCGATCAGGTCTGGGAGCATATGGGGGAGTGGCTGATTTCTGCCCAAGACAGAGAGTGT 1187  
DB 841 GCGATCAGGTCTGGGAGCATATGGGGGAGTGGCTGATTTCTGCCCAAGACAGAGAGTGT 900

QY 1188 GCTGTGCTGGCAG--TGTAGTCCCGCACTGTCTGTGTCAGAGAGCCACAGTGGGGTGG 1246  
DB 901 GCTGTGCTGGGAGTGTAGTCCCGCACTGTCTGTGTCAGAGAGCCACAGTGGGGTGG 960

QY 1247 CTTCTCTTCTGCT 1306  
DB 961 CTTCTCTTCTGCT 1020

QY 1307 GCCCTTTTCTCA--GAGATCACTCAATAACCTAAGACCCCTCAATAAAAA 1364  
DB 1021 GCCCTTTTCTCAAGATCACTCAATAAAGACCCCTCAATAAAAA 1080

Search completed: June 21, 2003, 09:46:23  
Job time : 376 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 09:40:55 ; Search time 79 Seconds  
(without alignments)  
5345.492 Million cell updates/sec

Title: US-09-944-944-41  
Perfect score: 1377  
Sequence: 1 gactagtcctctgagtc.....aaaaaaaaaaaaaa 1377

Scoring table: IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq:\*  
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6: /cgn2\_6/ptodata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1322.2	96.0	1347	US-09-140-804-1	Sequence 1, Appl
2	1296.6	94.2	1338	US-09-336-536-1	Sequence 1, Appl
3	717	52.1	728	US-09-336-536-2	Sequence 2, Appl
4	692.8	50.3	1263	US-09-336-536-8	Sequence 8, Appl
5	606	44.0	1001	US-09-188-930-218	Sequence 210, App
6	605	43.9	1015	US-09-188-930-30	Sequence 30, Appl
7	564.2	41.0	729	US-09-336-536-9	Sequence 9, Appl
8	504	36.6	729	US-09-140-804-10	Sequence 10, Appl
9	257.8	18.7	601	US-09-336-536-74	Sequence 74, Appl
10	149.6	10.9	393	US-09-188-930-26	Sequence 26, Appl
11	90.6	6.6	1276	US-08-463-911-1	Sequence 1, Appl
12	82.2	6.0	1313	US-08-463-911-6	Sequence 6, Appl
13	82.2	6.0	4517	US-09-140-804-9	Sequence 9, Appl
14	77.4	5.6	843	US-09-118-408-23	Sequence 23, Appl
15	77.4	5.6	843	US-09-506-855-23	Sequence 23, Appl
16	73	5.3	144	US-09-140-804-28	Sequence 28, Appl
17	72	5.2	144	US-09-140-804-29	Sequence 29, Appl
18	72	5.2	144	US-09-140-804-31	Sequence 31, Appl
19	71.8	5.2	147	US-09-140-804-30	Sequence 30, Appl
20	68.4	5.0	4411529	US-09-103-840A-1	Sequence 1, Appl
21	65.2	4.7	2543	US-08-555-669-11	Sequence 11, Appl
22	65.2	4.7	2543	US-09-073-663-11	Sequence 11, Appl
23	62	4.5	985	US-09-056-556-182	Sequence 182, App
24	62	4.5	985	US-09-072-556-177	Sequence 177, App
25	62	4.5	4403765	US-09-103-840A-2	Sequence 2, Appl
26	60.8	4.4	756	US-08-642-255-50	Sequence 50, Appl
27	60.8	4.4	1839	US-08-383-744-1	Sequence 1, Appl

28	60.8	4.4	1839	US-08-999-336-1	Sequence 1, Appl
29	60.8	4.4	1839	PCT-US96-01427-1	Sequence 1, Appl
30	59.8	4.3	1333	US-09-227-357-51	Sequence 51, Appl
31	59.6	4.3	801	US-08-770-379-16	Sequence 16, Appl
32	59.6	4.3	801	US-08-757-669A-16	Sequence 16, Appl
33	59.6	4.3	801	US-09-230-371A-16	Sequence 16, Appl
34	59.2	4.3	432	US-08-642-255-48	Sequence 48, Appl
35	58.2	4.2	2769	US-09-118-408-1	Sequence 1, Appl
36	58.2	4.2	2769	US-09-506-855-1	Sequence 1, Appl
37	58	4.2	3181	US-08-655-086-1	Sequence 1, Appl
38	57.4	4.2	4411529	US-09-103-840A-1	Sequence 1, Appl
39	56.6	4.1	4403765	US-09-103-840A-2	Sequence 2, Appl
40	56.4	4.1	444	US-09-397-787-161	Sequence 161, App
41	56.4	4.1	4488	US-08-406-030A-3	Sequence 3, Appl
42	56	4.1	4257	US-08-690-473-1	Sequence 1, Appl
43	56	4.1	4257	US-09-259-821A-1	Sequence 1, Appl
44	56	4.1	4257	US-08-843-659-1	Sequence 1, Appl
45	54.8	4.0	801	US-09-298-568-3	Sequence 3, Appl

ALIGNMENTS

```
RESULT 1
US-09-140-804-1
; Sequence 1, Application US/09140804
; Patent No. 6197930
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Humes, Jacqueline M.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-49
; CURRENT APPLICATION NUMBER: US/09/140,804
; CURRENT FILING DATE: 1998-08-26
; EARLIER APPLICATION NUMBER: 60/056,983
; EARLIER FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1347
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (198)..(926)
US-09-140-804-1

Query Match          96.0%; Score 1322.2; DB 4; Length 1347;
Best Local Similarity 99.8%; Pred. No. 5.7e-257;
Matches 1324; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

40 CGGCGAGGAGCGACGAGACTGGGTGACGCGACGCGAGGGGGCGCTGGCGGGGAGA 99
   ||
11 CGAGAGGAGCGACGACGAGACTGGGTGACGCGACGCGAGGGGGCGCTGGCGGGAGA 70
100 AGCGGGGGGGCGGAGCGACGACGAGGAGGTCGCGAGTACGAGGCGCCCGAGAGAG 159
   |||||
71 AGCGGGGGGGCGTGGAGCGACGACGAGGAGGTCGCGAGTACGAGGCGCCCGAGAGAG 130
   |||||
160 GCCATCGGGGAGCGCGGAGGAGGAGGAGCGAGAGAGCCCGCGTCCGGGCTCCCGATGC 219
   |||||
131 GCCATCGGGGAGCGCGGAGGAGGAGGAGCGAGAGAGCCCGCGTCCGGGCTCCCGATGC 190
   |||||
220 CAGCGCTTATGAGCGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 279
   |||||
191 CAGCGCTTATGAGCGCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 250
   |||||
280 ACTGAGCAGCAACAGATCCCGAGCTGCGCCGCGGAGCCCGCGCTTCCAGGAGCGC 339
   |||||
251 ACTGAGCAGCAACAGATCCCGAGCTGCGCCGCGGAGCCCGCGCTTCCAGGAGCGC 310
   |||||
340 GGGCCACCATGCGACCGAGGCTTCCGCGCGCGCGATGCGCGAGCGCGCGAGGCGCGC 399
   |||||
```



QY	834	ACCAAGTGTGGGTGACAGTGGGTGGGTGGTACATCATATGGATGTATGACAGCAATCAAGA	893
Db	794	ACCAAGTGTGGGTGACAGTGGGTGGGTGGTACATCATATGGATGTATGACAGCAATCAAGA	853
QY	894	CAGACAGACACTTCTCCGATTTCTGGTATGCTCCGACTGGACACAGCTCCACAGTCTTGG	953
Db	854	CAGACAGACACTTCTCCGATTTCTGGTATGCTCCGACTGGACACAGCTCCACAGTCTTGG	913
QY	954	CTTAGTGCCCACTGCAAAGTAGTGCATAGCTCATCTACCTTAGAAGGAGGGTGTAGGCTG	1013
Db	914	CTTAGTGCCCACTGCAAAGTAGTGCATAGCTCATCTACCTTAGAAGGAGGGTGTAGGCTG	973
QY	1014	ACAACCAAGTATCCAGAGAGGGCTGGCCCCCTCGAATATGTGTAATGACTAGGAGAGGTG	1073
Db	974	ACAACCTGTGTCATCCAGAGAGGGCTGGCCCCCTCGAATATGTGTAATGACTAGGAGAGGTG	1033
QY	1074	GGGTAAGAGCACTCCGCTCCGCTGCTGCTGGCAAGAAAGGAAGGAAAGTGGCTCTGCTCATC	1133
Db	1034	GGGTAAGAGCACTCCGCTCCGCTGCTGCTGGCAAGAAAGGAAGGAAAGTGGCTCTGCTCATC	1093
QY	1134	AGGTCTGGCAACATGGGGCAGTGGCTGATTTTCGCCCAACACAGAGAGATGTGCTGTG	1193
Db	1094	AGGTCTGGCAACATGGGGCAGTGGCTGATTTTCGCCCAACACAGAGAGATGTGCTGTG	1153
QY	1194	CTGGCAAGTGTAAATCCCCCAAGTTGCTGTGGTCCAGAGAGCCACAGGTGGGTGCTCTCTT	1253
Db	1154	CTGGCAAGTGTAAATCCCCCAAGTTGCTGTGGTCCAGAGAGCCACAGGTGGGTGCTCTCTT	1213
QY	1254	CCCTGGTCCCTGCTCTCTCTGTGATCTCTCCACACCCCTCTCTCTCTGGGGGCGGGCCCTTT	1313
Db	1214	CCCTGGTCCCTGCTCTCTCTGTGATCTCTCCACACCCCTCTCTCTCTGGGGGCGGGCCCTTT	1273
QY	1314	TCTAGAGATCTACATATAAACCCTTAGAAGACCCCTATATAAAAAAAAAAAAAAAAAA	1368
Db	1274	TCTAGAGATCTACATATAAACCCTTAGAAGACCCCTATATAAAAAAAAAAAAAAAAAA	1328

RESULT 3  
US-09-336-536-2  
; Sequence 2, Application US/09336536

```

1  APPLICANT: BOSSCORE, S.
2  TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
3  FILE REFERENCE: 7853-144
4  CURRENT APPLICATION NUMBER: US/09/336,536
5  CURRENT FILING DATE: 1999-06-18
6  NUMBER OF SEQ ID NOS: 75
7  SOFTWARE: PatentIn Ver. 2.0
8  SEQ ID NO 2
9  LENGTH: 728
10 TYPE: DNA
11 ORGANISM: Homo sapiens
12 OS-09-336-536-2

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Query Match	52.1%	Score 717	DB 4	Length 728
Best Local Similarity	99.9%	Pred. No. 1.4e-135		
Matches 728; Conservative	0	Mismatches	0	Indels 1; Gaps 1;

[illegible]

OY	407	GCTCCGGAGAGAAAGGCGAGGGGCGGAGAGCCGGGACTCCCGGAGACTCGAGGGGAGCCCC	466
Db	181	GCTCCGGAGAGAAAGGCGAGGGGCGGAGAG -CGGAGCTGGCCGGAGACTCGAGGGGAGCCCC	239
OY	467	GGGCGCGAGAGAGAGCGGAGACCCCGGGGGGCCACCGGGGCTGCGCGGGGAGTGTCTGGTG	526
Db	240	GGGCGCGAGAGAGAGCGGAGACCCCGGGGGGCCACCGGGGCTGTCCGGGGAGTGTCTGGTG	239
OY	527	CCTCCGCGATCCGCGCTTCAGCGCCAAAGCGCTCCGAGAGCGCGGGTGGCTTCGCGCGTCTGAC	586
Db	300	CCTCCGCGATCCGCGCTTCAGCGCCAAAGCGCTCCGAGAGCGCGGGTGGCTTCGCGCGTCTGAC	359
OY	587	GCACCCCTTGCCCTTGACCGCGCTGCTGTGTGTGAACAGAGAGAGGACATTACAGACGCGCTCAC	646
Db	360	GCACCCCTTGCCCTTGACCGCGCTGCTGTGTGTGAACAGAGAGGACATTACAGACGCGCTCAC	419
OY	647	GGCAAGTTCACCTGCGAGGTGCTGGGGCTCTACTGATGGCCGCTCATCGACCGCTCTAC	706
Db	420	GGCAAGTTCACCTGCGAGGTGCTGGGGCTCTACTGATGGCCGCTCATCGACCGCTCTAC	479
OY	707	CGGGCGACCTGACAGTTTGATCTGGTGAAGAAATGGCGAATCCATTGCGCTTTCTTCTCAG	766
Db	480	CGGGCGACCTGACAGTTTGATCTGGTGAAGAAATGGCGAATCCATTGCGCTTTCTTCTCAG	539
OY	767	TTTTTTCGGGGGGGTGGCCCCAAGCCACCTGCTGCTCGGGGGGGCCATGTTGAAGCTGGAG	826
Db	540	TTTTTTCGGGGGGGTGGCCCCAAGCCACCTGCTGCTCGGGGGGGCCATGTTGAAGGCTGGAG	599
OY	827	CCTGAGGACCAAGTGTGGGTGCAAGGTGGGTGTGGGTGATCTACATTGGCATTCATGTGCAC	886
Db	600	CCTGAGGACCAAGTGTGGGTGCAAGGTGGGTGTGGGTGATCTACATTGGCATTCATGTGCAC	659
OY	887	ATCAAGACAGACAGCACCTTCTCCGAGATTTCTGATCTACATCCGATCGCAGACAGCTCCCA	946
Db	660	ATCAAGACAGACAGCACCTTCTCCGAGATTTCTGATCTACATCCGATCGCAGACAGCTCCCA	719
OY	947	GTCCTTGGCT 955	
Db	720	GTCCTTGGCT 728	

RESULT 4  
US-09-336-536-8  
; Sequence 8, Application US/09336536

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? TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
? FILE REFERENCE: 7853-144
? CURRENT APPLICATION NUMBER: US/09/336,536
? CURRENT FILING DATE: 1999-06-18
? NUMBER OF SEQ ID NOS: 75
? SOFTWARE: Patentin Ver. 2.0
? SEQ ID NO 8
? LENGTH: 1263
? TYPE: DNA
? ORGANISM: Mus musculus
? US-09-336536-8

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Query Match	50.3%	Score 692.8;	DB 4;	Length 1263;
Best Local Similarity	78.0%;	Pred. No. 1.1e-130;		
Matches 917; Conservative	0;	Mismatches 237;	Indels 22;	Gaps 6;

QY 189 GAGAGGACCCCGGCGCGCGGCTCCCGGGGCGAGCGCTATGAGCGCACTCTGCTCTGC 24.8  
 Db 97 GAGAGGTTCTGGAGCTGATGCGCTCGGGGGTACCAACATAGAGCGACATCTTCTCCCTTC 156  
 QY 249 TGCCTCTGGGCGCTGGCGCGCGGCTGCCCCCACTGGAGCAAGCAAGATGCCAGCTCT 308  
 Db 157 TCGTCTGGGCTGGGAGTCAAGCGCTCTCCCTCTGTGAGCAAGCAAGATCCCCAGCTGT 216

QY 309 GCGGCGGCGACCCGCGCTTCCAGGACGCGGCGCATGTGAGCCAGGCGTTGCCG 368  
Db 217 GTCCCGGCGACCGCGCTTCCAGGACGCGGCGCATGTGAGCCAGGCGTTGCCG 276  
QY 369 GCGGCGATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 428  
Db 277 GCGGCGATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 336  
QY 429 GCGGCGATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 488  
Db 337 GCGGCGATGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 396  
QY 489 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 548  
Db 397 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 456  
QY 549 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 608  
Db 457 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 516  
QY 609 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 668  
Db 517 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 576  
QY 669 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 728  
Db 577 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 636  
QY 729 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 788  
Db 637 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 696  
QY 789 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 848  
Db 697 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 756  
QY 849 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 908  
Db 757 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 816  
QY 909 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 968  
Db 817 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 876  
QY 969 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1028  
Db 877 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 936  
QY 1029 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1088  
Db 937 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 995  
QY 1089 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1148  
Db 996 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1049  
QY 1149 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1208  
Db 1050 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1108  
QY 1209 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1265  
Db 1109 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1157  
QY 1266 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1325  
Db 1158 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1217  
QY 1326 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1361  
Db 1218 GCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1253

RESULT 5  
US-09-188-930-218  
Sequence 218. Application US/09188930A  
Patent No. 6150502  
GENERAL INFORMATION:  
APPLICANT: Watson, James D.  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Onrust, Rene  
APPLICANT: Muriel, James Greg  
TITLE OF INVENTION: Compositions Isolated From Skin Cells  
FILE REFERENCE: 11000.1011C1  
CURRENT APPLICATION NUMBER: US/09/188.930A  
CURRENT FILING DATE: 1998-11-09  
NUMBER OF SEQ ID NOS: 348  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 218  
LENGTH: 1001  
TYPE: DNA  
ORGANISM: Rat  
US-09-188-930-218

Query Match 44.0% Score 606; DB 3; Length 1001;  
Best Local Similarity 78.6% Pred. No. 2.7e-113;  
Matches 739; Conservative 0; Mismatches 195; Indels 6; Gaps 1;

QY 66 TGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 125  
Db 31 TGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 90  
QY 126 TGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 185  
Db 91 TGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 150  
QY 186 TG-----CGAGAGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 239  
Db 151 AGACTACAGAGAGAGATCTGGCGTCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 210  
QY 240 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 299  
Db 211 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 270  
QY 300 CGAGCGTCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 359  
Db 271 CGAGCGTCTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 330  
QY 360 GCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 419  
Db 331 GCTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 390  
QY 420 AAGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 479  
Db 391 AAGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 450  
QY 480 AAGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 539  
Db 451 AAGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 510  
QY 540 CTTTACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 599  
Db 511 CTTTACGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 570  
QY 600 TCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 659  
Db 571 TCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 630  
QY 660 GCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 719  
Db 631 GCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 690  
QY 720 AGTTGATCTGCTGAGAGATGGGCGATTCATTCGCTCTTCTTCCAGTTTTCGGGGGGT 779











; Sequence 9, Application US/09140804  
; Patent No. 6197930  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Humes, Jacqueline M.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
; FILE REFERENCE: 97-49  
; CURRENT APPLICATION NUMBER: US/09/140,804  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: 60/056,983  
; EARLIER FILING DATE: 1997-08-26  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 4517  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-140-804-9

Query Match 6.0%; Score 82.2; DB 4; Length 4517;  
Best Local Similarity 50.1%; Pred. No. 4.4e-08;  
Matches 316; Conservative 0; Mismatches 303; Indels 12; Gaps 4;

QY 331 CCGGCTTCACGACGCCGGGCGACATGSCAGCCAGGCTTCCGGGCGCGATGGCC 380  
DB 148 CGGGCATCCAGAGGCGATCCGGGCGATTAATGGGGCCCGAGCGGTGATGACAGATGGCA 207  
QY 381 GCGAGCGCGGCGGCG 440  
DB 208 CCGCTGTGTAGAGAGGAGGAGAGAGATCCAGGCTTATTTGCTCTTAAGGAGACATCG 267  
QY 441 GACTCCCGGACCTTCAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500  
DB 268 GTGAACCGGAGTACCGCGGCGTGAAGGTCGCCGAGGCTTCCGGGAATCCAGAGCAGA 327  
QY 501 CCGGCGCTCCGGGAGTGTGCTGCTCCGCGATCCGCTTCAGCGCGCAAGCGCTCCG 560  
DB 338 AAGGAGAACCTGGAAGAGGTGCTTATGATACCGCTCAGCATTCAGTGT---GGGATTGG 384  
QY 561 AGAGCGGGGTGCTCCGCGCTGTGACGACCCCTTCCAGCGCGCGCGCGCGCGCGCGCG 620  
DB 385 AGACTTACGTACTATTC---CCAACTATGCGCCCTTCCAGAGATCTTCTACAAATC 441  
QY 621 AGCAGGACATTAACGACCGCTCAGCGCAAGTTCACCTGCGAGGTGCTGGGCTTACT 680  
DB 442 AGCAAAACCATATGATGGCTCAGCTGTAATTCACCTGCAACATTCCTGGGCTTACT 501  
QY 681 ACTTCGCGCTCCAGCCAGCTGTACCGGGCGAGCGCTGCAGTTGATCTGTGGAAGATG 740  
DB 502 ACTTGGCTACACATCAAGCTCTATGATGAAGATGTGAAGGTGACGCTTCAAGAAAG 561  
QY 741 GCGATCCATTCCTCTTCTTCCAGATTTTTCGGGGGGGGGGCGCAAGCAGCTGCTCT 800  
DB 562 ACAAGGCTATGCTTTCACCTATGATGATACAGAGAAAT---AATGTGACCCAGGCT 618  
QY 801 CGGGGGGGGCGCATGCTGAGGCTGAGCGCTGAGAGCAAGTGTGGGTGAGGTTGG- 859  
DB 619 CCGGCTGTGCTCTGCTGATCTGGAGGTGGGAGCAAGTCTGGCTCCAGGTGTATGGG 678  
QY 860 --GGTACTACATTGGCATCTATGCGACATCAAGACAGACAGCCTTCTCCGATTTTC 917  
DB 679 AAGGAGACGTAATGAGCTATGCTGATATGACAAATGATCCACCTTCAAGGCTTTC 738  
QY 918 TGGTACTCCGACTGGGACAGCTCCCACT 948  
DB 739 TTCTCTACCATGACACCAACTGATCCACACT 769

RESULT 14  
US-09-118-408-23  
; Sequence 23, Application US/09118408A  
; Patent No. 6265544  
; GENERAL INFORMATION:

; APPLICANT: Sheppard, Paul O.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
; FILE REFERENCE: 97-30  
; CURRENT APPLICATION NUMBER: US/09/118,408A  
; CURRENT FILING DATE: 1998-07-17  
; EARLIER APPLICATION NUMBER: 60/053,154  
; EARLIER FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 23  
; LENGTH: 843  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Degenerate nucleotide sequence encoding zs1937  
; NAME/KEY: variation  
; LOCATION: (1)...(843)  
; OTHER INFORMATION: Each N is independently any nucleotide.  
; US-09-118-408-23

Query Match 5.6%; Score 77.4; DB 4; Length 843;  
Best Local Similarity 30.0%; Pred. No. 3e-07;  
Matches 209; Conservative 99; Mismatches 384; Indels 5; Gaps 2;

QY 233 CCACATCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 292  
DB 131 CWSNCCNCNCAGATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 190  
QY 293 AAGATCCCGAGCTTCCCGCGGCGACCCCGGCTTCCAGGACCGCGGCGGCGGCGGCGG 352  
DB 191 ARGATCARGANTNC 250  
QY 353 AGCCAGGCTTCCCGGCGCGCA--TGCGCGGACGCGCGCGAGCGCGCGCGCGCGCGCG 410  
DB 251 AYCNC 310  
QY 411 CCGGAGAGAAAGCGAGGCGGCGGAGCGCGGAGCTCCGCGGACCTGAGGAGACCCCGGCG 470  
DB 311 GNGGAGATYNGNNGNTNCCAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 370  
QY 471 CCGGAGAGAGGCGGAGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 530  
DB 371 ATACNGNCNCNARAGNCNARAGNCNARAGNCNARAGNCNARAGNCNARAGNCNARAG 430  
QY 531 CGCGATCCGCTTCAAGCGCGCAAGCGCTCCGAGAGCGCGGCTCCGCGCTGACGCGAC 590  
DB 431 AYTAYGNCNCNTTWSNGTNGMGAARARCNATGCAWYNAAYCAVYATYACARA 490  
QY 591 CCTTGGCCCTTCAGCCGCGTGTGTGAACGAGAGGACATTAACGACCGCTCACCAGCA 650  
DB 491 CNGTNAHTTAYGAYCNGARTYGTNAAYTTTAAGACAYTTAAYATGTTAYACNGNA 550  
QY 651 AGTTACCGGAGGAGGCTGCGTCTACTACTACTACTACTACTACTACTACTACTACTACT 707  
DB 551 ARTTATATGTATGTATGTCNCNGNTATATTTTWSNTNAAYGTCNAYACNTGGAAYC 610  
QY 708 GGGCGAGCGTGCAGTTGATCTGTGAAGATGCGAATCCATTCCTCTTCTTCCAGT 767  
DB 611 ABAAGARACNTAAYTCAAYATHTATGAARABAGARAGRTGNTATHTYNTTYGNC 670  
QY 768 TTTTGGGGGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 827  
DB 671 ARGINGGAGAYGNNNSNATHTATGCAWWSNCARMSVYTNATGTYNARNTNMGARGARG 730  
QY 828 CTGAGGACCAAGTGTGGGCGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 887  
DB 731 AYCARGTGTGGTNGNTNTNTAAYARAGNGARAGMGAARAYCNAHTTWSNGARGARY 790  
QY 888 TCAAGACAGACAGACCTTCCCGGATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 924  
DB 791 TNGAYACNTATATACNTTWSNGNTAYTTGTGTA 827



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 13:56:00 ; Search time 252 Seconds  
(Without alignments)  
8018.441 Million cell updates/sec

Title: US-09-944-944-41

Perfect score: 1377

Sequence: 1 gactagtctctcttgaggtct.....aaaaaaaaaaaaaaaaaa 1377

Scoring table:

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Gapop 60.0 , Gapext 60.0

Searched: 1042519 seqs, 733713590 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

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14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1377	100.0	1377	9	US-09-944-413-41
2	1377	100.0	1377	9	US-09-944-403-41
3	1377	100.0	1377	9	US-09-944-896-41
4	1377	100.0	1377	9	US-09-944-884-41
5	1377	100.0	1377	9	US-09-944-907-41
6	1377	100.0	1377	9	US-09-944-929-41
7	1377	100.0	1377	9	US-10-028-072-361
8	1377	100.0	1377	9	US-10-121-049-361
9	1377	100.0	1377	9	US-10-123-904-361
10	1377	100.0	1377	9	US-10-140-470-361
11	1377	100.0	1377	9	US-10-176-746-361
12	1377	100.0	1377	9	US-10-176-918-361
13	1377	100.0	1377	9	US-10-137-865-361
14	1377	100.0	1377	9	US-10-140-474-361
15	1377	100.0	1377	9	US-10-142-431-361
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17	1377	100.0	1377	9	US-10-140-002-361
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20	1377	100.0	1377	9	US-10-123-262-361	Sequence 361, App
21	1377	100.0	1377	9	US-10-142-423-361	Sequence 361, App
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23	1377	100.0	1377	9	US-10-141-755-361	Sequence 361, App
24	1377	100.0	1377	9	US-10-143-032-361	Sequence 361, App
25	1377	100.0	1377	9	US-10-123-108-361	Sequence 361, App
26	1377	100.0	1377	9	US-10-123-236-361	Sequence 361, App
27	1377	100.0	1377	9	US-10-123-261-361	Sequence 361, App
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29	1377	100.0	1377	9	US-10-140-928-361	Sequence 361, App
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35	1377	100.0	1377	9	US-10-140-925-361	Sequence 361, App
36	1377	100.0	1377	9	US-10-160-498-361	Sequence 361, App
37	1377	100.0	1377	9	US-09-944-884-41	Sequence 41, App
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43	1377	100.0	1377	9	US-10-123-908-361	Sequence 361, App
44	1377	100.0	1377	9	US-10-123-909-361	Sequence 361, App
45	1377	100.0	1377	9	US-10-123-910-361	Sequence 361, App

#### ALIGNMENTS

RESULT 1  
US-09-944-413-41  
Sequence 41, Application US/09944413  
Patent No. US20020156004A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Batstein, David  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerlitsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Hillan, Kenneth  
APPLICANT: Kijavlin, Ivar  
APPLICANT: Napier, Mary  
APPLICANT: Roy, Margaret  
APPLICANT: Tomas, Daniel  
APPLICANT: Wood, William  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P2548P1C1  
CURRENT APPLICATION NUMBER: US/09/944, 413  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 09/866, 028  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/067, 411  
PRIOR FILING DATE: December 3, 1997  
PRIOR APPLICATION NUMBER: 60/069, 334  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069, 335  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069, 278  
PRIOR FILING DATE: December 11, 1997  
PRIOR APPLICATION NUMBER: 60/069, 425  
PRIOR FILING DATE: December 12, 1997  
PRIOR APPLICATION NUMBER: 60/069, 696  
PRIOR FILING DATE: December 16, 1997  
PRIOR APPLICATION NUMBER: 60/069, 694  
PRIOR FILING DATE: December 16, 1997

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1 PRIOR APPLICATION NUMBER: 60/069,702
2 PRIOR FILING DATE: December 16, 1997
3 PRIOR APPLICATION NUMBER: 60/069,870
4 PRIOR FILING DATE: December 17, 1997
5 PRIOR APPLICATION NUMBER: 60/069,873
6 PRIOR FILING DATE: December 17, 1997
7 PRIOR APPLICATION NUMBER: 60/068,017
8 PRIOR FILING DATE: December 18, 1997
9 PRIOR APPLICATION NUMBER: 60/070,440
10 PRIOR FILING DATE: January 5, 1998
11 PRIOR APPLICATION NUMBER: 60/074,086
12 PRIOR FILING DATE: February 9, 1998
13 PRIOR APPLICATION NUMBER: 60/074,092
14 PRIOR FILING DATE: February 9, 1998
15 PRIOR APPLICATION NUMBER: 60/075,945
16 PRIOR FILING DATE: February 25, 1998
17 PRIOR APPLICATION NUMBER: 60/112,850
18 PRIOR FILING DATE: December 16, 1998
19 PRIOR APPLICATION NUMBER: 60/113,296
20 PRIOR FILING DATE: December 22, 1998
21 PRIOR APPLICATION NUMBER: 60/146,222
22 PRIOR FILING DATE: July 28, 1999
23 PRIOR APPLICATION NUMBER: PCT/US98/19330
24 PRIOR FILING DATE: September 16, 1998
25 PRIOR APPLICATION NUMBER: PCT/US98/25108
26 PRIOR FILING DATE: December 1, 1998
27 PRIOR APPLICATION NUMBER: 09/216,021
28 PRIOR FILING DATE: December 16, 1998
29 PRIOR APPLICATION NUMBER: 09/218,517
30 PRIOR FILING DATE: December 22, 1998
31 PRIOR APPLICATION NUMBER: 09/254,311
32 PRIOR FILING DATE: March 3, 1999
33 PRIOR APPLICATION NUMBER: PCT/US99/12252
34 PRIOR FILING DATE: June 22, 1999
35 PRIOR APPLICATION NUMBER: PCT/US99/21090
36 PRIOR FILING DATE: September 15, 1999
37 PRIOR APPLICATION NUMBER: PCT/US99/28409
38 PRIOR FILING DATE: No. US20020136004A1ember 30, 1999
39 PRIOR APPLICATION NUMBER: PCT/US99/28313
40 PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
41 PRIOR APPLICATION NUMBER: PCT/US99/28301
42 PRIOR FILING DATE: December 1, 1999
43 PRIOR APPLICATION NUMBER: PCT/US99/30095
44 PRIOR FILING DATE: December 16, 1999
45 PRIOR APPLICATION NUMBER: PCT/US00/03565
46 PRIOR FILING DATE: February 11, 2000
47 PRIOR APPLICATION NUMBER: PCT/US00/04414
48 PRIOR FILING DATE: February 22, 2000
49 PRIOR APPLICATION NUMBER: PCT/US00/05841
50 PRIOR FILING DATE: March 2, 2000
51 PRIOR APPLICATION NUMBER: PCT/US00/08439
52 PRIOR FILING DATE: March 30, 2000
53 PRIOR APPLICATION NUMBER: PCT/US00/14042
54 PRIOR FILING DATE: May 22, 2000
55 PRIOR APPLICATION NUMBER: PCT/US00/20710
56 PRIOR FILING DATE: July 28, 2000
57 PRIOR APPLICATION NUMBER: PCT/US00/32678
58 PRIOR FILING DATE: December 1, 2000
59 PRIOR APPLICATION NUMBER: PCT/US01/06520
60 PRIOR FILING DATE: February 28, 2001
61 NUMBER OF SEQ ID NOS: 120
62 SEQ ID NO 41
63 LENGTH: 1377
64 TYPE: DNA
65 ORGANISM: Homo Sapien
66 US-09-944-413-41

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Db	1	GACTAGTTCTCTTGGAGTCTGGAGAGAGAAAGCCGAGACCCCGCAGGACGCAACCAAGAC	60
Qy	61	TGGGTGACGCGCAGAGGAGGGGGCCCTGCGCCGGGAGAGCGCGGGGGCTGGACACCA	120
Db	61	TGGGTGACGCGCAGAGGAGGGGGCCCTGCGCCGGGAGAGCGCGGGGGCTGGACACCA	120
Qy	121	CCAACTGGAGGGTCCGGAGTACGAGAGCGCCCGCAAGAGAGCCATGGGGAGCGCGGAGG	180
Db	121	CCAACTGGAGGGTCCGGAGTACGAGAGCGCCCGCAAGAGAGCCATGGGGAGCGCGGAGG	180
Qy	181	GGAGCTGCGAGAGAGACCCCGCGCTCCGGGCTCCGGGTGCGACGGCTATGAGGCACTCT	240
Db	181	GGAGCTGCGAGAGAGACCCCGCGCTCCGGGCTCCGGGTGCGACGGCTATGAGGCACTCT	240
Qy	241	GTCCTGCTGCTCGTGGGGCTGGGGGGCGGCTCGGCCACTGAGAGCAACAATATCC	300
Db	241	GTCCTGCTGCTCGTGGGGCTGGGGGGCGGCTCGGCCACTGAGAGCAACAATATCC	300
Qy	301	CAGCCTTGCCCGGGGCAACCCCGGCTTCCAGGCAAGCGCGGGCCACATGCGACGACAGG	360
Db	301	CAGCCTTGCCCGGGGCAACCCCGGCTTCCAGGCAAGCGCGGGCCACATGCGACGACAGG	360
Qy	361	CTTGGCCGGCCCGCATTGGCCCGGAGCGCCGCGACGGCGCGCCGGGGGCTCCGGGAGAGA	420
Db	361	CTTGGCCGGCCCGCATTGGCCCGGAGCGCCGCGACGGCGCGCCGGGGGCTCCGGGAGAGA	420
Qy	421	AGCGAGAGGGGAGGAGCGGGGACTCCGGGACTCGAGGGAGCCCGGGGCGCGAGAGA	480
Db	421	AGCGAGAGGGGAGGAGCGGGGACTCCGGGACTCGAGGGAGCCCGGGGCGCGAGAGA	480
Qy	481	GGCGGGACCCCGCGGGGCCACCGGGGCTGCGGGGAGTCTCGGTGCTCGGATCCG	540
Db	481	GGCGGGACCCCGCGGGGCCACCGGGGCTGCGGGGAGTCTCGGTGCTCGGATCCG	540
Qy	541	CTTCAGGCGCAAGGCTCCGAGAGCGGGGTGGCTCGCGCTGAGCGACCTTACCCCT	600
Db	541	CTTCAGGCGCGAGGCTCCGAGAGCGGGGTGGCTCGCGCTGAGCGACCTTACCCCT	600
Qy	601	CGACCGCTGCTGTGAACGAGCAGAGGACATTCAGACCCCGCAGCAAGTTCACTG	660
Db	601	CGACCGCTGCTGTGAACGAGCAGAGGACATTCAGACCCCGCAGCAAGTTCACTG	660
Qy	661	CGAGGTGCTGGGGTCTACTACTTCCGCTGCATGCGACCGCTACCGGGGAGCTGCA	720
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Qy	781	GCCCAAGCAACCTCGCTCGGGGGGGGCCATGCTGAGGCTGAGAGCTTGAGAGCAAGT	840
Db	781	GCCCAAGCAACCTCGCTCGGGGGGGGCCATGCTGAGGCTGAGAGCTTGAGAGCAAGT	840
Qy	841	GTGGGTGAGGTGGGTGTGGGTGACTACATTGGCATTTGTCATCCAGCATCAAGACAGAG	900
Db	841	GTGGGTGAGGTGGGTGTGGGTGACTACATTGGCATTTGTCATCCAGCATCAAGACAGAG	900
Qy	901	CACCTTCCGGATTTCTGTGTACTCCGACTGGCAGCAGTCCCAAGTCTTGTCTTAGTG	960
Db	901	CACCTTCCGGATTTCTGTGTACTCCGACTGGCAGCAGTCCCAAGTCTTGTCTTAGTG	960
Qy	961	CCCACTGCAAGGTGAGTCATGCTCACTCCCTGAAAGAGAGGGGTGAGGCTGACAACCA	1020
Db	961	CCCACTGCAAGGTGAGTCATGCTCACTCCCTGAAAGAGAGGGGTGAGGCTGACAACCA	1020
Qy	1021	GGTCATCCAGAGGGCTGCGCCCTCGGAATATTGTGAATGACTAGGAGGCTGGGTAGA	1080
Db	1021	GGTCATCCAGAGGGCTGCGCCCTCGGAATATTGTGAATGACTAGGAGGCTGGGTAGA	1080
Qy	1081	GCACTTCCGCTGCTGCTGTGGCAAGAAATGGGAACAATGGCTGTCTGCGCATCAGGCTG	1140
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OY      1141  GCACATGGGGGCACTGGCTGGATTCTTCCGCAAGACCAAGAGAGTGTGCTGGCCAA 1200
Db      1141  GCACATGGGGGCACTGGCTGGATTCTTCCGCAAGACCAAGAGATGTGCTGGCCAA 1200
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OY      1261  CTGCTGTTCTCTGGATCTCTGCCACGCCCTCTCTCTCTGGGGCGCGCCCTTTTCTAGA 1320
Db      1261  CTGCTGTTCTCTGGATCTCTGCCACGCCCTCTCTCTCTGGGGCGCGCCCTTTTCTAGA 1320
OY      1321  GATTCACATCAATAAACCTACAGACCCCTATATAAAAAAAAAAAAAAAAAAAAAA 1377
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RESULT 2
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: Sequence 41, Application US/09944403
: Patent No. US20020165143A1
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: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gertlisen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavlin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
:
: TITLE OR INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE OR INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P2548PICI
:
: CURRENT APPLICATION NUMBER: US/09/944,403
: CURRENT FILING DATE: 2001-09-26
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: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
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: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
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: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
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: PRIOR APPLICATION NUMBER: 60/069,335
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: PRIOR FILING DATE: December 12, 1997
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: PRIOR FILING DATE: December 16, 1997
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: PRIOR FILING DATE: December 16, 1997
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: PRIOR FILING DATE: December 17, 1997
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: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
:
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
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: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
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: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
:
: PRIOR APPLICATION NUMBER: 60/074,092

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: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,830
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
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: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090
: PRIOR FILING DATE: September 15, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28409
: PRIOR FILING DATE: No. US20020165143A1emder 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28313
: PRIOR FILING DATE: No. US20020165143A1emder 30, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/28301
: PRIOR FILING DATE: December1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 41
: LENGTH: 1377
: TYPE: DNA
: ORGANISM: Homo Saplen
US-09-944-403-41

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Best Local Similarity 100.0%; Prid. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 GACTAGTCTCTTGAGAGTCTGGGAGAGGAAGAAGCGGAGCCGCGACAGGAGCGAACCAAGAC 60

QY      61 TGGGGTACGCGCAGGCGAGGGGGGGCCCTTGCGCCGGGGAGAAACCGGGGGCTGGAGCACCA 120
DB      61 TGGGGTACGCGCAGGCGAGGGGGGGCCCTTGCGCCGGGGAGAAACCGGGGGCTGGAGCACCA 120

QY      121 CCAACTGAGAGGCTCCGAGTAGCGAGCGCCCGGAAGAGAGGCATTCGGGGAGCCGGGAGGG 180
DB      121 CCAACTGAGAGGCTCCGAGTAGCGAGCGCCCGGAAGAGAGGCATTCGGGGAGCCGGGAGGG 180

QY      181 GGAAGTCGAGAGAGACCCCGGCGTCCGGGCTCCAGCGCTATAGGCCACTCT 240
DB      181 GGAAGTCGAGAGAGACCCCGGCGTCCGGGCTCCAGCGCTATAGGCCACTCT 240

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OY	241	CGTCTGTCGCTCCCTGGGCGCTGGGCGCGGCTCGGCCCACTGAGCAACAAATATCC	300
Db	241	CGTCTGTCGCTCCCTGGGCGCTGGGCGCGGCTCGGCCCACTGAGCAACAAATATCC	300
OY	301	CAGCCTCCTGCCCCGGGCAACCCCGGCTTTCAGAGCAAGCCGGGCAACATGAGCAAGG	360
Db	301	CAGCCTCCTGCCCCGGGCAACCCCGGCTTTCAGAGCAAGCCGGGCAACATGAGCAAGG	360
OY	361	CTTGGCGGGGGCCCGGATGAGCCCGGAGAGGCGCGAGCCGCCCGGGGGCTCCGGGAGAGA	420
Db	361	CTTGGCGGGGGCCCGGATGAGCCCGGAGAGGCGCGAGCCGCCCGGGGGCTCCGGGAGAGA	420
OY	421	AGGCGAGAGGGCGGAGAGCCGGGAGCTCCGGGACCTTGAGAGGAGACCCCGGGCGCGAGAGAG	480
Db	421	AGGCGAGAGGGCGGAGAGCCGGGAGCTCCGGGAGCTCCGGGAGAGGAGAGGAGAGAG	480
OY	481	GGCGGGAGACCCCGGGGGCCCAACCGGGCTCCGGGGGAGTGTCTGGTGTCTCCGATCCCG	540
Db	481	GGCGGGAGACCCCGGGGGCCCAACCGGGCTCCGGGGGAGTGTCTGGTGTCTCCGATCCCG	540
OY	541	CTTCAGCGCCAAAGCCTCTCGAGAGCGGGGTGCTCGCGCTGTGACGCAACCTTCCTCT	600
Db	541	CTTCAGCGCCAAAGCCTCTCGAGAGCGGGGTGCTCGCGCTGTGACGCAACCTTCCTCT	600
OY	601	CGACCGGCTGCTGGTGAACAGACAGAGCAATTAGAGCGCGCTACCGGCAAGTTCACCTG	660
Db	601	CGACCGGCTGCTGGTGAACAGACAGAGCAATTAGAGCGCGCTACCGGCAAGTTCACCTG	660
OY	661	CCAGGTGCTGGGGGTCTACTACTTGGCGCTGCATCCAGCCGCTACCGGGGAGCTGTCA	720
Db	661	CCAGGTGCTGGGGGTCTACTACTTGGCGCTGCATCCAGCCGCTACCGGGGAGCTGTCA	720
OY	721	GTTTGATCTGTGTGAAGATGGCGAATGCCATTTGCCCTTTCTTCCAGTTTTCGGGGGGTG	780
Db	721	GTTTGATCTGTGTGAAGATGGCGAATGCCATTTGCCCTTTCTTCCAGTTTTCGGGGGGTG	780
OY	781	GCCCAAGCGCAACCTCGCTCGGGGGGGGGCCATGCTAGAGGCTGAGAGCCTGAGAGCAAGT	840
Db	781	GCCCAAGCGCAACCTCGCTCGGGGGGGGGCCATGCTAGAGGCTGAGAGCCTGAGAGCAAGT	840
OY	841	GTGGGTGAGGTGGGTGTGGGTGATACATTGGCATTTGATGCGACATCAAGACAGACAG	900
Db	841	GTGGGTGAGGTGGGTGTGGGTGATACATTGGCATTTGATGCGACATCAAGACAGACAG	900
OY	901	CACCTTCTCCGGATTTTCTGTGTACTCCGACTGGGCAKAGCTCCCAAGTCTTTGCTTAAGTG	960
Db	901	CACCTTCTCCGGATTTTCTGTGTACTCCGACTGGGCAKAGCTCCCAAGTCTTTGCTTAAGTG	960
OY	961	CCCACTGCAAAAGTGAAGTCAATGCTCTCACTCTTAGAAGAGAGGTGTAGAGGCTGACAACCA	1020
Db	961	CCCACTGCAAAAGTGAAGTCAATGCTCTCACTCTTAGAAGAGAGGTGTAGAGGCTGACAACCA	1020
OY	1021	GGTCATCCAGAGAGGGCTGGCCCCCTGGGAATTTGTGAATACATAGAGGAGGTGGGGTAGA	1080
Db	1021	GGTCATCCAGAGAGGGCTGGCCCCCTGGGAATTTGTGAATACATAGAGGAGGTGGGGTAGA	1080
OY	1081	GCACCTCCGTCCTGTGCTGTGGCAAGAAATGGGAAATAGTGGCTGTCTCCGATCCAGAGTGTG	1140
Db	1081	GCACCTCCGTCCTGTGCTGTGGCAAGAAATGGGAAATAGTGGCTGTCTCCGATCCAGAGTGTG	1140
OY	1141	GCAGCATGGGCGAGTGGCTGGATTTTCTGCCAAGACAGAGAGAGTGTCTGTGCGCA	1200
Db	1141	GCAGCATGGGCGAGTGGCTGGATTTTCTGCCAAGACAGAGAGAGTGTCTGTGCGCA	1200
OY	1201	GTGTAAAGTCCCAAGTTGTCTGTGTCCAGAGACCCAGGTGGGGGTCTCTTCTCTGGTTC	1260
Db	1201	GTGTAAAGTCCCAAGTTGTCTGTGTCCAGAGACCCAGGTGGGGGTCTCTTCTCTGGTTC	1260
OY	1261	CTTGCGTTCTGTGATCTCTCCCAACCCCTCTGTCTCTGGGGCGGCGCTTTTCTTCAGA	1320
Db	1261	CTTGCGTTCTGTGATCTCTCCCAACCCCTCTGTCTCTGGGGCGGCGCTTTTCTTCAGA	1320

Oy 1321 GATACGCAATAAACCTAAGAACCCCTCTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1377  
 Db 1321 GATACGCAATAAACCTAAGAACCCCTCTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1377  
 RESULT 3  
 US-09-944-896-41  
 Sequence 41, Application US/09944896  
 Patent No. US20020168715A1  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin  
 APPLICANT: Botstein, David  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Gerritsen, Mary  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul  
 APPLICANT: Grimaldi, Christopher  
 APPLICANT: Gurney, Austlin  
 APPLICANT: Hillan, Kenneth  
 APPLICANT: Kljavin, Ivar  
 APPLICANT: Napier, Mary  
 APPLICANT: Roy, Margaret  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Wood, William  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 FILE REFERENCE: P2548P1C1  
 CURRENT APPLICATION NUMBER: US/09/944,896  
 CURRENT FILING DATE: 2001-08-31  
 PRIOR APPLICATION NUMBER: 09/866,028  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: 60/069,334  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,335  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,278  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,425  
 PRIOR FILING DATE: December 12, 1997  
 PRIOR APPLICATION NUMBER: 60/069,696  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,684  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,702  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,870  
 PRIOR FILING DATE: December 17, 1997  
 PRIOR APPLICATION NUMBER: 60/069,873  
 PRIOR FILING DATE: December 17, 1997  
 PRIOR APPLICATION NUMBER: 60/068,017  
 PRIOR FILING DATE: December 18, 1997  
 PRIOR APPLICATION NUMBER: 60/070,440  
 PRIOR FILING DATE: January 5, 1998  
 PRIOR APPLICATION NUMBER: 60/074,086  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/074,092  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/075,945  
 PRIOR FILING DATE: February 25, 1998  
 PRIOR APPLICATION NUMBER: 60/112,850  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: 60/113,286  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 60/146,222  
 PRIOR FILING DATE: July 28, 1999  
 PRIOR APPLICATION NUMBER: PCT/US98/19330  
 PRIOR FILING DATE: September 16, 1998  
 PRIOR APPLICATION NUMBER: PCT/US98/225108  
 PRIOR FILING DATE: December 1, 1996  
 PRIOR APPLICATION NUMBER: 09/216,021  
 PRIOR FILING DATE: December 16, 1998



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; PRIOR APPLICATION NUMBER: 09/218,517
; PRIOR FILING DATE: December 22, 1998
; PRIOR APPLICATION NUMBER: 09/254,311
; PRIOR FILING DATE: March 3, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: June 22, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020168715A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 11, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 41
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-896-41

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Query Match      100.0%  Score 1377:  DB 9:  Length 1377:
Best Local Similarity 100.0%:  Pred. No. 0;
Matches 1377:  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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QY 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGAGCCGGCAGAGGAGCAACAGAGAC 60
DB 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGAGCCGGCAGAGGAGCAACAGAGAC 60
QY 61 TGGGTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
DB 61 TGGGTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY 121 CCAACTGGAGGAGTCCGGAGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
DB 121 CCAACTGGAGGAGTCCGGAGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 181 GGGAGTGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
DB 181 GGGAGTGGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 241 GCTGCTGCTGCTCTGGAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 241 GCTGCTGCTGCTCTGGAGCTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 301 CAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
DB 301 CAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360
QY 361 CTGGCGGGGCGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
DB 361 CTGGCGGGGCGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
QY 421 AGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
DB 421 AGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480

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DB 421 AGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
QY 481 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 481 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY 541 CTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 541 CTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 601 GAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 601 GAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 661 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
DB 661 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
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DB 721 GTTATGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 780
QY 781 GCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
DB 781 GCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
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DB 841 GTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
QY 901 CACCTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
DB 901 CACCTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 960
QY 961 CCCACTGCAAGTGAAGTCAATGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 1020
DB 961 CCCACTGCAAGTGAAGTCAATGCTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 1020
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DB 1021 GGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
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QY 1141 GCAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
DB 1141 GCAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
QY 1201 GTTAAAGTCCCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB 1201 GTTAAAGTCCCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY 1261 CTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
DB 1261 CTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
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DB 1321 GATCACTCAATTAACCTTAAGAACCTCTCACTCACTCACTCACTCACTCACTCACTCACTCA 1377

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RESULT 4
US-09-944-944-41
; Sequence 41, Application US/09944944
; Patent No. US20020173463A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen

```

APPLICANT: Gerritsen, Mary  
 APPLICANT: Goddard, Andrew  
 APPLICANT: Godowski, Paul  
 APPLICANT: Grimaldi, Christopher  
 APPLICANT: Gurney, Austin  
 APPLICANT: Hillan, Kenneth  
 APPLICANT: Kijaviri, Ivar  
 APPLICANT: Napier, Mary  
 APPLICANT: Roy, Margaret  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Wood, William  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 FILE OF INVENTION: ACIDS ENCODING THE SAME  
 FILE REFERENCE: P2548P1C1  
 CURRENT APPLICATION NUMBER: US/09/944,944  
 CURRENT FILING DATE: 2001-09-26  
 PRIOR APPLICATION NUMBER: 09/866,028  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: 60/067,411  
 PRIOR FILING DATE: December 3, 1997  
 PRIOR APPLICATION NUMBER: 60/069,334  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,335  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,278  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,425  
 PRIOR FILING DATE: December 12, 1997  
 PRIOR APPLICATION NUMBER: 60/069,696  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,694  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,702  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,870  
 PRIOR FILING DATE: December 17, 1997  
 PRIOR APPLICATION NUMBER: 60/069,873  
 PRIOR FILING DATE: December 17, 1997  
 PRIOR APPLICATION NUMBER: 60/068,017  
 PRIOR FILING DATE: December 18, 1997  
 PRIOR APPLICATION NUMBER: 60/070,440  
 PRIOR FILING DATE: January 5, 1998  
 PRIOR APPLICATION NUMBER: 60/074,086  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/074,092  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/075,945  
 PRIOR FILING DATE: February 25, 1998  
 PRIOR APPLICATION NUMBER: 60/112,850  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: 60/113,296  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 60/146,222  
 PRIOR FILING DATE: July 28, 1999  
 PRIOR APPLICATION NUMBER: PCT/US98/19330  
 PRIOR FILING DATE: September 16, 1998  
 PRIOR APPLICATION NUMBER: PCT/US98/25108  
 PRIOR FILING DATE: December 1, 1998  
 PRIOR APPLICATION NUMBER: 09/216,021  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: 09/218,517  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 09/224,311  
 PRIOR FILING DATE: March 3, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/12252  
 PRIOR FILING DATE: June 22, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: September 15, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28409  
 PRIOR FILING DATE: No. US20020173463A1member 30, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28313  
 PRIOR FILING DATE: No. US20020173463A1member 30, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28301

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: PRIOR FILING DATE: December1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 41
: TYPE: DNA
: LENGTH: 1377
: ORGANISM: Homo Sapien
US-09-944-944-41

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Query Match	100.0%	Score 1377	DB 9	Length 1377	
Best Local Similarity	100.0%	Pred. No. 0			
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				0	Gaps
					0
OY	1	GACTAGTTCCTTGAGACTCTGGGAGAGAGAAAGCCGAGCCGCGACGAGACCGAACCGACGAC	60		
Db	1	GACTAGTTCCTTGAGACTCTGGGAGAGAGAAAGCCGAGCCGCGACGAGACCGAACCGACGAC	60		
OY	61	TGGGTGACGCGAGGGCGAGGGGGCCCTTGCCCGGGGAGAAAGGCGGGGGCTGGACACCA	120		
Db	61	TGGGTGACGCGAGGGCGAGGGGGCCCTTGCCCGGGGAGAAAGGCGGGGGCTGGACACCA	120		
OY	121	CCAACTGAGAGGCTCCGAGTAAGCAGAGCCGCCCGAAAGAGAGCCATCGGGAGCGCGGAGGG	180		
Db	121	CCAACTGAGAGGCTCCGAGTAAGCAGAGCCGCCCGAAAGAGAGCCATCGGGAGCGCGGAGGG	180		
OY	181	GGGAGCTGGGAGAGAGACCCCGGCGTCCGGGGCTCCCGGTCCAGAGCGCTATGAGGGCCACTCT	240		
Db	181	GGGAGCTGGGAGAGAGACCCCGGCGTCCGGGGCTCCCGGTCCAGAGCGCTATGAGGGCCACTCT	240		
OY	241	CGTCCGTGCTGCTCCTGAGGGCTTGCGCGCGCGGCTCGGCCCCACTGAGCAGCAACAAAGATCCC	300		
Db	241	CGTCCGTGCTGCTCCTGAGGGCTTGCGCGCGCGGCTCGGCCCCACTGAGCAGCAACAAAGATCCC	300		
OY	301	CAGCCTCTGCCCCGGGGGCACCCCGGCTTTCAGAGCACGCGCGGGCCACCAATGGCAGCGAGGG	360		
Db	301	CAGCCTCTGCCCCGGGGGCACCCCGGCTTTCAGAGCACGCGCGGGCCACCAATGGCAGCGAGGG	360		
OY	361	CTTGGCGGGGCGCGATTGCGCGGAGAGGCGCGGAGCGCGCCCGGGGGCTCCGGGAGAGAA	420		
Db	361	CTTGGCGGGGCGCGATTGCGCGGAGAGGCGCGGAGCGCGCGCCCGGGGGCTCCGGGAGAGAA	420		
OY	421	AGGCGAGGGCGGAGGCCGGGAGCTCCGGGACTTCGAGGGGAGACCCCGGGCGCGAGGAGA	480		
Db	421	AGGCGAGGGCGGAGGCCGGGAGCTCCGGGACTTCGAGGGGAGACCCCGGGCGCGAGGAGA	480		
OY	481	GGGCGGAGCCGCGGGGGGCCACCGGGGCGTGGCGGGGAGTGCCTTCGGCGATTCGCG	540		
Db	481	GGGCGGAGCCGCGGGGGGCCACCGGGGCGTGGCGGGGAGTGCCTTCGGCGATTCGCG	540		
OY	541	CTTTCAGGCGCCAAAGCGCTCCGAGAGCGGGGTGCTCTCCGGCTGTGACGACCCCTTGCCCTT	600		
Db	541	CTTTCAGGCGCCAAAGCGCTCCGAGAGCGGGGTGCTCTCCGGCTGTGACGACCCCTTGCCCTT	600		
OY	601	CGACCGCGTGTGTGTAACGAGCAGAGGACATTAGACGCGCTGCACCGGCAAGTTACCTG	660		
Db	601	CGACCGCGTGTGTGTAACGAGCAGGACATTAGACGCGCTGCACCGGCAAGTTACCTG	660		

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QY 661 CCAGTGGCTGGGGGCTCTACTTCCGCGTCATGCGCACGGTCTACCGGGCCAGCTGCA 720
Db 661 CCAGTGGCTGGGGGCTCTACTTCCGCGTCATGCGCACGGTCTACCGGGCCAGCTGCA 720
QY 721 GTTGTATCTGTGAAGAAATGCGAATCCATTCCTCTTCTTCCAGTTTTCGGGGGGTG 780
Db 721 GTTGTATCTGTGAAGAAATGCGAATCCATTCCTCTTCTTCCAGTTTTCGGGGGGTG 780
QY 781 GCCCAAGCCAGCTTCGCTCTCGGGGGGGGGCCATGATGAGGCTGAGAGCCATCAAGT 840
Db 781 GCCCAAGCCAGCTTCGCTCTCGGGGGGGGGCCATGATGAGGCTGAGAGCCATCAAGT 840
QY 841 GTGGGTGAGAGTGGGTGTGGGTGACTACTATGATGATGATGATGATGATGATGATGAT 900
Db 841 GTGGGTGAGAGTGGGTGTGGGTGACTACTATGATGATGATGATGATGATGATGATGAT 900
QY 901 CACCTTCTCCGGAATTTCTGTGTACTCCGACTGGCAGACGTCGCCAGTCTTGTAGTG 960
Db 901 CACCTTCTCCGGAATTTCTGTGTACTCCGACTGGCAGACGTCGCCAGTCTTGTAGTG 960
QY 961 CCCACTGCAAGTAGTCACTGCTCTCCTCTAGAAAGAGAGGTGTAGGCTGACCAACA 1020
Db 961 CCCACTGCAAGTAGTCACTGCTCTCCTCTAGAAAGAGAGGTGTAGGCTGACCAACA 1020
QY 1021 GGTCTATCCAGAGAGGAGGCTGGCCCTCGAATATTTGTGAATGACTAGAGAGTGGAGT 1080
Db 1021 GGTCTATCCAGAGAGGAGGCTGGCCCTCGAATATTTGTGAATGACTAGAGAGTGGAGT 1080
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Db 1081 GCATCTCTCCGCTCTGTCTGTCTGCAAGAAATGGAACAGTGTCTGTCTGCAATGAGT 1140
QY 1141 GCACATGAGGAGGAGGCTGTGATTTCTGCTCCCAAGACAGAGAGTGTGTGTGTGTGT 1200
Db 1141 GCACATGAGGAGGAGGCTGTGATTTCTGCTCCCAAGACAGAGAGTGTGTGTGTGTGT 1200
QY 1201 GTGTAAGTCCGCCAGATGCTGTGTGTCAGAGAGCCAGAGTGGGTGTCTCTCTGCTG 1260
Db 1201 GTGTAAGTCCGCCAGATGCTGTGTGTCAGAGAGCCAGAGTGGGTGTCTCTCTGCTG 1260
QY 1261 CTCGCTCTCTGTGATCTCTCCCAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Db 1261 CTCGCTCTCTGTGATCTCTCCCAACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
QY 1321 GATCACTCAATTAACCTTAAGAACCTCTATTAATAAAAAAAAAAAAAAAAAAAAAA 1377
Db 1321 GATCACTCAATTAACCTTAAGAACCTCTATTAATAAAAAAAAAAAAAAAAAAAAAA 1377

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RESULT 5
US-09-944-907-41
: Sequence 41, Application US/09944907
: Publication NO. US20020198147A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fliviaroff, Ellen
: APPLICANT: Geffrisen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kijavir, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: ACIDS ENCODING THE SAME

```

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: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944,907
: CURRENT FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 41
: LENGTH: 1377
: TYPE: DNA
: ORGANISM: Homo Sapien
US-09-944-907-41

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Query Match 100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GACTAGTCTCTTGGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
Db 1 GACTAGTCTCTTGGAGTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
QY 61 TGGGTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 61 TGGGTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
QY 121 CCAACTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Db 121 CCAACTGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
QY 181 GGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
Db 181 GGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 GGTCTGTCTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 241 GGTCTGTCTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
QY 301 CAGCTCTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 301 CAGCTCTGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
QY 361 CTTGCGGGGCGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 361 CTTGCGGGGCGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 AGGCGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 421 AGGCGAGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 GCGCGGAGCCGCGGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 481 GCGCGGAGCCGCGGGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 CTTAGCGCCCAAGGCTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 541 CTTAGCGCCCAAGGCTCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
QY 601 CGAGCGGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 601 CGAGCGGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 CCAGTGGCTGGGGGCTCTACTTCCGCGTCATGCGCACGGTCTACCGGGCCAGCTGCA 720
Db 661 CCAGTGGCTGGGGGCTCTACTTCCGCGTCATGCGCACGGTCTACCGGGCCAGCTGCA 720
QY 721 GTTGTATCTGTGAAGAAATGCGAATCCATTCCTCTTCTTCCAGTTTTCGGGGGGTG 780
Db 721 GTTGTATCTGTGAAGAAATGCGAATCCATTCCTCTTCTTCCAGTTTTCGGGGGGTG 780
QY 781 GCCCAAGCCAGCTTCGCTCTCGGGGGGGGGCCATGATGAGGCTGAGAGCCATCAAGT 840
Db 781 GCCCAAGCCAGCTTCGCTCTCGGGGGGGGGCCATGATGAGGCTGAGAGCCATCAAGT 840
QY 841 GTGGGTGAGAGTGGGTGTGGGTGACTACTATGATGATGATGATGATGATGATGATGAT 900

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|||||  
Db 841 GTGGCTCAGATGGCTGGGTGACTACATGGCATATGCCAGCATCAAGACAGACAG 900  
QY 901 CACCTTCCGAGATTTCGGGTGATCTCCGACTGGCAGACAGTCCCGAGCTTTGGTTAGT 960  
Db 901 CACCTTCCGAGATTTCGGGTGATCTCCGACTGGCAGACAGTCCCGAGCTTTGGTTAGT 960  
QY 961 CCCACTGCAAAAGTAGCTCATGCTCTCATCTCTAGAAAGAGAGGTGTAGAGCTGCAACCA 1020  
Db 961 CCCACTGCAAAAGTAGCTCATGCTCTCATCTCTAGAAAGAGAGGTGTAGAGCTGCAACCA 1020  
QY 1021 GGTTCATCCAGAGAGGGGTGGCCCCCTGGAAATATTGTGAATGACTAGGAGGTGGGTAGA 1080  
Db 1021 GGTTCATCCAGAGAGGGGTGGCCCCCTGGAAATATTGTGAATGACTAGGAGGTGGGTAGA 1080  
QY 1081 GCACCTCCGCTCCGTGCTGCTGGCAAGAAATGGAAACAGTGGCTGTGCGATCAGGTCTG 1140  
Db 1081 GCACCTCCGCTCCGTGCTGCTGGCAAGAAATGGAAACAGTGGCTGTGCGATCAGGTCTG 1140  
QY 1141 GCAGCATGGGGGAGTGGCTGGATTTCGCCCAAGACAGAGAGTGTGCTGTGGCAA 1200  
Db 1141 GCAGCATGGGGGAGTGGCTGGATTTCGCCCAAGACAGAGAGTGTGCTGTGGCAA 1200  
QY 1201 GTGTAATCCCCCAGTGTGCTGTGCTGAGAGAGCCAGAGGTGGGTGCTCTCTGCTGTC 1260  
Db 1201 GTGTAATCCCCCAGTGTGCTGTGCTGAGAGAGCCAGAGGTGGGTGCTCTCTGCTGTC 1260  
QY 1261 CTCTGCTTCTGTGATCTCTCCCAACCCCTCTCTGCTGTGGGGCCGCTTTCTAGA 1320  
Db 1261 CTCTGCTTCTGTGATCTCTCCCAACCCCTCTCTGCTGTGGGGCCGCTTTCTAGA 1320  
QY 1321 GATCACTCAATAAACCTAGAACCCCTATATAAAAAAAAAAAAAAAAAAAAAA 1377  
Db 1321 GATCACTCAATAAACCTAGAACCCCTATATAAAAAAAAAAAAAAAAAAAAAA 1377

## RESULT 6

US-09-944-929-41  
; Sequence 41, Application US/09444929  
; Publication No. US20020197612A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Baton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Geriltsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kijavlin, Ivar  
; APPLICANT: Napier, Margaret  
; APPLICANT: Roy, Margaret  
; APPLICANT: Thomas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944, 929  
; PRIOR FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: 09/866, 028  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 41  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-944-929-41

Query Match 100.0%; Score 1377; DB 9; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GACTAGTTCTCTGAGCTGGGAGGAGGAAAGCGGAGCCGGAGGAGCGCAACAGAGAC 60  
Db 1 GACTAGTTCTCTGAGCTGGGAGGAGGAAAGCGGAGCCGGAGGAGCGCAACAGAGAC 60  
QY 61 TGGGGTACGCGCAGGAGGAGGCGGCTGGCCGGGGAGAAAGCGGGGGGCTGAGACCA 120  
Db 61 TGGGGTACGCGCAGGAGGAGGCGGCTGGCCGGGGAGAAAGCGGGGGGCTGAGACCA 120  
QY 121 CCAACTGGAGGATCCGAGATAGCAGAGCGCCCGAAGAGAGCCATCGGGAGCCGGAGGG 180  
Db 121 CCAACTGGAGGATCCGAGATAGCAGAGCGCCCGAAGAGAGCCATCGGGAGCCGGAGGG 180  
QY 181 GGGACTGCGAGAGAGACCCCGGCGCTCCGGGCTCCGGGTGCCAGCGCTATGAGGCGCATCT 240  
Db 181 GGGACTGCGAGAGAGACCCCGGCGCTCCGGGCTCCGGGTGCCAGCGCTATGAGGCGCATCT 240  
QY 241 CGTCTGCTGCTCTGAGGCTGGGCGGCTGGCGGCGGCTCGCCCACTGGAGACAAAGATCCC 300  
Db 241 CGTCTGCTGCTCTGAGGCTGGGCGGCTGGCGGCGGCTCGCCCACTGGAGACAAAGATCCC 300  
QY 301 CAGCTCTGCGCCGGGGGAGACCCCGGCTTCAGAGACCGCGGCGCCACCATGGACAGCGAGG 360  
Db 301 CAGCTCTGCGCCGGGGGAGACCCCGGCTTCAGAGACCGCGGCGCCACCATGGACAGCGAGG 360  
QY 361 CTTCGCGGCGCGCATGAGCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGAGAA 420  
Db 361 CTTCGCGGCGCGCATGAGCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGAGAA 420  
QY 421 AGCGGAGGCGGAGGCGCGGAGCTGCCGGAAGCTCGAGAGGAGACCCCGGCGCGAGAGAA 480  
Db 421 AGCGGAGGCGGAGGCGCGGAGCTGCCGGAAGCTCGAGAGGAGACCCCGGCGCGAGAGAA 480  
QY 481 GCGGCGAGCCCGGGGGGCGACCGGGGCTGCCGGGAGTGTCTGGTGGCTCCGGATCCG 540  
Db 481 GCGGCGAGCCCGGGGGGCGACCGGGGCTGCCGGGAGTGTCTGGTGGCTCCGGATCCG 540  
QY 541 CTTCAGCGCGCAAGGCGCTCCAGAGCCCGGGTCCCGCTCTGACGACCCCTTGCCCTT 600  
Db 541 CTTCAGCGCGCAAGGCGCTCCAGAGCCCGGGTCCCGCTCTGACGACCCCTTGCCCTT 600  
QY 601 CGACCGCGCTCTGCTGTAACGACGAGGACATTTACGACCGCTCACCGGCAAGTTACCTG 660  
Db 601 CGACCGCGCTCTGCTGTAACGACGAGGACATTTACGACCGCTCACCGGCAAGTTACCTG 660  
QY 661 CCAAGTCTGGGGTCTACTACTTGGCGGTCATGCGCACCGGTACCGGGGCGAGCTGCA 720  
Db 661 CCAAGTCTGGGGTCTACTACTTGGCGGTCATGCGCACCGGTACCGGGGCGAGCTGCA 720  
QY 721 GTTGTATCTGGTGAAGATGGCGAATCCATTGCTCTTTCTTCAGTTTTCGGGGGTG 780  
Db 721 GTTGTATCTGGTGAAGATGGCGAATCCATTGCTCTTTCTTCAGTTTTCGGGGGTG 780  
QY 781 GCGCAAGCCAGCTCTGCTGCGGGGGGCGCATGCTGAGCTGAGGCTTAGAGCAAGT 840  
Db 781 GCGCAAGCCAGCTCTGCTGCGGGGGGCGCATGCTGAGCTGAGGCTTAGAGCAAGT 840  
QY 841 GTGGGTCAGAGTGGGTGGGTGACTAATTTGATATGATGATGATGATGATGATGATGATGAT 900  
Db 841 GTGGGTCAGAGTGGGTGGGTGACTAATTTGATATGATGATGATGATGATGATGATGATGAT 900  
QY 901 CACCTTCTCGGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
Db 901 CACCTTCTCGGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
QY 961 CCCACTGCAAAAGTAGCTCATGCTCTCATCTCTAGAAAGAGAGGTGTAGAGCTGCAACCA 1020  
Db 961 CCCACTGCAAAAGTAGCTCATGCTCTCATCTCTAGAAAGAGAGGTGTAGAGCTGCAACCA 1020  
QY 1021 GGTTCATCCAGAGAGGGGTGGCCCCCTGGAAATATTGTGAATGACTAGGAGGTGGGTAGA 1080  
Db 1021 GGTTCATCCAGAGAGGGGTGGCCCCCTGGAAATATTGTGAATGACTAGGAGGTGGGTAGA 1080

QY 1081 GCACTCTCCGCTGCTGCTGCAAGAAATGGAAAGTGGCTGCTGCAATCAGGCTG 1140  
Db 1081 GCACTCTCCGCTGCTGCTGCTGCAAGAAATGGAAAGTGGCTGCTGCAATCAGGCTG 1140  
QY 1141 GCACCAATGGGGGCACTGGCTGATTTCTGCCCAAGACAGAGAGTGTGCTGCTGCA 1200  
Db 1141 GCACCAATGGGGGCACTGGCTGATTTCTGCCCAAGACAGAGAGTGTGCTGCTGCA 1200  
QY 1201 GTGTAATGCCCCGAGTGTGCTGCTGCAAGAGCCAGAGTGGTGTCTCTGCTGCTG 1260  
Db 1201 GTGTAATGCCCCGAGTGTGCTGCTGCAAGAGCCAGAGTGGTGTCTCTGCTGCTG 1260  
QY 1261 CTCTGCTTCTGCTGATCTCCCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
Db 1261 CTCTGCTTCTGCTGATCTCCCAACCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
QY 1321 GATCAGTCATTAACCTAAGAACCCCTCATATAAAAAAAAAAAAAAAAAAAAA 1377  
Db 1321 GATCAGTCATTAACCTAAGAACCCCTCATATAAAAAAAAAAAAAAAAAAAAA 1377

RESULT 7  
US-10-028-072-361  
Sequence 361, Application US/10028072  
Publication No. US20030004311A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Defoige, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tunas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang  
TITLE OF INVENTION:  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/028,072  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059836  
PRIOR FILING DATE: 1997-09-24  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062285

PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062814  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/062816  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063045  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063082  
PRIOR FILING DATE: 1997-10-31  
PRIOR APPLICATION NUMBER: 60/063127  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063327  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063329  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063550  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063561  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063704  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063733  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063735  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063738  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063755  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064248  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/064809  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065846  
PRIOR FILING DATE: 1997-11-17  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/066453  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066511  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/069212  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069278  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069334  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069694  
PRIOR FILING DATE: 1997-12-16  
PRIOR APPLICATION NUMBER: 60/072320  
PRIOR FILING DATE: 1998-01-23  
PRIOR APPLICATION NUMBER: 60/073612  
PRIOR FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: 60/074086  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/074092  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-02-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27

[illegible]

QY 961 CCCACTGCAAAAGTGAAGTCTATGCTCTCACTCTCTAGAGAGAGGGTGTGAGGCTGACACCA 1020  
Db 961 CCCACTGCAAAAGTGAAGTCTATGCTCTCACTCTCTAGAGAGAGGGTGTGAGGCTGACACCA 1020  
QY 1021 GGTCAATCCAGAGAGGGCTGGCCCCCTGGAAATTTGTGAATGACTAGAGAGGTGGGGTGA 1080  
Db 1021 GGTCAATCCAGAGAGGGCTGGCCCCCTGGAAATTTGTGAATGACTAGAGAGGTGGGGTGA 1080  
QY 1081 GCACATCGCTGCTCTGCTGGCAGGAATGGGAACATGGCTGTCTGCTGATGAGTGTG 1140  
Db 1081 GCACATCGCTGCTCTGCTGGCAGGAATGGGAACATGGCTGTCTGCTGATGAGTGTG 1140  
QY 1141 GCAGCATGGGGCAGTGGCTGATTTCTGCCCAAGACAGAGAGTGTGCTGTGCA 1200  
Db 1141 GCAGCATGGGGCAGTGGCTGATTTCTGCCCAAGACAGAGAGTGTGCTGTGCA 1200  
QY 1201 GTGTAAATCCCAATGCTGTGCTGCAAGAGCCACAGGTGGGTGCTCTCTCTGTC 1260  
Db 1201 GTGTAAATCCCAATGCTGTGCTGCAAGAGCCACAGGTGGGTGCTCTCTCTGTC 1260  
QY 1261 CTCTGCTCTGCTGATGCTCCACCCCTCTCTGCTGCTGGGGCCGGCCCTTTCACGA 1320  
Db 1261 CTCTGCTCTGCTGATGCTCCACCCCTCTCTGCTGCTGGGGCCGGCCCTTTCACGA 1320  
QY 1321 GATCACTCAATTAACCTTAAGAACCTCTCATTAATAAAAAAAAAAAAAAAAAAAAA 1377  
Db 1321 GATCACTCAATTAACCTTAAGAACCTCTCATTAATAAAAAAAAAAAAAAAAAAAAA 1377

RESULT 8  
US-10-121-049-361  
; Sequence 361, Application US/10121049  
; Publication No. US2003002239A1

GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvarioff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE OF INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P3330R1C17  
CURRENT FILING DATE: 2002-04-12  
Prior Application removed - See File Wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 361  
LENGTH: 1377  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-121-049-361

Query Match 100.0%; Score 1377; DB 9; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGTCTCTGTGAGTCTGGAGAGAGAAAGCGGAGCGGACAGGAGCGAAGCAGAC 60  
Db 1 GACTAGTCTCTGTGAGTCTGGAGAGAGAAAGCGGAGCGGACAGGAGCGAAGCAGAC 60

QY 61 TGGGGTGAAGGAGGAGGAGGCGCTGAGCCGGGGAGAGAGCGCGGGGCTGAGCACCA 120  
Db 61 TGGGGTGAAGGAGGAGGAGGCGCGCTGAGCCGGGGAGAGAGCGCGGGGCTGAGCACCA 120  
QY 121 CCACTGGAAGGCTCCGGAGTACAGAGCGCCCCGAAGAGAGCCATGCGGAGCGGAGG 180  
Db 121 CCACTGGAAGGCTCCGGAGTACAGAGCGCCCCGAAGAGAGCCATGCGGAGCGGAGG 180  
QY 181 GGGAGTGGAGAGAGAGCCCGGGCTCCGGGGTCCGGGTCCAGCGCTATGAGGCCATCCT 240  
Db 181 GGGAGTGGAGAGAGAGCCCGGGCTCCGGGGTCCGGGTCCAGCGCTATGAGGCCATCCT 240  
QY 241 GGTCTGCTGCTCTGAGGCTTGGCCGGCTGCGCGCCCTCCACATGAGCAGCAACAGATCC 300  
Db 241 GGTCTGCTGCTCTGAGGCTTGGCCGGCTGCGCGCCCTCCACATGAGCAGCAACAGATCC 300  
QY 301 CAGCTCTGCCCCGGGGGACACCCGGCTTTCAGAGCACCGCGGGCCACCATGGCAGCCAGG 360  
Db 301 CAGCTCTGCCCCGGGGGACACCCGGCTTTCAGAGCACCGCGGGCCACCATGGCAGCCAGG 360  
QY 361 CTGGCCGGGGCCGATGGGCGGAGAGGCGGAGGCGGAGGCGGCGGCGGCGGAGAGA 420  
Db 361 CTGGCCGGGGCCGATGGGCGGAGAGGCGGAGGCGGAGGCGGCGGCGGCGGAGAGA 420  
QY 421 AGCGAGGAGCGGAGAGCGCGGACTGCGCGGAGCTTCGAGAGGAGACCCCGGGCCGCGAGAGA 480  
Db 421 AGCGAGGAGCGGAGAGCGCGGACTGCGCGGAGCTTCGAGAGGAGACCCCGGGCCGCGAGAGA 480  
QY 481 GCGGGGAGCCCGGGGGGCCACCGGGCTGCGCGGGAGTGTGCTGCTCCGCGATCCG 540  
Db 481 GCGGGGAGCCCGGGGGGCCACCGGGCTGCGCGGGAGTGTGCTGCTCCGCGATCCG 540  
QY 541 CTTGAGCGCAAGCGCTCCGAGAGCGGGGTGCTCGCGCGTGTGAGCGCAACCCCTTCCCT 600  
Db 541 CTTGAGCGCAAGCGCTCCGAGAGCGGGGTGCTCGCGCGTGTGAGCGCAACCCCTTCCCT 600  
QY 601 CGACCGCGTGTGTGAAGAGAGCAGAGGAGCATTAACAGCCGCTCACCGGCAATTCACCTG 660  
Db 601 CGACCGCGTGTGTGAAGAGAGCAGAGGAGCATTAACAGCCGCTCACCGGCAATTCACCTG 660  
QY 661 CCAGTGTCTGGGGTCTACTACTTTCGCGTCCATCCACCGTCAACCGGGCCAGCTGCA 720  
Db 661 CCAGTGTCTGGGGTCTACTACTTTCGCGTCCATCCACCGTCAACCGGGCCAGCTGCA 720  
QY 721 GTTGTATGCTGGAAGAAATGGGAATTCATGCGCTTCTTCCAGTTTTCGGGGGG 780  
Db 721 GTTGTATGCTGGAAGAAATGGGAATTCATGCGCTTCTTCTTCCAGTTTTCGGGGGG 780  
QY 781 GCCCAAGCAGGCTGCTCTGCGGGGGGCCATGCTGAGAGGCTGAGAGCCAGCAAGT 840  
Db 781 GCCCAAGCAGGCTGCTCTGCGGGGGGCCATGCTGAGAGGCTGAGAGCCAGCAAGT 840  
QY 841 GTGGTGAAGTGGGTGTGAGTACTATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 900  
Db 841 GTGGTGAAGTGGGTGTGAGTACTATGAGCAATGAGCAATGAGCAATGAGCAATGAGCA 900  
QY 901 CACCTTCCGGAATTTGAGTACTCGAGCTGAGAGAGCTCCCAAGCTTTTGTAGTG 960  
Db 901 CACCTTCCGGAATTTGAGTACTCGAGCTGAGAGAGCTCCCAAGCTTTTGTAGTG 960  
QY 961 CCCACTGCAAAAGTGAAGTCTATGCTCTCACTCTCTAGAGAGAGGGTGTGAGGCTGACACCA 1020  
Db 961 CCCACTGCAAAAGTGAAGTCTATGCTCTCACTCTCTAGAGAGAGGGTGTGAGGCTGACACCA 1020  
QY 1021 GGTCAATCCAGAGAGGGCTGGCCCCCTGGAAATTTGTGAATGACTAGAGAGGTGGGGTGA 1080  
Db 1021 GGTCAATCCAGAGAGGGCTGGCCCCCTGGAAATTTGTGAATGACTAGAGAGGTGGGGTGA 1080  
QY 1081 GCACATCGCTGCTCTGCTGGCAGGAATGGGAACATGGCTGTCTGCTGATGAGTGTG 1140  
Db 1081 GCACATCGCTGCTCTGCTGGCAGGAATGGGAACATGGCTGTCTGCTGATGAGTGTG 1140  
QY 1141 GCAGCATGGGGCAGTGGCTGATTTCTGCCCAAGACAGAGAGTGTGCTGTGCA 1200



Db 1141 GCACCAATGAGGAGTGTGCTGATTTCTGCCCCAGACAGAGAGTGTGCTGTGCAAA 1200  
QY 1201 GTGAAGTCCCGCCAGTTGCTGTGTCAGAGAGCCACAGGTGGGTGCTTCTGCTGTC 1260  
Db 1201 GTGAAGTCCCGCCAGTTGCTGTGTCAGAGAGCCACAGGTGGGTGCTTCTGCTGTC 1260  
QY 1261 CTCTGCTTCTGTGATCCCTCCACCCCTCTCTCTCTGAGGCGCCCTTTTCTGAGA 1320  
Db 1261 CTCTGCTTCTGTGATCCCTCCACCCCTCTCTCTCTGAGGCGCCCTTTTCTGAGA 1320  
QY 1321 GATCACTCAATTAACCTTAAGAACCTCTATAAAAAAAAAAAAAAAAAAAAAA 1377  
Db 1321 GATCACTCAATTAACCTTAAGAACCTCTATAAAAAAAAAAAAAAAAAAAAAA 1377

RESULT 9  
US-10-123-904-361  
Sequence 361, Application US/10123904  
Publication No. US20030022328A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey E.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Matanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
TITLE OR INVENTION: ACIDS ENCODING THE SAME  
FILE REFERENCE: P330R1C54  
CURRENT APPLICATION NUMBER: US/10/123,904  
CURRENT FILING DATE: 2002-04-16  
Prior Application removed - See file wrapper or Palm  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 361  
LENGTH: 1377  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-10-123-904-361

Query Match 100.0%; Score 1377; DB 9; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGTCTCTGTGAGTCTGTGGAGAGGAAAGCGGAGCCGCGAGAGAGCGAAACAGAC 60  
Db 1 GACTAGTCTCTGTGAGTCTGTGGAGAGGAAAGCGGAGCCGCGAGAGAGCGAAACAGAC 60  
QY 61 TGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
Db 61 TGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
QY 121 CCAACTGAGAGGTCCGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
Db 121 CCAACTGAGAGGTCCGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 180  
QY 181 GGGAGTGGAG 240  
Db 181 GGGAGTGGAG 240  
QY 241 CGTCTGCTGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
Db 241 CGTCTGCTGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300

Db 241 CGTCTGCTGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300  
QY 301 CAGCCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
Db 301 CAGCCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360  
QY 361 CTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
Db 361 CTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420  
QY 421 AGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
Db 421 AGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
QY 481 GGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
Db 481 GGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
QY 541 CTTCAGGCGCAAGCGCTCCGAGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
Db 541 CTTCAGGCGCAAGCGCTCCGAGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
QY 601 CGAGCCGCTGCTGTGAG 660  
Db 601 CGAGCCGCTGCTGTGAG 660  
QY 661 CCAAGTGTCTGAGGAGTCTACTACTTCCGCTGATGATGATGATGATGATGATGATGAT 720  
Db 661 CCAAGTGTCTGAGGAGTCTACTACTTCCGCTGATGATGATGATGATGATGATGATGAT 720  
QY 721 GTTTGATCTGTGAG 780  
Db 721 GTTTGATCTGTGAG 780  
QY 781 GCCCAAGCGAGCGCTCCGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
Db 781 GCCCAAGCGAGCGCTCCGCTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840  
QY 841 GTGGGTGAGAGTGTGGGTGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 900  
Db 841 GTGGGTGAGAGTGTGGGTGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 900  
QY 901 CACCTTCTCCGAGT 960  
Db 901 CACCTTCTCCGAGT 960  
QY 961 CCCACTGCAAGT 1020  
Db 961 CCCACTGCAAGT 1020  
QY 1021 GGTTCATCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
Db 1021 GGTTCATCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
QY 1081 GCACTCTCCGCTCTGT 1140  
Db 1081 GCACTCTCCGCTCTGT 1140  
QY 1141 GCAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
Db 1141 GCAGCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
QY 1201 GTGTAAGTCCCGCCAGTTGCTGTGTCAGAGAGCCACAGGTGGGTGCTTCTGCTGTC 1260  
Db 1201 GTGTAAGTCCCGCCAGTTGCTGTGTCAGAGAGCCACAGGTGGGTGCTTCTGCTGTC 1260  
QY 1261 CTCTGCTTCTGTGATCCCTCCACCCCTCTCTCTGAGGCGCCCTTTTCTGAGA 1320  
Db 1261 CTCTGCTTCTGTGATCCCTCCACCCCTCTCTCTGAGGCGCCCTTTTCTGAGA 1320  
QY 1321 GATCACTCAATTAACCTTAAGAACCTCTATAAAAAAAAAAAAAAAAAAAAAA 1377  
Db 1321 GATCACTCAATTAACCTTAAGAACCTCTATAAAAAAAAAAAAAAAAAAAAAA 1377



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RESULT 10
US-10-140-470-361
; Sequence 361, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C160
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 361
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-470-361

Query Match      100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGTCTCTGTTGAGTCTGGAGAGAGAAAGCGGACCGCAGAGGAGCGAAGCCAGGAC 60
DB 1 GACTAGTCTCTGTTGAGTCTGGAGAGAGAAAGCGGACCGCAGAGGAGCGAAGCCAGGAC 60
QY 61 TGGGGTACGCGCAGAGGCGAGGGGGCGCTGGCGGGGAGAAAGCGGGGGCTGGAGACACA 120
DB 61 TGGGGTACGCGCAGAGGCGAGGGGGCGCTGGCGGGGAGAAAGCGGGGGCTGGAGACACA 120
QY 121 CCAACTGGAGGTCGCGAGTAGCGAGCGCCCGAAGAGGAGCATCGGGGAGCCGGAGAGG 180
DB 121 CCAACTGGAGGTCGCGAGTAGCGAGCGCCCGAAGAGGAGCATCGGGGAGCCGGAGAGG 180
QY 181 GGAAGTGGAGAGAGACCCCGCGTCCGGGGCTCCCGGTCCAGCGCTATGAGGCCACTCT 240
DB 181 GGAAGTGGAGAGAGACCCCGCGTCCGGGGCTCCCGGTCCAGCGCTATGAGGCCACTCT 240
QY 241 CGTCTGCTGCTCTGCGGCGTGGGGCGGGCGGCTCCCGCACTGAGAGCAACAGATCCC 300
DB 241 CGTCTGCTGCTCTGCGGCGTGGGGCGGGCGGCTCCCGCACTGAGAGCAACAGATCCC 300
QY 301 CAGCCTCTGCGCGGGGACACCCGGCTTCAGAGCAGCGGGGCCACCATGAGCAGCAGG 360
DB 301 CAGCCTCTGCGCGGGGACACCCGGCTTCAGAGCAGCGGGGCCACCATGAGCAGCAGG 360
QY 361 CTTCGCGGGCGCGATGGCGCGAGCGCGGAGCGCGCGCGGGGCTCCGGGAGAGAA 420
DB 361 CTTCGCGGGCGCGATGGCGCGAGCGCGGAGCGCGCGCGGGGCTCCGGGAGAGAA 420
QY 421 AGCGGAGGGCGGAGCGCGGAGCTGCGGGAGCTTCGAGAGGAGACCCCGGGCGCGAGAGA 480
DB 421 AGCGGAGGGCGGAGCGCGGAGCTGCGGGAGCTTCGAGAGGAGACCCCGGGCGCGAGAGA 480
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QY 481 GCGGAGACCCGCGGGGACCCAGCGGGGCTGCGGGGAGAGTCTGGGCTCTCCGCATCCGC 540
DB 481 GCGGAGACCCGCGGGGACCCAGCGGGGCTGCGGGGAGAGTCTGGGCTCTCCGCATCCGC 540
QY 541 CTTCAGCGCCAAAGCGCTCCGAGAGCCGGGTCCTCCGCGCTGAGAGCACCCTTGCCCTT 600
DB 541 CTTCAGCGCCAAAGCGCTCCGAGAGCCGGGTCCTCCGCGCTGAGAGCACCCTTGCCCTT 600
QY 601 CGAGCGCGTCTGCTGGAACGAGCAGGAGCATTTAGACGCGCTCACCGGCAAGTTCACCTG 660
DB 601 CGAGCGCGTCTGCTGGAACGAGCAGGAGCATTTAGACGCGCTCACCGGCAAGTTCACCTG 660
QY 661 CCAGGTGCTGGGGCTCTACTCTTCGCGCTCATGCCACGCTTACCGGGCAGCGCTCA 720
DB 661 CCAGGTGCTGGGGCTCTACTCTTCGCGCTCATGCCACGCTTACCGGGCAGCGCTCA 720
QY 721 GTTTGATCTGTTGAGAAATGCGAATCCATTGCTCTTCTTCAGTTTTCGGGGGTG 780
DB 721 GTTTGATCTGTTGAGAAATGCGAATCCATTGCTCTTCTTCAGTTTTCGGGGGTG 780
QY 781 GCCCAAGCAGACCTCTCTCTGGGGGGGGCCATGTAAGCTGAGAGCCTGAGACCAAGT 840
DB 781 GCCCAAGCAGACCTCTCTCTGGGGGGGGCCATGTAAGCTGAGAGCCTGAGACCAAGT 840
QY 841 GTGGGTGAGGTGGGTGGGTGACTATGATGATGATGATGATGATGATGATGATGATGAT 900
DB 841 GTGGGTGAGGTGGGTGGGTGACTATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 CACCTTCTCCGAAATTTCTGTTGTTACTCGACTGCGACAGCTCCCAAGTCTTTGCTTAGT 960
DB 901 CACCTTCTCCGAAATTTCTGTTGTTACTCGACTGCGACAGCTCCCAAGTCTTTGCTTAGT 960
QY 961 CCCACTGGAAGTAGTCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
DB 961 CCCACTGGAAGTAGTCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
QY 1021 GGTATCTCCAGAGAGGCTGGCGCCCTCGAATATTGTAATGATGATGATGATGATGATGAT 1080
DB 1021 GGTATCTCCAGAGAGGCTGGCGCCCTCGAATATTGTAATGATGATGATGATGATGATGAT 1080
QY 1081 GCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
DB 1081 GCACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
QY 1141 GCAGATGAGGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
DB 1141 GCAGATGAGGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1201 GTGTAAGTCCCGCAGTTGCTCTGTTGTCAGAGCCACAGTGGGTGCTCTCTCTCTCTCT 1260
DB 1201 GTGTAAGTCCCGCAGTTGCTCTGTTGTCAGAGCCACAGTGGGTGCTCTCTCTCTCTCT 1260
QY 1261 CTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
DB 1261 CTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
QY 1321 GATCACTCAATTAACCTTAAGAACCTCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1377
DB 1321 GATCACTCAATTAACCTTAAGAACCTCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1377

RESULT 11
US-10-175-746-361
; Sequence 361, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
```

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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C35
; CURRENT APPLICATION NUMBER: US/10/175,746
; PRIOR APPLICATION DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 361
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-175-746-361

```

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Query Match      100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGAGCCGCGAGGAGCGAACCAGAGAC 60
D 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGAGCCGCGAGGAGCGAACCAGAGAC 60
QY 61 TGGGAGTACGCGAGGAGGAGGCGCTGCGCGGAGAAAGCGGAGGCTGGAGACCA 120
D 61 TGGGAGTACGCGAGGAGGAGGCGCTGCGCGGAGAAAGCGGAGGCTGGAGACCA 120
QY 121 CCAACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
D 121 CCAACTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 180
QY 181 GGGAGTGCAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
D 181 GGGAGTGCAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 241 GGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
D 241 GGTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 301 CAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
D 301 CAGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
QY 361 CTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
D 361 CTTCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
QY 421 AGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
D 421 AGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 481 GGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
D 481 GGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
QY 541 CTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
D 541 CTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY 601 CGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
D 601 CGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
QY 661 CGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
D 661 CGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720

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D 661 CGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
QY 721 GTTGTGATCTGCTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
D 721 GTTGTGATCTGCTGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
QY 781 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
D 781 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
QY 841 GTGGGTCAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
D 841 GTGGGTCAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
QY 901 CACCTTCTCCGAGATTTCTGCTGATCTGCTGATCTGCTGATCTGCTGATCTGCT 960
D 901 CACCTTCTCCGAGATTTCTGCTGATCTGCTGATCTGCTGATCTGCTGATCTGCT 960
QY 961 CCCACTGCAAAAGTAGAGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
D 961 CCCACTGCAAAAGTAGAGCTCATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1020
QY 1021 GGTCTATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
D 1021 GGTCTATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
QY 1081 GCACTCTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
D 1081 GCACTCTCCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1141 GCAAGCATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
D 1141 GCAAGCATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
QY 1201 GTGTAGTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
D 1201 GTGTAGTCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260
QY 1261 CTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
D 1261 CTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
QY 1321 GATCAGTCAATTAACCTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1377
D 1321 GATCAGTCAATTAACCTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1377

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RESULT 12
US-10-176-918-361
; Sequence 361, Application US/10176918
; Publication No. US2003027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerlitsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Thomas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P330R1C382
; CURRENT APPLICATION NUMBER: US/10/176, 918

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; CURRENT FILING DATE: 2002-06-20  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 361  
 ; LENGTH: 1377  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-10-176-918-361

Query Match 100.0%; Score 1377; DB 9; Length 1377;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGGACCGGACCGAGCCAGACAGAC 60  
 DB 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGGACCGGACCGAGCCAGACAGAC 60  
 QY 61 TGGGAGTGGAG 120  
 DB 61 TGGGAGTGGAG 120  
 QY 121 CCAACTGGAG 180  
 DB 121 CCAACTGGAG 180  
 QY 181 GGGAGTGGAG 240  
 DB 181 GGGAGTGGAG 240  
 QY 241 GGTGCTGCTGCTCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
 DB 241 GGTGCTGCTGCTCTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
 QY 301 CAGCTCTGCT 360  
 DB 301 CAGCTCTGCT 360  
 QY 361 CAGCTCTGCT 420  
 DB 361 CAGCTCTGCT 420  
 QY 421 AGGCGAG 480  
 DB 421 AGGCGAG 480  
 QY 481 GGGCGAG 540  
 DB 481 GGGCGAG 540  
 QY 541 CTTGAG 600  
 DB 541 CTTGAG 600  
 QY 601 CGACCGAG 660  
 DB 601 CGACCGAG 660  
 QY 661 CAGAGTGGAG 720  
 DB 661 CAGAGTGGAG 720  
 QY 721 GTTGGATGAG 780  
 DB 721 GTTGGATGAG 780  
 QY 781 GGGCGAG 840  
 DB 781 GGGCGAG 840  
 QY 841 GTGGGTGAG 900  
 DB 841 GTGGGTGAG 900

QY 901 CACCTTCTCCGAGATTTCTGTACTCCGAGTGGACAGCTCCCAAGTCTTGTAGT 960  
 DB 901 CACCTTCTCCGAGATTTCTGTACTCCGAGTGGACAGCTCCCAAGTCTTGTAGT 960  
 QY 961 CCCACTGCAAGTGAAGTCTGATGCTCTCACTCTCTCAAGAGAGAGAGAGAGAGAGAG 1020  
 DB 961 CCCACTGCAAGTGAAGTCTGATGCTCTCACTCTCTCAAGAGAGAGAGAGAGAGAGAG 1020  
 QY 1021 GGTATCCAG 1080  
 DB 1021 GGTATCCAG 1080  
 QY 1081 GCATCTCTCCGCT 1140  
 DB 1081 GCATCTCTCCGCT 1140  
 QY 1141 GCAGCATGGAG 1200  
 DB 1141 GCAGCATGGAG 1200  
 QY 1201 GTGTAACTCCCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 DB 1201 GTGTAACTCCCAAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260  
 QY 1261 CTCTGCT 1320  
 DB 1261 CTCTGCT 1320  
 QY 1321 GATCAGCTCAATTAACCTTAAGAACCTCTCAATTAATTAATTAATTAATTAATTA 1377  
 DB 1321 GATCAGCTCAATTAACCTTAAGAACCTCTCAATTAATTAATTAATTAATTAATTA 1377

RESULT 13  
 US-10-176-921-361  
 ; Sequence 361, Application US/10176921  
 ; Publication No. US20030027276A1

; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumanabe, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3330R1C288  
 ; CURRENT APPLICATION NUMBER: US/10176,921  
 ; CURRENT FILING DATE: 2002-06-20  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 361  
 ; LENGTH: 1377  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 ; US-10-176-921-361

Query Match 100.0%; Score 1377; DB 9; Length 1377;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGGACCGGACCGAGAGAGAGAGAGAG 60



OY	241	GTCTCGTGTGCTCTGAGGACCTGAGGAGCGAGCTGCGCCCACTGGACGACAAAGATGCC	300
Db	241	GTCTCGTGTGCTCTGAGGACCTGAGGAGCGAGCTGCGCCCACTGGACGACAAAGATGCC	300
OY	301	CAGCCTCTGCCCGGAGCAACCCGGCCCTTCCAGGCAGCGCGGGCCACCATGGACCCAGGG	360
Db	301	CAGCCTCTGCCCGGAGCAACCCGGCCCTTCCAGGCAGCGCGGGCCACCATGGACCCAGGG	360
OY	361	CTTGCGGGGGCCGCANTGGCCGCGACAGGCGCGGAGCGGGCGCCGGGGCTCCGGGAGAA	420
Db	361	CTTGCGGGGGCCGCANTGGCCGCGACAGGCGCGGAGCGGGCGCCGGGGCTCCGGGAGAA	420
OY	421	AGCGGAGGGCGGAGAGCCGGGACTGCGGGAGCTCGAGGGGACCCTGGCGCGAGAGAGA	480
Db	421	AGCGGAGGGCGGAGAGCCGGGACTGCGGGAGCTCGAGGGGACCCTGGCGCGAGAGAGA	480
OY	481	GGCGGGACCCGCGGGGGCCACCGGGGCTGCGCGGGGAGAGGCTCGGGCTCCGCGCATCGC	540
Db	481	GGCGGGACCCGCGGGGGCCACCGGGGCTGCGCGGGGAGAGGCTCGGGCTCCGCGCATCGC	540
OY	541	CTTCAAGCGCCAAAGCGCTCCAGAGACCGGGGTCTCTCGCGCTGTAGCGACCCCTTGCCCTT	600
Db	541	CTTCAAGCGCCAAAGCGCTCCAGAGACCGGGGTCTCTCGCGCTGTAGCGACCCCTTGCCCTT	600
OY	601	CGACCGCGCTGTGGGAAACGAGACAGGACATTTACGAGCGCTGCACCGGCAAGTTCACCTG	660
Db	601	CGACCGCGCTGTGGGAAACGAGACAGGACATTTACGAGCGCTGCACCGGCAAGTTCACCTG	660
OY	661	CCAGGTGCTTGGGGTCTACTACTTTCGCCCTCCATGCCACCGGTCTACCGGGCCAGCTGCA	720
Db	661	CCAGGTGCTTGGGGTCTACTACTTTCGCCCTCCATGCCACCGGTCTACCGGGCCAGCTGCA	720
OY	721	GTTTGATCTGTGTAAGAAATGCGAATCCATTGACCTCTTCTCCAGTTTTCGGGGGGTG	780
Db	721	GTTTGATCTGTGTAAGAAATGCGAATCCATTGACCTCTTCTCCAGTTTTCGGGGGGTG	780
OY	781	GCCCAAGCAACCTTCGCTCGGGGGGGGGCCATGTAGAGCTGAGACCTGAGACAAAGT	840
Db	781	GCCCAAGCAACCTTCGCTCGGGGGGGGGCCATGTAGAGCTGAGACCTGAGACAAAGT	840
OY	841	GTGGGTGAGGTGGGTGTGGGTGACTACATTGGGATCTATGCCACATCAAGACAGACAG	900
Db	841	GTGGGTGAGGTGGGTGTGGGTGACTACATTGGGATCTATGCCACATCAAGACAGACAG	900
OY	901	CACCTTCCCGGATTTCTGTGTACTCCGACTGGCAGACAGTCCCAAGTCTTTGCTTAATG	960
Db	901	CACCTTCCCGGATTTCTGTGTACTCCGACTGGCAGACAGTCCCAAGTCTTTGCTTAATG	960
OY	961	CCCACTCGAAGTGAAGCTCATGCTCACTCCTTGAAGAGGAGGTGTAGGCTGCACAAACA	1020
Db	961	CCCACTCGAAGTGAAGCTCATGCTCACTCCTTGAAGAGGAGGTGTAGGCTGCACAAACA	1020
OY	1021	GGTCACTCAGAGAGGGCTGGCCCCCTGGAAATATGTGATATCAATAGGAGGTGGGTAGA	1080
Db	1021	GGTCACTCAGAGAGGGCTGGCCCCCTGGAAATATGTGATATCAATAGGAGGTGGGTAGA	1080
OY	1081	GCACCTCCGCTCTGCTGCTGGCAAGAGAAATGGGAAACAGTGGCTGCTCGATCAAGGTG	1140
Db	1081	GCACCTCCGCTCTGCTGCTGGCAAGAGAAATGGGAAACAGTGGCTGCTCGATCAAGGTG	1140
OY	1141	GCAGCATGGGGCAGTGGGTGGATTTCTGCCCAAGACACAGAGAGTGTCTGTGCTGGCAA	1200
Db	1141	GCAGCATGGGGCAGTGGGTGGATTTCTGCCCAAGACACAGAGAGTGTCTGTGCTGGCAA	1200
OY	1201	GTTGAAGTCCCCCAAGTTGCTCTGTGCTCAGAGACCCAGTGGGGGTCTCTTCCCTGGCTC	1260
Db	1201	GTTGAAGTCCCCCAAGTTGCTCTGTGCTCAGAGACCCAGTGGGGGTCTCTTCCCTGGCTC	1260
OY	1261	CTGTGCTTCTGTGATCTCCCAACCCCTCTGTCTGTGGGGCGCGCCCTTTTCTCAGA	1320
Db	1261	CTGTGCTTCTGTGATCTCCCAACCCCTCTGTCTGTGGGGCGCGCCCTTTTCTCAGA	1320

QY	1321	GATCAGCTCAATAAACCTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAAA	1377
Db	1321	GATCAGCTCAATAATAACCTAAGAACCTCATATAAAAAAAAAAAAAAAAAAAAAA	1377
		RESULT 15	
		US-10-140-474-361	
		; Sequence 361, Application US/10140474	
		; Publication No. US20030032156A1	
		; GENERAL INFORMATION:	
		; APPLICANT: Baker, Kevin P.	
		; APPLICANT: Beresinski, Maureen	
		; APPLICANT: DeForge, Laura	
		; APPLICANT: Desnoyers, Luc	
		; APPLICANT: Filvaroff, Ellen	
		; APPLICANT: Gao, Wei-Qiang	
		; APPLICANT: Gerritsen, Mary E.	
		; APPLICANT: Goddard, Audrey	
		; APPLICANT: Godowski, Paul J.	
		; APPLICANT: Gurney, Austin L.	
		; APPLICANT: Sherwood, Steven	
		; APPLICANT: Smith, Victoria	
		; APPLICANT: Stewart, Timothy A.	
		; APPLICANT: Tamas, Daniel	
		; APPLICANT: Watanabe, Colin K	
		; APPLICANT: Wood, William	
		; APPLICANT: Zhang, Zhenli	
		; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC	
		; TITLE OF INVENTION: ACIDS ENCODING THE SAME	
		; FILE REFERENCE: P3330R1C162	
		; CURRENT APPLICATION NUMBER: US/10/140,474	
		; CURRENT FILING DATE: 2002-05-06	
		; Prior Application removed - See Palm or File Wrapper	
		; NUMBER OF SEQ ID NOS: 550	
		; SEQ ID NO 361	
		; LENGTH: 1377	
		; TYPE: DNA	
		; ORGANISM: Homo Sapien	
		US-10-140-474-361	
		Query Match	100.0%; Score 1377; DB 9; Length 1377;
		Best Local Similarity	100.0%; Pred. No. 0;
		Matches 1377; Conservative	0; Mismatches 0; Indels 0; Gaps 0
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QY	61	TGGGTGACGGCAGGAGGAGGAGGCGCTTGGCCGGGAGAAAGCGCGGGGCTTGAGCACCA	120
Db	61	TGGGTGACGGCAGGAGGAGGAGGCGCTTGGCCGGGAGAAAGCGCGGGGCTTGAGCACCA	120
QY	121	CCAACTGGAGGCTCCGGAGTAGCGAGCGCCCGCGAAGGAAGGACCATCGGGAGCGCGAGG	180
Db	121	CCAACTGGAGGCTCCGGAGTAGCGAGCGCCCGCGAAGGAAGGACCATCGGGAGCGCGAGG	180
QY	181	GGGAGTCGAGAGAACCCCGCGCTCGGGCTCCCGGTGCGACGCTATGAGGCCACTCT	240
Db	181	GGGAGTCGAGAGAACCCCGCGCTCGGGCTCCCGGTGCGACGCTATGAGGCCACTCT	240
QY	241	CGTCCGTCGTCGTCGGGGCGCTGGCGCGGCTCGGCCCGGCTCGGCGGAGCAACAAGATCC	300
Db	241	CGTCCGTCGTCGTCGGGGCGCTGGCGCGGCTCGGCCCGGCTCGGCGGAGCAACAAGATCC	300
QY	301	CAGCCTTCGCCCCGGGACACCCGCGCTTCAGGACGAGCGCGGCGCACATGCGACCGAGG	360
Db	301	CAGCCTTCGCCCCGGGACACCCGCGCTTCAGGACGAGCGCGGCGCACATGCGACCGAGG	360
QY	361	CTTGGCGGGCGCGATGGCGCGGAGCGGCGGAGCGGCGCGCGCGCGCGCGGAGAGAA	420
Db	361	CTTGGCGGGCGCGATGGCGCGGAGCGGCGGAGCGGCGCGCGCGCGCGCGGAGAGAA	420
QY	421	AGCGAGGCGGAGCGCGGAGCTGCGGGGACCTGAGGAGAACCCCGGCGCGAGAGAA	480



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-09-944-944-41

Perfect score: 1377

Sequence: 1.gactagttctcttgagctc.....aaaaaaaaaaaaaaaaa 1377

Scoring table:

Gapop 10.0 , Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1377	100.0	1377	9	US-09-944-403-41
3	1377	100.0	1377	9	US-09-944-896-41
4	1377	100.0	1377	9	US-09-944-944-41
5	1377	100.0	1377	9	US-09-944-907-41
6	1377	100.0	1377	9	US-09-944-929-41
7	1377	100.0	1377	9	US-10-028-072-361
8	1377	100.0	1377	9	US-10-121-049-361
9	1377	100.0	1377	9	US-10-123-904-361
10	1377	100.0	1377	9	US-10-140-470-361
11	1377	100.0	1377	9	US-10-175-746-361
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13	1377	100.0	1377	9	US-10-176-921-361
14	1377	100.0	1377	9	US-10-137-865-361
15	1377	100.0	1377	9	US-10-140-474-361
16	1377	100.0	1377	9	US-10-142-431-361
17	1377	100.0	1377	9	US-10-143-114-361
18	1377	100.0	1377	9	US-10-140-002-361
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20	1377	100.0	1377	9	US-10-123-262-361	Sequence 361, App
21	1377	100.0	1377	9	US-10-142-423-361	Sequence 361, App
22	1377	100.0	1377	9	US-10-121-050-361	Sequence 361, App
23	1377	100.0	1377	9	US-10-141-755-361	Sequence 361, App
24	1377	100.0	1377	9	US-10-143-032-361	Sequence 361, App
25	1377	100.0	1377	9	US-10-123-108-361	Sequence 361, App
26	1377	100.0	1377	9	US-10-123-236-361	Sequence 361, App
27	1377	100.0	1377	9	US-10-123-261-361	Sequence 361, App
28	1377	100.0	1377	9	US-10-140-921-361	Sequence 361, App
29	1377	100.0	1377	9	US-10-140-928-361	Sequence 361, App
30	1377	100.0	1377	9	US-10-121-045-361	Sequence 361, App
31	1377	100.0	1377	9	US-10-123-292-361	Sequence 361, App
32	1377	100.0	1377	9	US-10-123-903-361	Sequence 361, App
33	1377	100.0	1377	9	US-10-124-819-361	Sequence 361, App
34	1377	100.0	1377	9	US-10-124-822-361	Sequence 361, App
35	1377	100.0	1377	9	US-10-140-925-361	Sequence 361, App
36	1377	100.0	1377	9	US-10-160-498-361	Sequence 361, App
37	1377	100.0	1377	9	US-09-944-884-41	Sequence 41, App
38	1377	100.0	1377	9	US-10-121-041-361	Sequence 361, App
39	1377	100.0	1377	9	US-10-121-043-361	Sequence 361, App
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41	1377	100.0	1377	9	US-10-123-215-361	Sequence 361, App
42	1377	100.0	1377	9	US-10-123-902-361	Sequence 361, App
43	1377	100.0	1377	9	US-10-123-908-361	Sequence 361, App
44	1377	100.0	1377	9	US-10-123-909-361	Sequence 361, App
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## ALIGNMENTS

RESULT 1  
US-09-944-413-41  
; Sequence 41, Application US/09944413  
; Patent No. US20020156004A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerlitsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kijavlin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P2548P1  
; CURRENT APPLICATION NUMBER: US/09/944,413  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 06/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997

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1 PRIOR APPLICATION NUMBER: 60/069,702
2 PRIOR FILING DATE: December 16, 1997
3 PRIOR APPLICATION NUMBER: 60/069,870
4 PRIOR FILING DATE: December 17, 1997
5 PRIOR APPLICATION NUMBER: 60/069,873
6 PRIOR FILING DATE: December 17, 1997
7 PRIOR APPLICATION NUMBER: 60/068,017
8 PRIOR FILING DATE: December 18, 1997
9 PRIOR APPLICATION NUMBER: 60/070,440
10 PRIOR FILING DATE: January 5, 1998
11 PRIOR APPLICATION NUMBER: 60/074,086
12 PRIOR FILING DATE: February 9, 1998
13 PRIOR APPLICATION NUMBER: 60/074,092
14 PRIOR FILING DATE: February 9, 1998
15 PRIOR APPLICATION NUMBER: 60/075,945
16 PRIOR FILING DATE: February 25, 1998
17 PRIOR APPLICATION NUMBER: 60/112,850
18 PRIOR FILING DATE: December 16, 1998
19 PRIOR APPLICATION NUMBER: 60/113,296
20 PRIOR FILING DATE: December 22, 1998
21 PRIOR APPLICATION NUMBER: 60/146,222
22 PRIOR FILING DATE: July 28, 1999
23 PRIOR APPLICATION NUMBER: PCT/US98/19330
24 PRIOR FILING DATE: September 16, 1998
25 PRIOR APPLICATION NUMBER: PCT/US98/25108
26 PRIOR FILING DATE: December 1, 1998
27 PRIOR APPLICATION NUMBER: 09/216,021
28 PRIOR FILING DATE: December 16, 1998
29 PRIOR APPLICATION NUMBER: 09/218,517
30 PRIOR FILING DATE: December 22, 1998
31 PRIOR APPLICATION NUMBER: 09/254,311
32 PRIOR FILING DATE: March 3, 1999
33 PRIOR APPLICATION NUMBER: PCT/US99/12252
34 PRIOR FILING DATE: June 22, 1999
35 PRIOR APPLICATION NUMBER: PCT/US99/21090
36 PRIOR FILING DATE: September 15, 1999
37 PRIOR APPLICATION NUMBER: PCT/US99/28409
38 PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
39 PRIOR APPLICATION NUMBER: PCT/US99/28313
40 PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
41 PRIOR APPLICATION NUMBER: PCT/US99/28301
42 PRIOR FILING DATE: December1, 1999
43 PRIOR APPLICATION NUMBER: PCT/US99/30095
44 PRIOR FILING DATE: December 16, 1999
45 PRIOR APPLICATION NUMBER: PCT/US00/03555
46 PRIOR FILING DATE: February 11, 2000
47 PRIOR APPLICATION NUMBER: PCT/US00/04414
48 PRIOR FILING DATE: February 22, 2000
49 PRIOR APPLICATION NUMBER: PCT/US00/05841
50 PRIOR FILING DATE: March 2, 2000
51 PRIOR APPLICATION NUMBER: PCT/US00/08439
52 PRIOR FILING DATE: March 30, 2000
53 PRIOR APPLICATION NUMBER: PCT/US00/14042
54 PRIOR FILING DATE: May 22, 2000
55 PRIOR APPLICATION NUMBER: PCT/US00/20710
56 PRIOR FILING DATE: July 28, 2000
57 PRIOR APPLICATION NUMBER: PCT/US00/32678
58 PRIOR FILING DATE: December 1, 2000
59 PRIOR APPLICATION NUMBER: PCT/US01/06520
60 PRIOR FILING DATE: February 28, 2001
61 NUMBER OF SEQ ID NOS: 120
62 SEQ ID NO 41
63 LENGTH: 1377
64 TYPE: DNA
65 ORGANISM: Homo Sapien
66 IS-09-944-413-41

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Query Match	100.0%	Score 1377	DB 9	Length 1377
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O	y	61	TGGGTGAGCGCAGGGCAGAGGGGGCGCTGGCCGGGAGAGAGCGGGGGCTGGAGCACCA	120
D	b	61	TGGGTGAGCGCAGGGCAGAGGGGGCGCTGGCCGGGAGAGAGCGGGGGCTGGAGCACCA	120
O	y	121	CCAACTGGAAGGCTCCGGAGTAGCCAGGCGCCCGAAGAGAGGCCATGGGGAGCGCCGGAGG	180
D	b	121	CCAACTGGAAGGCTCCGGAGTAGCCAGGCGCCCGAAGAGAGGCCATGGGGAGCGCCGGAGG	180
O	y	181	GGAGCTGGAGAGAGACCCCGGGGCTCCGGGCTCCCGTGCACAGCGCTATGAGGCGCACTCT	240
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O	y	241	CGTCCGTGCTGCTCTGGGGCTGGGCGCCGGGCTCGCCCACTGACGACAAACAGATCCC	300
D	b	241	CGTCCGTGCTGCTCTGGGGCTGGGCGCCGGGCTCGCCCACTGACGACAAACAGATCCC	300
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D	b	361	CTTGGCGGGCGCGCATGGCCCGAGAGCGCGCGAGCGCGCGCCCGGGGGCTCCGGAGAGAA	420
O	y	421	AGCGCAGGGCGGGAGCGCGGAGCTCCGGGACCTTCAGAGGGAGACCCCGGGCGCGAGAGA	480
D	b	421	AGCGCAGGGCGGGAGCGCGGAGCTCCGGGACCTTCAGAGGGAGACCCCGGGCGCGAGAGA	480
O	y	481	GGCGGGACCGCGGGGGCCACCGGGGCTCGCGGGGAGTGTGGGTGGCTCCGGCATTCGCG	540
D	b	481	GGCGGGACCGCGGGGGCCACCGGGGCTCGCGGGGAGTGTGGGTGGCTCCGGCATTCGCG	540
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D	b	541	CTTCAAGCGCAGAGCGCTCCGAGAGCGGGGTGCTCCGCGCTGACAGCACTTGGCCCTT	600
O	y	601	CGACCGCGTGTGTGAACGAGACAGAGGACATTACAGCGCCGTACACGGCAAGTTCACCTG	660
D	b	601	CGACCGCGTGTGTGAACGAGACAGAGGACATTACAGCGCCGTACACGGCAAGTTCACCTG	660
O	y	661	CCAGGTGCTGGGGTCTACTTACCTTCCGCGTCCATGCGCAACGCTTACCGGGCAGGCTGCA	720
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D	b	721	GTTTGATCTGTGAAGAAATGGCGAATCCATTGCGCTTTCACAGTTTTCGGGGGGTG	780
O	y	781	GCCCCAAGCCACCTCGCTTCGGGGGGGGCCATGGTGAAGGCTGAGGCTGAGGACCAAGT	840
D	b	781	GCCCCAAGCCACCTCGCTTCGGGGGGGGCCATGGTGAAGGCTGAGGCTGAGGACCAAGT	840
O	y	841	GTGGGTGAGGTGGGTGTGGTGACTTATGGCATTTATGCCATCAAGACAAGACAG	900
D	b	841	GTGGGTGAGGTGGGTGTGGTGACTTATGGCATTTATGCCATCAAGACAAGACAG	900
O	y	901	CACCTTCGCGGAATTTTCGGTGTACTCGACTGGGACAGCTCCCAAGCTTGTGCTATGTG	960
D	b	901	CACCTTCGCGGAATTTTCGGTGTACTCGACTGGGACAGCTCCCAAGCTTGTGCTATGTG	960
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OY	241	CGTCTGCTGTCCTCGGGGCGTCGGGGGCGCGGGTCCGCCCATCTGGACGCAACAAAGATCC	300
Db	241	CGTCTGCTGTCCTCGGGGCGTCGGGGGCGCGGGTCCGCCCATCTGGACGCAACAAAGATCC	300
OY	301	CAGCCTTCGCCCCGGGGGCACCCCGACCTTCCAGAGCAAGCCGGGGCCACATATGGACAGCCAGG	360
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OY	361	CTTCGCGGGGGCCGCAATGGCCCGCGGACAGCGCGGAGCGCGCGCCGGGGGTCCGGGAGAA	420
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Db	361	CTTCGCGGGGGCCGCAATGGCCCGCGGACAGCGCGGAGCGCGCGCCGGGGGTCCGGGAGAA	420
OY	421	AGGGGAGGGGCGGAGGCGCGGACCTGCGCGGACCTTCGAGGGGACCCCGGGCGCGAGAG	480
OY	421	AGGGGAGGGGCGGAGGCGCGGACCTGCGCGGACCTTCGAGGGGACCCCGGGCGCGAGAG	480
Db	421	AGGGGAGGGGCGGAGGCGCGGACCTGCGCGGACCTTCGAGGGGACCCCGGGCGCGAGAG	480
OY	481	GGCGGGACCCGCGGGGGCCACCGGGGCTCCCGGGGAGTGTCTGGTGGCTCCGCGATCCG	540
OY	481	GGCGGGACCCGCGGGGGCCACCGGGGCTCCCGGGGAGTGTCTGGTGGCTCCGCGATCCG	540
Db	481	GGCGGGACCCGCGGGGGCCACCGGGGCTCCCGGGGAGTGTCTGGTGGCTCCGCGATCCG	540
OY	541	CTTCAGCGCCCAAGGCGCTCGAGAGCGGGGTGCTCCCGCGCGTGCAGCGACCCCTTGCCCT	600
OY	541	CTTCAGCGCCCAAGGCGCTCGAGAGCGGGGTGCTCCCGCGCGTGCAGCGACCCCTTGCCCT	600
Db	541	CTTCAGCGCCCAAGGCGCTCGAGAGCGGGGTGCTCCCGCGCGTGCAGCGACCCCTTGCCCT	600
OY	601	CGACCGCGTGTGTGAACGAGCAGGAGACATTCAGACGCGGTCAACCGGCAAGTTCACCTG	660
OY	601	CGACCGCGTGTGTGAACGAGCAGGAGACATTCAGACGCGGTCAACCGGCAAGTTCACCTG	660
Db	601	CGACCGCGTGTGTGAACGAGCAGGAGACATTCAGACGCGGTCAACCGGCAAGTTCACCTG	660
OY	661	CCAGGTGCTGGGGGCTACTACTTCGCGCGTGCATATGCGACGCGTCAACCGGGGACGCTGCA	720
OY	661	CCAGGTGCTGGGGGCTACTACTTCGCGCGTGCATATGCGACGCGTCAACCGGGGACGCTGCA	720
Db	661	CCAGGTGCTGGGGGCTACTACTTCGCGCGTGCATATGCGACGCGTCAACCGGGGACGCTGCA	720
OY	721	GTTTGATCTGTGTGAAGAAATGGCGAATTCATTCCTTCTTCCAGTTTTCGGGGGGTG	780
OY	721	GTTTGATCTGTGTGAAGAAATGGCGAATTCATTCCTTCTTCCAGTTTTCGGGGGGTG	780
Db	721	GTTTGATCTGTGTGAAGAAATGGCGAATTCATTCCTTCTTCCAGTTTTCGGGGGGTG	780
OY	781	GCCCAAGCCACCTTCGCTCTCGGGGGGGGCCATGTGAGGCTGTGAAGCTGTGAGGACCAAGT	840
OY	781	GCCCAAGCCACCTTCGCTCTCGGGGGGGGCCATGTGAGGCTGTGAGGCTGTGAGGACCAAGT	840
Db	781	GCCCAAGCCACCTTCGCTCTCGGGGGGGGCCATGTGAGGCTGTGAGGCTGTGAGGACCAAGT	840
OY	841	GTGGGTGAGGTGGGGTGTGGGTGAGTACTATTCGATCTATTCGACGACATCAAGACAGACAG	900
OY	841	GTGGGTGAGGTGGGGTGTGGGTGAGTACTATTCGATCTATTCGACGACATCAAGACAGACAG	900
Db	841	GTGGGTGAGGTGGGGTGTGGGTGAGTACTATTCGATCTATTCGACGACATCAAGACAGACAG	900
OY	901	CACCTTCTCGGATTTCTGTGTGTACTCCGACTGGACAGCTCCGACGTCTTGTCTAGTG	960
OY	901	CACCTTCTCGGATTTCTGTGTGTACTCCGACTGGACAGCTCCGACGTCTTGTCTAGTG	960
Db	901	CACCTTCTCGGATTTCTGTGTGTACTCCGACTGGACAGCTCCGACGTCTTGTCTAGTG	960
OY	961	CCCACTGCAAGTGTAGCTCATGCTCACTCACTCTGAAAGAGAGGGTGTAGGGCTGCAACCA	1020
OY	961	CCCACTGCAAGTGTAGCTCATGCTCACTCACTCTGAAAGAGAGGGTGTAGGGCTGCAACCA	1020
Db	961	CCCACTGCAAGTGTAGCTCATGCTCACTCACTCTGAAAGAGAGGGTGTAGGGCTGCAACCA	1020
OY	1021	GGTCATCCAGAGGGGCTGGCCCCCTGGGAATATTGTGAATGACTAAGGAGGTGGGGTGA	1080
OY	1021	GGTCATCCAGAGGGGCTGGCCCCCTGGGAATATTGTGAATGACTAAGGAGGTGGGGTGA	1080
Db	1021	GGTCATCCAGAGGGGCTGGCCCCCTGGGAATATTGTGAATGACTAAGGAGGTGGGGTGA	1080
OY	1081	GCACTTCGCCGTCTGTCTGTGGCAAGAAATGGGAACAATGGCTGTCTGTCCATCAGGTGTG	1140
OY	1081	GCACTTCGCCGTCTGTCTGTGGCAAGAAATGGGAACAATGGCTGTCTGTCCATCAGGTGTG	1140
Db	1081	GCACTTCGCCGTCTGTCTGTGGCAAGAAATGGGAACAATGGCTGTCTGTCCATCAGGTGTG	1140
OY	1141	GCACCATGGGGCAATGGCTGGAATTTCTCCCAAGACAGAGAGAGTGTCTGTGCGCA	1200
OY	1141	GCACCATGGGGCAATGGCTGGAATTTCTCCCAAGACAGAGAGAGTGTCTGTGCGCA	1200
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OY	1201	GTGTAAAGTCCCAAGTTGTCTGTGCTCAAGAGCCGAGGTGGGGTGTCTCTTCCGTGTC	1260
OY	1201	GTGTAAAGTCCCAAGTTGTCTGTGCTCAAGAGCCGAGGTGGGGTGTCTCTTCCGTGTC	1260
Db	1201	GTGTAAAGTCCCAAGTTGTCTGTGCTCAAGAGCCGAGGTGGGGTGTCTCTTCCGTGTC	1260
OY	1261	CTTGCGCTTCTGTGAATCTCCCAACCCCTCTGTCTCTGTGGGGCGGGCCCTTTTCTCAGA	1320
OY	1261	CTTGCGCTTCTGTGAATCTCCCAACCCCTCTGTCTCTGTGTGGGGCGGGCCCTTTTCTCAGA	1320
Db	1261	CTTGCGCTTCTGTGAATCTCCCAACCCCTCTGTCTCTGTGTGGGGCGGGCCCTTTTCTCAGA	1320

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1377 Db      1321 GATCAGTCATTAACCTCTAGAACCTCTATAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1377
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1379 RESULT 3
1380 US-09-944-896-41
1381 Sequence 41, Application US/09944896
1382 Patent No. US20020168715A1
1383 GENERAL INFORMATION:
1384 APPLICANT: Baker, Kevin
1385 APPLICANT: Botstein, David
1386 APPLICANT: Eaton, Dan
1387 APPLICANT: Ferrara, Napoleone
1388 APPLICANT: Filvaroff, Ellen
1389 APPLICANT: Gerritsen, Mary
1390 APPLICANT: Goddard, Audrey
1391 APPLICANT: Godowski, Paul
1392 APPLICANT: Grimaldi, Christopher
1393 APPLICANT: Gurney, Austin
1394 APPLICANT: Hillan, Kenneth
1395 APPLICANT: Kijavlin, Ivar
1396 APPLICANT: Napier, Mary
1397 APPLICANT: Roy, Margaret
1398 APPLICANT: Tumas, Daniel
1399 APPLICANT: Wood, William
1400 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
1401 FILE REFERENCE: P2548P1C1
1402 CURRENT APPLICATION NUMBER: US/09/944, 896
1403 CURRENT FILING DATE: 2001-08-31
1404 PRIOR APPLICATION NUMBER: 09/866, 028
1405 PRIOR FILING DATE: 2001-05-25
1406 PRIOR APPLICATION NUMBER: 60/069, 334
1407 PRIOR FILING DATE: December 11, 1997
1408 PRIOR APPLICATION NUMBER: 60/069, 335
1409 PRIOR FILING DATE: December 11, 1997
1410 PRIOR APPLICATION NUMBER: 60/069, 278
1411 PRIOR FILING DATE: December 11, 1997
1412 PRIOR APPLICATION NUMBER: 60/069, 425
1413 PRIOR FILING DATE: December 12, 1997
1414 PRIOR APPLICATION NUMBER: 60/069, 696
1415 PRIOR FILING DATE: December 15, 1997
1416 PRIOR APPLICATION NUMBER: 60/069, 694
1417 PRIOR FILING DATE: December 16, 1997
1418 PRIOR APPLICATION NUMBER: 60/069, 702
1419 PRIOR FILING DATE: December 16, 1997
1420 PRIOR APPLICATION NUMBER: 60/069, 870
1421 PRIOR FILING DATE: December 17, 1997
1422 PRIOR APPLICATION NUMBER: 60/069, 873
1423 PRIOR FILING DATE: December 17, 1997
1424 PRIOR APPLICATION NUMBER: 60/068, 017
1425 PRIOR FILING DATE: December 18, 1997
1426 PRIOR APPLICATION NUMBER: 60/070, 440
1427 PRIOR FILING DATE: January 5, 1998
1428 PRIOR APPLICATION NUMBER: 60/074, 086
1429 PRIOR FILING DATE: February 9, 1998
1430 PRIOR APPLICATION NUMBER: 60/074, 092
1431 PRIOR FILING DATE: February 9, 1998
1432 PRIOR APPLICATION NUMBER: 60/075, 945
1433 PRIOR FILING DATE: February 25, 1998
1434 PRIOR APPLICATION NUMBER: 60/112, 850
1435 PRIOR FILING DATE: December 16, 1998
1436 PRIOR APPLICATION NUMBER: 60/113, 296
1437 PRIOR FILING DATE: December 22, 1998
1438 PRIOR APPLICATION NUMBER: 60/146, 222
1439 PRIOR FILING DATE: July 28, 1999
1440 PRIOR APPLICATION NUMBER: PCT/US98/19330
1441 PRIOR FILING DATE: September 16, 1998
1442 PRIOR APPLICATION NUMBER: PCT/US98/25108
1443 PRIOR FILING DATE: December 1, 1998
1444 PRIOR APPLICATION NUMBER: 09/216, 021
1445 PRIOR FILING DATE: December 16, 1998
1446

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APPLICANT: Gerltsen, Mary  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul  
 APPLICANT: Grimaldi, Christopher  
 APPLICANT: Gurney, Austin  
 APPLICANT: Hallan, Kenneth  
 APPLICANT: Kijavini, Ivar  
 APPLICANT: Napier, Mary  
 APPLICANT: Roy, Margaret  
 APPLICANT: Tumes, Daniel  
 APPLICANT: Wood, William  
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 FILE OF INVENTION: ACIDS ENCODING THE SAME  
 FILE REFERENCE: P2548P1C1  
 CURRENT APPLICATION NUMBER: US/09/944,944  
 CURRENT FILING DATE: 2001-09-26  
 PRIOR APPLICATION NUMBER: 09/866,028  
 PRIOR FILING DATE: 2001-05-25  
 PRIOR APPLICATION NUMBER: 60/067,411  
 PRIOR FILING DATE: December 3, 1997  
 PRIOR APPLICATION NUMBER: 60/069,334  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,335  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,728  
 PRIOR FILING DATE: December 11, 1997  
 PRIOR APPLICATION NUMBER: 60/069,425  
 PRIOR FILING DATE: December 12, 1997  
 PRIOR APPLICATION NUMBER: 60/069,696  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,694  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,702  
 PRIOR FILING DATE: December 16, 1997  
 PRIOR APPLICATION NUMBER: 60/069,870  
 PRIOR FILING DATE: December 17, 1997  
 PRIOR APPLICATION NUMBER: 60/069,873  
 PRIOR FILING DATE: December 17, 1997  
 PRIOR APPLICATION NUMBER: 60/068,017  
 PRIOR FILING DATE: December 18, 1997  
 PRIOR APPLICATION NUMBER: 60/070,440  
 PRIOR FILING DATE: January 5, 1998  
 PRIOR APPLICATION NUMBER: 60/074,086  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/074,092  
 PRIOR FILING DATE: February 9, 1998  
 PRIOR APPLICATION NUMBER: 60/075,945  
 PRIOR FILING DATE: February 25, 1998  
 PRIOR APPLICATION NUMBER: 60/112,850  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: 60/113,296  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 60/146,222  
 PRIOR FILING DATE: July 28, 1999  
 PRIOR APPLICATION NUMBER: PCT/US98/19330  
 PRIOR FILING DATE: September 16, 1998  
 PRIOR APPLICATION NUMBER: PCT/US98/25108  
 PRIOR FILING DATE: December 1, 1998  
 PRIOR APPLICATION NUMBER: 09/216,021  
 PRIOR FILING DATE: December 16, 1998  
 PRIOR APPLICATION NUMBER: 09/218,517  
 PRIOR FILING DATE: December 22, 1998  
 PRIOR APPLICATION NUMBER: 09/254,311  
 PRIOR FILING DATE: March 3, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/12252  
 PRIOR FILING DATE: June 22, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/21090  
 PRIOR FILING DATE: September 15, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28409  
 PRIOR FILING DATE: No. US20020173463A1member 30, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28313  
 PRIOR FILING DATE: No. US20020173463A1member 30, 1999  
 PRIOR APPLICATION NUMBER: PCT/US99/28301

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: PRIOR FILING DATE: December1, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/30095
: PRIOR FILING DATE: December 16, 1999
: PRIOR APPLICATION NUMBER: PCT/US00/03565
: PRIOR FILING DATE: February 11, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/04414
: PRIOR FILING DATE: February 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/05841
: PRIOR FILING DATE: March 2, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/08439
: PRIOR FILING DATE: March 30, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/14042
: PRIOR FILING DATE: May 22, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/20710
: PRIOR FILING DATE: July 28, 2000
: PRIOR APPLICATION NUMBER: PCT/US00/32678
: PRIOR FILING DATE: December 1, 2000
: PRIOR APPLICATION NUMBER: PCT/US01/06520
: PRIOR FILING DATE: February 28, 2001
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 41
: LENGTH: 1377
: TYPE: DNA
: ORGANISM: Homo Sapien
US-09-944-944-41

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Query Match	100.0%	Score 1377	DB 9	Length 1377	
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				0	Gaps
					0
QY	1	GACTAGTTCCTTGGAGTCTGGGAGGAGAAAGCGAGCCGCGACGAGACGAC	60		
Db	1	GACTAGTTCCTTGGAGTCTGGGAGGAGAAAGCGAGCCGCGACGAGACGAGAC	60		
QY	61	TGGGGTGACGCGAGGGCCAGGGGGCGCCCTGCCCCGGGGAGAGCGCGGGGCTGGACACCA	120		
Db	61	TGGGGTGACGCGAGGGCCAGGGGGCGCCCTGCCCCGGGGAGAGCGCGGGGCTGGACACCA	120		
QY	121	CCAACTGAGAGGCTCCGAGTAGCGACGACCCCGGAAGGAGAGCCATCGGGAGCGCGGAGGG	180		
Db	121	CCAACTGAGAGGCTCCGAGTAGCGAGCGCCCGGAAGGAGAGCCATCGGGAGCGCGGAGGG	180		
QY	181	GGGACGTGGAGAGNACCCCGGCGTCCGGGCTCCCGGTGCGACGCTATGAGGCACTCT	240		
Db	181	GGGACGTGGAGAGNACCCCGGCGTCCCGGCTCCCGGTGCGACGCTATGAGGCACTCT	240		
QY	241	CGTCCGTGCTGCTCGGGGCTGCGCGCGCGCTCGGCCCTCCACTGAGACGACAAACAATCCC	300		
Db	241	CGTCCGTGCTGCTCGGGGCTGCGCGCGCGCTCGGCCCTCCACTGAGACGACAAACAATCCC	300		
QY	301	CAGCCTCTGCCCCGGGGCCACCCCGGCTTTCAGGCAACCGCGGCCACATGGCAGCCAGGG	360		
Db	301	CAGCCTCTGCCCCGGGGCCACCCCGGCTTTCAGGCAACCGCGGCCACATGGGACGACAGG	360		
QY	361	CTTCGCGGGGCGCGATGAGTCGCGAGAGGCGCGAGCGCGCCCGGGGCTCCGGAGAGNA	420		
Db	361	CTTCGCGGGGCGCGATGAGTCGCGAGAGGCGCGAGCGCGCCCGGGGCTCCGGAGAGNA	420		
QY	421	AGCGAGGCGCGGAGGCGCGGAGCTGCCGGACCTTGAGGGGACCCCGGGCGCGAGAGA	480		
Db	421	AGCGAGGCGCGGAGGCGCGGAGCTGCCGGAGCTTGAGGGGACCCCGGGCGCGAGAGA	480		
QY	481	GGCGGAAOCGCGGGGGCCACCGGGGCTGCGGGGAGAGTCTGGGTGCTCCGCGATCCGC	540		
Db	481	GGCGGAAOCGCGGGGGCCACCGGGGCTGCGGGGAGAGTCTGGGTGCTCCGCGATCCGC	540		
QY	541	CTTCAGGCGCCAAAGGCTCCGAGAGCGGGGTGCTTCGCGCTTGACGACCCCTTGCCCT	600		
Db	541	CTTCAGGCGCCAAAGGCTCCGAGAGCGGGGTGCTTCGCGCTTGACGACCCCTTGCCCT	600		
QY	601	CGACCGCGTGTGTGGTGAACGACGACGAGGACATTAGACGCGCTCACCGGCAAGTTACCTG	660		
Db	601	CGACCGCGTGTGTGGTGAACGACGAGGACATTAGACGCGCTCACCGGCAAGTTACCTG	660		

661 CCAGTGGCTGGGGTCTACTACTTCCGCTCCAGCAACCGTCTACCGGGCCAGGCTGCA 720  
661 CCAGTGGCTGGGGTCTACTACTTCCGCTCCAGCAACCGTCTACCGGGCCAGGCTGCA 720  
721 GTTGTATCTGTGGAAGAAATGGCGAATTCATTCCTCTTCTTCCAGTTTTCGGGGGGTG 780  
721 GTTGTATCTGTGGAAGAAATGGCGAATTCATTCCTCTTCTTCCAGTTTTCGGGGGGTG 780  
781 GCCCAAGCCAGCTGCTCTGCGGGGGGGCCATGTTGAGGCTGGAGCTGAGGACCAAGT 840  
781 GCCCAAGCCAGCTGCTCTGCGGGGGGGCCATGTTGAGGCTGGAGCTGAGGACCAAGT 840  
841 GTGGGTGAGAGGGGTGGGTGGGTGACTACATTCGATTCATGACATCAACAGACAGAC 900  
841 GTGGGTGAGAGGGGTGGGTGGGTGACTACATTCGATTCATGACATCAACAGACAGAC 900  
901 CACCTTCCCGGATTTCTGTGTACTCCGACTGCGACAGCTCCCGAGTCTTGTAGTG 960  
901 CACCTTCCCGGATTTCTGTGTACTCCGACTGCGACAGCTCCCGAGTCTTGTAGTG 960  
961 CCCACTGCAAGTGTGCTCATGCTCTCTACTCTTAAGAGAGGGGTGAGGCTGACACCA 1020  
961 CCCACTGCAAGTGTGCTCATGCTCTCTACTCTTAAGAGAGGGGTGAGGCTGACACCA 1020  
1021 GGTCTATCCAGAGGGGCTGGCCCGCTGGAAATTTGTGAATGACTAGGAGGTGGGTAGA 1080  
1021 GGTCTATCCAGAGGGGCTGGCCCGCTGGAAATTTGTGAATGACTAGGAGGTGGGTAGA 1080  
1081 GCATCTCCGCTCTGCTGCTGCGAGAGAAATGGGAAAGTGGCTGTCTGCGATCAGATCTG 1140  
1081 GCATCTCCGCTCTGCTGCTGCGAGAGAAATGGGAAAGTGGCTGTCTGCGATCAGATCTG 1140  
1141 GCAGATAGGGGAGAGGCTGGAATTTCTGCCCAAGACAGAGAGTGTGTGTGGTGGCA 1200  
1141 GCAGATAGGGGAGAGGCTGGAATTTCTGCCCAAGACAGAGAGTGTGTGTGGTGGCA 1200  
1201 GTGTAACTCCCGCAAGTGTGCTGCTGCTGCAAGAGCCAGGCTGGGTGCTCTCTCTGCTG 1260  
1201 GTGTAACTCCCGCAAGTGTGCTGCTGCTGCAAGAGCCAGGCTGGGTGCTCTCTCTGCTG 1260  
1261 CTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
1261 CTCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320  
1321 GATCCTCAATTAACCTTAAGAACTCTCAATTAACCTTAAGAACTCTCAATTAACCTTAAG 1377  
1321 GATCCTCAATTAACCTTAAGAACTCTCAATTAACCTTAAGAACTCTCAATTAACCTTAAG 1377  
Db 1321 GATCCTCAATTAACCTTAAGAACTCTCAATTAACCTTAAGAACTCTCAATTAACCTTAAG 1377

RESULT 5  
US-09-944-907-41  
; Sequence 41, Application US/09944907  
; Publication No. US20020198147A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerlitsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Guiney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kijavlin, Iyar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P2548P1  
CURRENT APPLICATION NUMBER: US/09/944, 907  
CURRENT FILING DATE: 2001-08-31  
PRIOR APPLICATION NUMBER: 09/866, 028  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 120  
SEQ ID NO 41  
LENGTH: 1377  
TYPE: DNA  
ORGANISM: Homo Sapien  
US-09-944-907-41

Query Match  
Best Local Similarity 100.0%; Score 1377; DB 9; Length 1377;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGAGCGGCGAGGAGCGAAGCAGAC 60  
1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGAGCGGCGAGGAGCGAAGCAGAC 60  
61 TGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
61 TGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120  
121 CCAACTGAGAGGAGTCCGAGATAGCAGAGCGCCCGAAGAGAGGAGGAGGAGGAGGAGGAG 180  
121 CCAACTGAGAGGAGTCCGAGATAGCAGAGCGCCCGAAGAGAGGAGGAGGAGGAGGAGGAG 180  
181 GGGAGTGCAGAGAGACCCCGGAGTCCGAGGAGTCCGAGGAGTCCGAGGAGTCCGAGGAGTCC 240  
181 GGGAGTGCAGAGAGACCCCGGAGTCCGAGGAGTCCGAGGAGTCCGAGGAGTCCGAGGAGTCC 240  
241 GGTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
241 GGTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300  
301 CAGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
301 CAGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
361 CTTGCGGGGCGCGATGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 420  
361 CTTGCGGGGCGCGATGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCGCGGAGCG 420  
421 AGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
421 AGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480  
481 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
481 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
541 CTTGAGCGGCAAGCGCTCCGAGAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
541 CTTGAGCGGCAAGCGCTCCGAGAGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
601 CGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
601 CGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
661 CCAGGTGCTGGGGTCTACTACTTCCGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
661 CCAGGTGCTGGGGTCTACTACTTCCGCTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720  
721 GTTGTATCTGTGGAAGAAATGGCGAATTCATTCCTCTTCTTCCAGTTTTCGGGGGGTG 780  
721 GTTGTATCTGTGGAAGAAATGGCGAATTCATTCCTCTTCTTCCAGTTTTCGGGGGGTG 780  
781 GCCCAAGCCAGCTGCTCTGCGGGGGGGCCATGTTGAGGCTGGAGCTGAGGACCAAGT 840  
781 GCCCAAGCCAGCTGCTCTGCGGGGGGGCCATGTTGAGGCTGGAGCTGAGGACCAAGT 840  
841 GTGGGTGAGAGGGGTGGGTGGGTGACTACATTCGATTCATGACATCAACAGACAGAC 900

Db 841 GTGGGTGAGGTGGGTGGGTGAGTACATGATGATCCAGCATCAAGACAGACAG 900  
Qy 901 CACCTTCCCGGATTTTGGGTGATCTCCGACGTGGACAGTCCCGAGCTTGGTATG 960  
Db 901 CACCTTCCCGGATTTTGGGTGATCTCCGACGTGGACAGTCCCGAGCTTGGTATG 960  
Qy 961 CCCACTGCAAGTGAAGTCAATGCTCACTCTGAAAGAGAGGTGTGAGGCTGACACCA 1020  
Db 961 CCCACTGCAAGTGAAGTCAATGCTCACTCTGAAAGAGAGGTGTGAGGCTGACACCA 1020  
Qy 1021 GGTATCCAGAGAGGCTGGGCCCCCTGAAATTTGTGAATGATAGAGAGGTGGGTAGA 1080  
Db 1021 GGTATCCAGAGAGGCTGGGCCCCCTGAAATTTGTGAATGATAGAGAGGTGGGTAGA 1080  
Qy 1081 GCATCTCCGCTGCTGCTGCTGGCAAGATGGAAACAGTGTCTGTCGATCAGGTCTG 1140  
Db 1081 GCATCTCCGCTGCTGCTGCTGGCAAGATGGAAACAGTGTCTGTCGATCAGGTCTG 1140  
Qy 1141 GCACATAGGGGCACTGGCTGGATTTCTGCCAAGACAGAGAGTGTGCTGGCAA 1200  
Db 1141 GCACATAGGGGCACTGGCTGGATTTCTGCCAAGACAGAGAGTGTGCTGGCAA 1200  
Qy 1201 GTGTAATGCCCCGAGTGTCTGTGTGTCAGAGAGCCAGGAGGTGTCTGTCTGTCTG 1260  
Db 1201 GTGTAATGCCCCGAGTGTCTGTGTGTCAGAGAGCCAGGAGGTGTCTGTCTGTCTG 1260  
Qy 1261 CTCTGCTTCTGTGATCTCTCCACCCCTCTCTCTGCTGGGCGGCTTTCTCAGA 1320  
Db 1261 CTCTGCTTCTGTGATCTCTCCACCCCTCTCTCTGCTGGGCGGCTTTCTCAGA 1320  
Qy 1321 GATCAGTCATATAAAGCTAGAACCTCTATATAAAAAAAAAAAAAAAAAAAAAA 1377  
Db 1321 GATCAGTCATATAAAGCTAGAACCTCTATATAAAAAAAAAAAAAAAAAAAAAA 1377

## RESULT 6

US-09-944-929-41

: Sequence 41, Application US/09444929  
: Publication No. US20020197612A1  
: GENERAL INFORMATION:

: APPLICANT: Baker, Kevin  
: APPLICANT: Botstein, David  
: APPLICANT: Eaton, Dan  
: APPLICANT: Ferrara, Napoleone  
: APPLICANT: Filvaroff, Ellen  
: APPLICANT: Gerltsen, Mary  
: APPLICANT: Goddard, Audrey  
: APPLICANT: Godowski, Paul  
: APPLICANT: Grimaldi, Christopher  
: APPLICANT: Gurney, Austin  
: APPLICANT: Hillan, Kenneth  
: APPLICANT: Kijavlin, Ivar  
: APPLICANT: Napier, Mary  
: APPLICANT: Roy, Margaret  
: APPLICANT: Tamas, Daniel  
: APPLICANT: Wood, William  
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
: FILE REFERENCE: P2548P1C1  
: CURRENT APPLICATION NUMBER: US/09/944, 929  
: PRIORITY FILING DATE: 2001-08-31  
: PRIOR APPLICATION NUMBER: 09/866, 028  
: PRIORITY FILING DATE: 2001-05-25  
: NUMBER OF SEQ ID NOS: 120  
: SEQ ID NO 41  
: LENGTH: 1377  
: TYPE: DNA  
: ORGANISM: Homo Sapien  
US-09-944-929-41

Query Match 100.0%; Score 1377; DB 9; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60  
Db 1 GACTAGTCTCTTGGAGTCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60  
Qy 61 TGGGATGAG 120  
Db 61 TGGGATGAG 120  
Qy 121 CCAACTGAG 180  
Db 121 CCAACTGAG 180  
Qy 181 GGGAGTGGAG 240  
Db 181 GGGAGTGGAG 240  
Qy 241 CGTCTGCTGCTCTGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 300  
Db 241 CGTCTGCTGCTCTGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 300  
Qy 301 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
Db 301 CAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
Qy 361 CTTCGCGGCGCGAGTGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
Db 361 CTTCGCGGCGCGAGTGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
Qy 421 AGCGAG 480  
Db 421 AGCGAG 480  
Qy 481 GGGGAG 540  
Db 481 GGGGAG 540  
Qy 541 CTTCAGGCGCAAGCGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
Db 541 CTTCAGGCGCAAGCGCTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600  
Qy 601 CGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Db 601 CGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Qy 661 CGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Db 661 CGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720  
Qy 721 GTTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
Db 721 GTTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780  
Qy 781 GCGCAAGCGAG 840  
Db 781 GCGCAAGCGAG 840  
Qy 841 GTGGGTGAG 900  
Db 841 GTGGGTGAG 900  
Qy 901 CACCTTCCCGGATTTTGGGTGATCTCCGACGTGGACAGTCCCGAGCTTGGTATG 960  
Db 901 CACCTTCCCGGATTTTGGGTGATCTCCGACGTGGACAGTCCCGAGCTTGGTATG 960  
Qy 961 CCCACTGCAAGTGAAGTCAATGCTCACTCTGAAAGAGAGGTGTGAGGCTGACACCA 1020  
Db 961 CCCACTGCAAGTGAAGTCAATGCTCACTCTGAAAGAGAGGTGTGAGGCTGACACCA 1020  
Qy 1021 GGTATCCAGAGAGGCTGGGCCCCCTGAAATTTGTGAATGATAGAGAGGTGGGTAGA 1080  
Db 1021 GGTATCCAGAGAGGCTGGGCCCCCTGAAATTTGTGAATGATAGAGAGGTGGGTAGA 1080

QY 1081 GCACCTCCGTCCTCTGTCGACAGATGGAGAACAGNGGCTGTCTGAGATCAGGTCTG 1140  
DB 1081 GCACCTCCGTCCTCTGTCGACAGATGGAGAACAGTGGCTGTCTGAGATCAGGTCTG 1140  
QY 1141 GCAGATGGGAGTGGTGTGATTTCTGCCCAAGACAGAGAGTGTCTGTGCGCAA 1200  
DB 1141 GCAGATGGGAGTGGTGTGATTTCTGCCCAAGACAGAGAGTGTCTGTGCGCAA 1200  
QY 1201 GTTAAGTCCCACTGTCTGTCTGTCAGAGACCAGCGTGGGTCTCTCTTCGTGTC 1260  
DB 1201 GTTAAGTCCCACTGTCTGTCTGTCAGAGACCAGCGTGGGTCTCTCTTCGTGTC 1260  
QY 1261 CTCTCTCTCTGTCGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320  
DB 1261 CTCTCTCTCTGTCGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320  
QY 1321 GATCCTCAATTAACCTTAAGAACCTCTCATTAATAAAAAAAAAAAAAAAAAAAAA 1377  
DB 1321 GATCCTCAATTAACCTTAAGAACCTCTCATTAATAAAAAAAAAAAAAAAAAAAAA 1377  
RESULT 7  
US-10-028-072-361  
Sequence 361, Application US/10028072  
Publication No. US20030004311A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang  
TITLE OF INVENTION:  
FILE REFERENCE:  
CURRENT APPLICATION NUMBER: US/10/028,072  
CURRENT FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 60/049911  
PRIOR FILING DATE: 1997-06-18  
PRIOR APPLICATION NUMBER: 60/056974  
PRIOR FILING DATE: 1997-08-26  
PRIOR APPLICATION NUMBER: 60/059113  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059115  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059117  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059122  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059184  
PRIOR FILING DATE: 1997-09-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059352  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059588  
PRIOR FILING DATE: 1997-09-19  
PRIOR APPLICATION NUMBER: 60/059836  
PRIOR FILING DATE: 1997-09-24  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062285  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062287  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/062814  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/062816  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063045  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063082  
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PRIOR APPLICATION NUMBER: 60/063127  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063327  
PRIOR FILING DATE: 1997-10-27  
PRIOR APPLICATION NUMBER: 60/063329  
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PRIOR APPLICATION NUMBER: 60/063550  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063561  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063704  
PRIOR FILING DATE: 1997-10-29  
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PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063735  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063738  
PRIOR FILING DATE: 1997-10-29  
PRIOR APPLICATION NUMBER: 60/063755  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064248  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/064809  
PRIOR FILING DATE: 1997-11-07  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065846  
PRIOR FILING DATE: 1997-11-17  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/066453  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066511  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/069212  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069278  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069334  
PRIOR FILING DATE: 1997-12-11  
PRIOR APPLICATION NUMBER: 60/069694  
PRIOR FILING DATE: 1997-12-16  
PRIOR APPLICATION NUMBER: 60/072320  
PRIOR FILING DATE: 1998-01-23  
PRIOR APPLICATION NUMBER: 60/073612  
PRIOR FILING DATE: 1998-02-04  
PRIOR APPLICATION NUMBER: 60/074086  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/074092  
PRIOR FILING DATE: 1998-02-09  
PRIOR APPLICATION NUMBER: 60/077791  
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PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-02-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: 60/080165  
 PRIOR FILING DATE: 1998-03-31  
 PRIOR APPLICATION NUMBER: 60/081203  
 PRIOR FILING DATE: 1998-04-09  
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 PRIOR APPLICATION NUMBER: 60/082999  
 PRIOR FILING DATE: 1998-04-24  
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 PRIOR FILING DATE: 1998-04-29  
 PRIOR APPLICATION NUMBER: 60/084600  
 PRIOR FILING DATE: 1998-05-07  
 PRIOR APPLICATION NUMBER: 60/084627  
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 PRIOR APPLICATION NUMBER: 60/085149  
 PRIOR FILING DATE: 1998-05-12  
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 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090445  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090538  
 PRIOR FILING DATE: 1998-06-24  
 PRIOR APPLICATION NUMBER: 60/090863  
 PRIOR FILING DATE: 1998-06-26  
 PRIOR APPLICATION NUMBER: 60/091360

PRIOR FILING DATE: 1998-07-01  
 PRIOR APPLICATION NUMBER: 60/091519  
 PRIOR FILING DATE: 1998-07-02  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 Query Match 100.0%; Score 1377; DB 9; Length 1377;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 GACTAGTCTCTGTGAGTCTGGAGAGAGAAAGGAGACCCGAGAGCAACCAAGAC 60  
 1 GACTAGTCTCTGTGAGTCTGGAGAGAGAAAGGAGACCCGAGAGCAACCAAGAC 60  
 61 TGGGGTGAAGGAG 120  
 61 TGGGGTGAAGGAG 120  
 121 CCAACTGAGAGGAG 180  
 121 CCAACTGAGAGGAG 180  
 181 GGGAGTGGAG 240  
 181 GGGAGTGGAG 240  
 241 CGTCTCTGCT 300  
 241 CGTCTCTGCT 300  
 301 CAGCCTTGCCCGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
 301 CAGCCTTGCCCGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
 301 CAGCCTTGCCCGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360  
 361 CTTCGCGGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
 361 CTTCGCGGGGGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
 421 AGCGAG 480  
 421 AGCGAG 480  
 481 GGGGGAG 540  
 481 GGGGGAG 540  
 541 CTTCAGCGGAG 600  
 541 CTTCAGCGGAG 600  
 601 CGAGCGGAG 660  
 601 CGAGCGGAG 660  
 661 CGAGGAG 720  
 661 CGAGGAG 720  
 721 GTTTGATCTGTGTAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
 721 GTTTGATCTGTGTAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780  
 781 GCCCAAGCGAG 840  
 781 GCCCAAGCGAG 840  
 841 GTGGGTGAG 900  
 841 GTGGGTGAG 900  
 901 CACCTTCTCGGAGATTTCTGGTGTATCTCCAGTGGCAGAGCTCCAGTCTTGTAG 960  
 901 CACCTTCTCGGAGATTTCTGGTGTATCTCCAGTGGCAGAGCTCCAGTCTTGTAG 960





Db 1141 GCACATGAGGAGTGGTGGATTCTGCCCCAAGACAGAGAGTGTGCTGTGCGCA 1200  
QY 1201 GTGTAAGTCCCGCATGTTGCTGTGTCAGAGAGCCAGCGTGGGTGCTCTTCTGTC 1260  
Db 1201 GTGTAAGTCCCGCATGTTGCTGTGTCAGAGAGCCAGCGTGGGTGCTCTTCTGTC 1260  
QY 1261 CTCTGCTTCTGTGATGCTCTCCCAACCCCTCTCTCTCTGCGGCGCCCTTTTCTCAGA 1320  
Db 1261 CTCTGCTTCTGTGATGCTCTCCCAACCCCTCTCTCTCTGCGGCGCCCTTTTCTCAGA 1320  
QY 1321 GATCACTCAATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAAA 1377  
Db 1321 GATCACTCAATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAAA 1377

RESULT 9  
US-10-123-904-361  
; Sequence 361, Application US/10123904  
; Publication No. US20030022328A1  
; GENERAL INFORMATION:  
; APPLICANT: Beresini, Laureen P.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P330R1C54  
; CURRENT APPLICATION NUMBER: US/10/123, 904  
; CURRENT FILING DATE: 2002-04-16  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 361  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-123-904-361

Query Match 100.0%; Score 1377; DB 9; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 241 GTCCTGCTGCTCTCTGAGGCTGTGCGGCCGTGCCCCACCTGAGCAGACAAGATCCC 300  
QY 301 CAGCCTGTGCCCCGAGGACCCCGGCTTTCAGAGACCCGCGGACCATGTGACAGCAGG 360  
Db 301 CAGCCTGTGCCCCGAGGACCCCGGCTTTCAGAGACCCGCGGACCATGTGACAGCAGG 360  
QY 361 CTTCGCGGCGCGATGAGCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCGCG 420  
Db 361 CTTCGCGGCGCGATGAGCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGCGCGCG 420  
QY 421 AGCGAGGAGGAGGAGGAGCGGAGCTGCGGAGCGCTGAGAGGAGACCGCGGCGCGAGAGA 480  
Db 421 AGCGAGGAGGAGGAGGAGCGGAGCTGCGGAGCGCTGAGAGGAGACCGCGGCGCGAGAGA 480  
QY 481 GCGCGAGACCGCGCGGAGCGCGACCGGCGCTGCGCGGAGATGCTCGGCTCCGCGATCCG 540  
Db 481 GCGCGAGACCGCGCGGAGCGCGACCGGCGCTGCGCGGAGATGCTCGGCTCCGCGATCCG 540  
QY 541 CTTCAGCGCAAGCGCTCCAGAGACCGGAGCTCTCGCGCGCTGAGCGCACCTTGCCCTT 600  
Db 541 CTTCAGCGCAAGCGCTCCAGAGACCGGAGCTCTCGCGCGCTGAGCGCACCTTGCCCTT 600  
QY 601 CGACCGGCTGTGTGTAACGAGAGCGAGGACATTAAGAGCGCGCTACCGCGCAAGTACCTG 660  
Db 601 CGACCGGCTGTGTGTAACGAGAGCGAGGACATTAAGAGCGCGCTACCGCGCAAGTACCTG 660  
QY 661 CAGAGTCTGAGGCTACTACTTCTGCGCTCATGCGCACCGCTACCGCGCGCGCGCGCA 720  
Db 661 CAGAGTCTGAGGCTACTACTTCTGCGCTCATGCGCACCGCTACCGCGCGCGCGCGCA 720  
QY 721 GTTTGATCTGTGTAAGATGAGGACATTCATTTGCTCTTCTTCCAGTTTTCGAGGGGTG 780  
Db 721 GTTTGATCTGTGTAAGATGAGGACATTCATTTGCTCTTCTTCCAGTTTTCGAGGGGTG 780  
QY 781 GCCCAAGCGACGCTCTGCGGAGGAGGAGCGCATGTGAGGCTGAGGCTGAGGACCAAGT 840  
Db 781 GCCCAAGCGACGCTCTGCGGAGGAGGAGCGCATGTGAGGCTGAGGCTGAGGACCAAGT 840  
QY 841 GTGGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 900  
Db 841 GTGGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 900  
QY 901 CACCTTCTCGGATTTGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGT 960  
Db 901 CACCTTCTCGGATTTGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGT 960  
QY 961 CCACGTGCAAGAGAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGT 1020  
Db 961 CCACGTGCAAGAGAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGTGTAAGTGT 1020  
QY 1021 GGTATCATCAGAGAGGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080  
Db 1021 GGTATCATCAGAGAGGCTGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1080  
QY 1081 GCACCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
Db 1081 GCACCTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
QY 1141 GCACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200  
Db 1141 GCACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200  
QY 1201 GTGTAAGTCCCGCATGTTGCTGTGTCAGAGAGCCAGCGTGGGTGCTCTTCTGTC 1260  
Db 1201 GTGTAAGTCCCGCATGTTGCTGTGTCAGAGAGCCAGCGTGGGTGCTCTTCTGTC 1260  
QY 1261 CTCTGCTTCTGTGATGCTCTCCCAACCCCTCTCTCTCTGCGGCGCCCTTTTCTCAGA 1320  
Db 1261 CTCTGCTTCTGTGATGCTCTCCCAACCCCTCTCTCTCTGCGGCGCCCTTTTCTCAGA 1320  
QY 1321 GATCACTCAATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAAA 1377  
Db 1321 GATCACTCAATTAACCTAAGAACCTCATTAATAAAAAAAAAAAAAAAAAAAAAA 1377

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RESULT 10
US-10-140-470-361
; Sequence 361, Application US/10140470
; Publication No. US2003002231A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvarioff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumanabe, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P33030R1C160
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 361
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-470-361

Query Match      100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGGACCGGACGAGGAGCGAAGCAGAGC 60
DB      1 GACTAGTCTCTTGGAGTCTGGAGAGAGAAAGCGGACCGGACGAGGAGCGAAGCAGAGC 60
QY      61 TGGGCTGACGCGAGGCGAGGGGGCGCTGGCGGGGAGAAAGCGGCGGGGCTGGAGCAGCA 120
DB      61 TGGGCTGACGCGAGGCGAGGGGGCGCTGGCGGGGAGAAAGCGGCGGGGCTGGAGCAGCA 120
QY      121 CCAACTGGAGGGTCCGAGTAGCGAGCGCCCGGAGAGAGCCATCGGGGAGCGGGAGAGG 180
DB      121 CCAACTGGAGGGTCCGAGTAGCGAGCGCCCGGAGAGAGCCATCGGGGAGCGGGAGAGG 180
QY      181 GGGAGCTGCGAGAGAGAGCCCGGGGCTCCGGTCCGAGCGCTATGAGGCCACTCT 240
DB      181 GGGAGCTGCGAGAGAGAGCCCGGGGCTCCGGTCCGAGCGCTATGAGGCCACTCT 240
QY      241 CGTCTGCTGCTCTCTGGGCGCTGGGCGCGGCTCCCGCCCACTGAGCAGCAACAAATCCC 300
DB      241 CGTCTGCTGCTCTCTGGGCGCTGGGCGCGGCTCCCGCCCACTGAGCAGCAACAAATCCC 300
QY      301 CAGCCTCTGCCCCGGGGACACCCCGGCTTCAAGGACGCGGGGCGACATGAGCAGCAGG 360
DB      301 CAGCCTCTGCCCCGGGGGACACCCCGGCTTCAAGGACGCGGGGCGACATGAGCAGCAGG 360
QY      361 CTGGCGGGGCGCGATGAGCGCGAGCGCGCGAGCGCGCGCGCGGGGCTCCGGAGAGAA 420
DB      361 CTGGCGGGGCGCGATGAGCGCGAGCGCGCGAGCGCGCGCGCGGGGCTCCGGAGAGAA 420
QY      421 AGGCGAGGGCGGGAGAGCGGGGAGCTCCGGGAGACTTGAGAGGAGAGAGAGAGAGAGAG 480
DB      421 AGGCGAGGGCGGGAGAGCGGGGAGCTCCGGGAGACTTGAGAGGAGAGAGAGAGAGAG 480
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QY      481 GGGCGGACCCGGGGGCGCCACCAGCGGCTGCGGGGAGTGTCTGCTCCGCGATCCGC 540
DB      481 GGGCGGACCCGGGGGCGCCACCAGCGGCTGCGGGGAGTGTCTGCTCCGCGATCCGC 540
QY      541 CTTCAGCGCCAAAGCGCTCCGAGAGCGGGGTGCTCCGCGTCTGACGACACCTTGCCCTT 600
DB      541 CTTCAGCGCCAAAGCGCTCCGAGAGCGGGGTGCTCCGCGTCTGACGACACCTTGCCCTT 600
QY      601 CGACCGCGTGGTGGGAGACGAGGAGGACATTTAGACGCGCGGACCGGCAAGTTCACCTG 660
DB      601 CGACCGCGTGGTGGGAGACGAGGAGGACATTTAGACGCGCGGACCGGCAAGTTCACCTG 660
QY      661 CCAGGTGCTGGGGGCTCTACTACTTGGCCGTCATCCACCGTCTACCGGGGAGCGCTCA 720
DB      661 CCAGGTGCTGGGGGCTCTACTACTTGGCCGTCATCCACCGTCTACCGGGGAGCGCTCA 720
QY      721 GTTGTATCTGTGAAGAAATGGGAAATCCATTGCTCTTCTTCCAGTTTTCGGGGGTG 780
DB      721 GTTGTATCTGTGAAGAAATGGGAAATCCATTGCTCTTCTTCCAGTTTTCGGGGGTG 780
QY      781 GCGCAAGCGACGCGTCTGGGGGGGGGCGCATGGTGAAGGCTGAGGACCAAGT 840
DB      781 GCGCAAGCGACGCTCTCTGGGGGGGGGCGCATGGTGAAGGCTGAGGACCAAGT 840
QY      841 GTGGTGACAGTGGGTGGGTGAATGACTATGATGCAATGCAATGCAATGCAATGCAATG 900
DB      841 GTGGTGACAGTGGGTGGGTGAATGACTATGATGCAATGCAATGCAATGCAATGCAATG 900
QY      901 CACCTTCTCCGAGTTTGTGTGTACTCCGACTGCGACAGCTCCCAAGTCTTGTCTTGTG 960
DB      901 CACCTTCTCCGAGTTTGTGTGTACTCCGACTGCGACAGCTCCCAAGTCTTGTCTTGTG 960
QY      961 CCCACTGCAAGTGAAGTGCATGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 1020
DB      961 CCCACTGCAAGTGAAGTGCATGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 1020
QY      1021 GGTATCCAGGAGGAGGCTGCCCCCTGGAAATATTTGTAATGACTAGGAGGTGGGGTGA 1080
DB      1021 GGTATCCAGGAGGAGGCTGCCCCCTGGAAATATTTGTAATGACTAGGAGGTGGGGTGA 1080
QY      1081 GCATCTCTCCGCTCTGCTCTGCTGCAAGAAATGGGAACAGTGTCTGCTGCTGCTGCTG 1140
DB      1081 GCATCTCTCCGCTCTGCTCTGCTGCAAGAAATGGGAACAGTGTCTGCTGCTGCTGCTG 1140
QY      1141 GCAGCATGGGAGAGGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
DB      1141 GCAGCATGGGAGAGGTGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1200
QY      1201 GTGTAGTCCCGCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
DB      1201 GTGTAGTCCCGCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1260
QY      1261 CTCTGCTCTCTGAGTCTCTCCACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
DB      1261 CTCTGCTCTCTGAGTCTCTCCACCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
QY      1321 GATCACTCAATTAACCTTAAGAAACCTCAATTAAGAAACCTCAATTAAGAAACCTCA 1377
DB      1321 GATCACTCAATTAACCTTAAGAAACCTCAATTAAGAAACCTCAATTAAGAAACCTCA 1377

RESULT 11
US-10-175-746-361
; Sequence 361, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Desforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvarioff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
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; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 361
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-918-361

Query Match      100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GACTAGTCTCTTGAGTCTGGAGAGAGAAAGCGGAGCGGAGGAGCGAAGCAGAGC 60
DB 1 GACTAGTCTCTTGAGTCTGGAGAGAGAAAGCGGAGCGGAGGAGCGAAGCAGAGC 60
QY 61 TGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
DB 61 TGGGGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY 121 CCAACTGAGAGGAGTCCGAGAGTACGAGAGCGCCCGAAGAGAGCCATGCGGAGG 180
DB 121 CCAACTGAGAGGAGTCCGAGAGTACGAGAGCGCCCGAAGAGAGCCATGCGGAGG 180
QY 181 GGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 181 GGGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
QY 241 GGTCTGCTGCTCTGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
DB 241 GGTCTGCTGCTCTGAGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 300
QY 301 CAGCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
DB 301 CAGCCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 361 CTTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
DB 361 CTTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
QY 421 AGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
DB 421 AGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 480
QY 481 GGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
DB 481 GGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY 541 CTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
DB 541 CTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 601 CGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
DB 601 CGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 660
QY 661 CCAAGTGGCTGGGGTCTACTACTTCCGCTCCATCCACCGCTCCAGCGGAGGAG 720
DB 661 CCAAGTGGCTGGGGTCTACTACTTCCGCTCCATCCACCGCTCCAGCGGAGGAG 720
QY 721 GTTGTATCTGTGAGAGATGAGGAGATTCATCTCTTCTTCCAGATTCTTGGGGG 780
DB 721 GTTGTATCTGTGAGAGATGAGGAGATTCATCTCTTCTTCCAGATTCTTGGGGG 780
QY 781 GCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
DB 781 GCCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 840
QY 841 GTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
DB 841 GTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900
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QY 901 CACCTTCGCGATTTCTGTGAGTCCGAGTGGACAGACAGCTCCCGAGTCTGTAGTG 960
DB 901 CACCTTCGCGATTTCTGTGAGTCCGAGTGGACAGACAGCTCCCGAGTCTGTAGTG 960
QY 961 CCCACTGCAAAAGTGAAGTCAATCTCTCTACTCTAGAGAGGAGGAGTGAAGTGA 1020
DB 961 CCCACTGCAAAAGTGAAGTCAATCTCTCTACTCTAGAGAGGAGGAGTGAAGTGA 1020
QY 1021 GGTCAATCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
DB 1021 GGTCAATCCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1080
QY 1081 GCACCTCCGCTCTGCTGTGGCAAGGAATGGGAAGAGGAGGAGGAGGAGGAGGAG 1140
DB 1081 GCACCTCCGCTCTGCTGTGGCAAGGAATGGGAAGAGGAGGAGGAGGAGGAGGAG 1140
QY 1141 GCAGCATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
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; Sequence 361, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3350R1C288
; CURRENT APPLICATION NUMBER: US/10/176,921
; PRIORITY FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 361
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-921-361

Query Match      100.0%; Score 1377; DB 9; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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841 GTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
841 GTGGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 900  
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; Sequence 361, Application US/10140474  
; Publication No. US20030032156A1  
GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P330R1C162  
; CURRENT APPLICATION NUMBER: US/10/140/474  
; PRIORITY FILING DATE: 2002-05-06  
; Prior Application removed - See Palm or File Wrapper  
; SEQ ID NO 361  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
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Best Local Similarity 100.0%; Pred. No. 0;  
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361 CTGGCGGGGGCGGAGTGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGAGAA 420  
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421 AGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480

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Job time : 259 secs







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 XX 01-DEC-1998; 98WO-US25108.  
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 XX 25-FEB-1998; 98US-0075945.  
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 XX  
 XX (GENENTECH INC.)  
 PA  
 PI Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;  
 PI Yuan J;  
 DR WPI; 1999-371118/31.  
 DR P-PSDB; AAY17827.  
 XX  
 XX Nucleic acids encoding PRO secreted and transmembrane proteins  
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 XX  
 XX Claim 2; Fig 20; 123pp; English.  
 PS  
 XX The present invention describes nucleic acids encoding PRO secreted and  
 CC transmembrane proteins used therapeutically. The PRO proteins have  
 CC cyostatic, anti-inflammatory, anti-proliferative and immunosuppressive  
 CC activity. The proteins and polynucleotides can be used in therapy,  
 CC identification of homologues, raising antibodies and design of probes  
 CC and primers. They can be used in a range of diseases related to proteins  
 CC that they have homology with, e.g. a PRO protein having homology to  
 CC complement proteins may be used in inflammatory responses.  
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 XX  
 XX Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;  
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 Query Match 100.0%; Score 1377; DB 20; Length 1377;  
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 Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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PD	08-JUN-2000.
PF	30-NOV-1999; 99WO-US28409.
PR	01-DEC-1998; 98MO-US25108.
PR	16-DEC-1998; 98US-0113850.
PR	22-DEC-1998; 98US-0113296.
PR	20-JUL-1999; 99US-0144758.
PR	26-JUL-1999; 99US-0145698.
PA	(GETH ) GENENTECH INC.
PI	Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;
DR	WPI: 2000-412325/35.
DR	P-PSDB: AAY71468.
PT	New composition useful for inhibiting neoplastic cell growth and for treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or their antagonists
PS	Claim 20; Fig 5; 108pp; English.
XX	The present sequence is the cDNA clone, designated as DNA40592-1242, encoding the human PRO344 polypeptide. It is isolated from human foetal lung tissue cDNA library, identified using probes based on a consensus sequence DNA33399, derived from secreted protein extracellular domain (ECD). Expressed Sequence Tag (EST). This clone is assigned ATCC deposit No: 209492. PRO344 functions as a neoplastic cell growth inhibitor and is used for treating tumours, using an effective amount of PRO655, PRO364 and PRO344. This composition is especially useful for treatment of human cancers such as breast, prostate, colon, lung, renal, ovarian and CNS, leukemia and melanoma.
XX	Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;
XX	Query Match 100.0%; Score 1377; DB 21; Length 1377;
XX	Best Local Similarity 100.0%; Pred. No. 0;
XX	Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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DB	1 GACTAGTCTCTTGAGAGTCTGGAGAGGAAAGCGAGCCGACGAGGACGAACGAGAC 60
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DB	61 TGGGTCAGCGCAGGCGAGGCGCCCTGCGCCGGGAGAAAGCGCGGGGCTTGAGCACC 120

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Db	121	CCAACTGGAGGGTCCGGAGTACGAGACGCCCCGAGAGAGGCCATGGGGAGCGCGGAGGG	180
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OY	301	CAGCCTCTGCCCCGGGGGCAACCCGGGCTTCAGGCAAGCGCGGGCCACAGTGGACGACAGG	360
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OY	1021	GGTATTCAGAGAGGGCTGGCCCCCTGGAAATTTGTGAAATCACTAGAGAGGTGGGTGGA	1080
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Db	1081	GCACCTTCGCTGCTGTGGTGGCAAGAAATGGGAAACAATGGCTGTGCTCGATCAGGTG	1140
OY	1141	GCAGCATGGGAGCAATGGCTGATTTTCTGCCAAGACAGAGAGAGTGTCTGTGCGCAA	1200
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RESULT 4  
ID AAA46907 standard; cDNA: 1377 BP.  
AC AAA46907;  
XX 03-OCT-2000 (first entry)  
XX cDNA encoding novel polypeptide PRO344.  
XX PRO201; PRO322; PRO1265; PRO344; PRO343; PRO347; PRO357;  
KW PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;  
KW tumorigenesis; cancer; neoplastic cell growth; cell proliferation; ss.  
XX Homo sapiens.  
OS  
FH Key Location/Qualifiers  
FT CDS 227..958  
FT /tag= a  
PN MO200037640-A2.  
XX 29-JUN-2000.  
PD 16-DEC-1999; 99WO-US30095.  
XX 22-DEC-1998; 98US-0113296.  
XX 08-MAR-1999; 99WO-US05028.  
PR 02-JUN-1999; 99WO-US12252.  
PR 01-SEP-1999; 99WO-US20111.  
PR 15-SEP-1999; 99WO-US21090.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 02-DEC-1999; 99WO-US28565.  
XX (GETH ) GENENTECH INC.  
PA  
PI Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;  
PI Wood WT;  
XX WPI: 2000-452188/39.  
DR P-PSDB: AAY93688.  
XX  
PT New anti-polypeptide antibody useful in the treatment and diagnosis of  
PT neoplastic cell growth and proliferation -  
XX  
PS Claim 50; Fig 9; 220pp; English.  
XX  
CC The present sequence encodes a novel human polypeptide. The  
CC specification describes novel polypeptides designated PRO201, PRO292,  
CC PRO327, PRO1265, PRO344, PRO343, PRO347, PRO357, PRO1017,  
CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in  
CC the genome of tumour cells. The polypeptides are believed to contribute  
CC to tumorigenesis. The polypeptides are useful target for the  
CC identification of certain cancers, and may act as predictors of the  
CC prognosis of tumour treatment. Antibodies against these polypeptides  
CC are useful in the treatment and diagnosis of neoplastic cell growth  
CC and proliferation in mammals.  
XX  
SO Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;

Query Match 100.0%; Score 1377; DB 21; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GACTAGTCTCTGTGAGTCTGTGAGAGAGAAAGCGAGACCGGACGAGAGCGAAGCAGAGAC 60  
Db 1 GACTAGTCTCTGTGAGTCTGTGAGAGAGAAAGCGAGACCGGACGAGAGCGAAGCAGAGAC 60  
QY 61 TGGGTTGACGCGAGGCGAGGGGGCGCTGCGCGGGGAGACAGCGGGGGCTGTGAGACCA 120  
Db 61 TGGGTTGACGCGAGGCGAGGGGGCGCTGCGCGGGGAGACAGCGGGGGCTGTGAGACCA 120  
QY 121 CCAAGTGGAGGGTCCGAGTATGCGAGCGCCCGGAGAGAGGCGATGCGGGAGCGGGAGG 180  
Db 121 CCAAGTGGAGGGTCCGAGTATGCGAGCGCCCGGAGAGAGGCGATGCGGGAGCGGGAGG 180  
QY 181 GGGAGTGGAGAGAGACCCCGGCGTCCGGGCTCCGCTGCGAGCGCTATGAGCGCACTCT 240  
Db 181 GGGAGTGGAGAGAGACCCCGGCGTCCGGGCTCCGCTGCGAGCGCTATGAGCGCACTCT 240  
QY 241 GCTCTGCTGCTCTGTGGGCTGTGGGCGCGGCTGCGCCCTGCGAGCGAACAAGATCC 300  
Db 241 GCTCTGCTGCTCTGTGGGCTGTGGGCGCGGCTGCGCCCTGCGAGCGAACAAGATCC 300  
QY 301 CAGCGTCCGCGGGGGGACCCCGGCTTCCAGAGGAGCGCGGGGCGACATGGCGAGCG 360  
Db 301 CAGCGTCCGCGGGGGGACCCCGGCTTCCAGAGGAGCGCGGGGCGACATGGCGAGCG 360  
QY 361 CTTGCGCGCGCGAGTGGCGCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGAGAGA 420  
Db 361 CTTGCGCGCGCGAGTGGCGCGCGAGCGCGCGAGCGCGCGCGCGCGCGCGAGAGA 420  
QY 421 AGCGAGGCGGAGAGCGCGGAGCTGCCGAGCTTGAGGAGACCCCGGGCGCGAGAGA 480  
Db 421 AGCGAGGCGGAGAGCGCGGAGCTGCCGAGCTTGAGGAGAGCCCGGGCGCGAGAGA 480  
QY 481 GGGCGGAGCGCGGGGGGCCACCGGGGCTGCCGGGAGTGTGCGTCCGCGATCCGC 540  
Db 481 GGGCGGAGCGCGGGGGGCCACCGGGGCTGCCGGGAGTGTGCGTCCGCGATCCGC 540  
QY 541 CTTAGCGCGCAAGCGCTCCGAGAGCGGGGCTGCTCGCGCTGAGCGACCCCTTCCCT 600  
Db 541 CTTAGCGCGCAAGCGCTCCGAGAGCGGGGCTGCTCGCGCTGAGCGACCCCTTCCCT 600  
QY 601 CGACCGGCTGCTGTGAGAGCGAGCGAGGACATTAGACCGCGTACCGGCAAGTTACTG 660  
Db 601 CGACCGGCTGCTGTGAGAGCGAGCGAGGACATTAGACCGCGTACCGGCAAGTTACTG 660  
QY 661 CCAAGTGCCTGGGGCTCTACTACTTTCGCGTCCAGTCCAGTTCAGTTCGCGGGGTG 720  
Db 661 CCAAGTGCCTGGGGCTCTACTACTTTCGCGTCCAGTTCAGTTCGCGGGGTG 720  
QY 721 GTTGTATCTGTGGAAGATGGCGAATTCATTCCTTCTTCAGTTCGCGGGGTG 780  
Db 721 GTTGTATCTGTGGAAGATGGCGAATTCATTCCTTCTTCAGTTCGCGGGGTG 780  
QY 781 GCCCAAGCAGCGTCTGTGCGGGGGGCGATGAGGCTGTGAGGAGCTGTGAGGAGCAAGT 840  
Db 781 GCCCAAGCAGCGTCTGTGCGGGGGGCGATGAGGAGCTGTGAGGAGCTGTGAGGAGCAAGT 840  
QY 841 GTGGTGCAGGTGGGTGTGGGTGACTATGATGGCATATGCGACATCAAGACAGACAG 900  
Db 841 GTGGTGCAGGTGGGTGTGGGTGACTATGATGGCATATGCGACATCAAGACAGACAG 900  
QY 901 CACCTTCCGCGAATTTCTGTGTACTGCGAGTGGCAGACGTCGCCAGTCTTGTCTTAGTG 960  
Db 901 CACCTTCCGCGAATTTCTGTGTACTGCGAGTGGCAGACGTCGCCAGTCTTGTCTTAGTG 960  
QY 961 CCCACTGCAAGTAGTCAATGCTTCACTCTCTAGAGAGAGGCTGTGAGGCTGTGACACCA 1020  
Db 961 CCCACTGCAAGTAGTCAATGCTTCACTCTCTAGAGAGAGGCTGTGAGGCTGTGACACCA 1020



Db	841	GTGGGTGACAGTGGGTGTGGGTGACTACTACATTGGCATTTGACCCAGCATCAAGACAGACAG	900
QY	901	CACCTTCGCCGATTTCTTGTTGTTGTACTCCGACTGGACAGCTCCCCAGCTTTTGCTTAGTG	960
Db	901	CACCTTCGCCGATTTCTTGTTGTTGTACTCCGACTGGACAGCTCCCCAGCTTTTGCTTAGTG	960
QY	961	CCCACTGCAAAAGTAGTCATAGCTCCTACACCTTAGAAGAGAGGTGTAGGCTGACAAACA	1020
Db	961	CCCACTGCAAAAGTAGTCATAGCTCCTACACCTTAGAAGAGAGGTGTAGGCTGACAAACA	1020
QY	1021	GGTCATCCAGAGGGCTGGCCCCCTCGAATATTGTGAATACACAGGAGGTGGGTAGAGA	1080
Db	1021	GGTCATCCAGAGGGCTGGCCCCCTCGAATATTGTGAATACACAGGAGGTGGGTAGAGA	1080
QY	1081	GCACCTCCCGCTCCGCTGCTGGCAAAAGAAATGGGAACAGTGGCTGTCTGTCATCAGGCTG	1140
Db	1081	GCACCTCCCGCTCCGCTGCTGGCAAAAGAAATGGGAACAGTGGCTGTCTGTCATCAGGCTG	1140
QY	1141	GCAGCATGGGGCAGATGGCTGGATTTCGTCCCAAGACCAGAGAGAGTGTGTGCTGGCAAA	1200
Db	1141	GCAGCATGGGGCAGATGGCTGGATTTCGTCCCAAGACCAGAGAGAGTGTGTGCTGGCAAA	1200
QY	1201	GTCGTAAGTCCCCCAGTTGCTCTTGCTGCCAGGAGCCCAAGGTGGGTGCTCTCTCTGCTG	1260
Db	1201	GTCGTAAGTCCCCCAGTTGCTCTTGCTGCCAGGAGCCCAAGGTGGGTGCTCTCTCTGCTG	1260
QY	1261	CTCTGCTCTCTCTGATGCTCTCCCAACCCCTCTGCTCTGGGGCCGGCCCTTTTCTCAGA	1320
Db	1261	CTCTGCTCTCTCTGATGCTCTCCCAACCCCTCTGCTCTGGGGCCGGCCCTTTTCTCAGA	1320
QY	1321	GATCATTCTAATAAAGCTTAGAACCTCTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1377
Db	1321	GATCATTCTAATAAAGCTTAGAACCTCTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1377

RESULT 6	
AA521428	
ID	AA521424 standard; cDNA: 1377 BP.
XX	
AC	
XX	
AA521424;	
XX	
DT	24-OCT-2001 (first entry)
XX	
DE	Human cDNA sequence encoding for PRO344 polypeptide.
XX	
KW	Human secretory and transmembrane; PRO; mammalian; cancer; lung;
KW	breast; prostate; cervical; tumour necrosis factor-alpha;
KW	cataliase; ear; proliferation; glucose free fatty acid; skeletal muscle;
KW	adipocyte; A-peptide; factor VIIa; gene therapy; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200140466-A2.
XX	
PD	07-JUN-2001.
XX	
PF	01-DEC-2000; 2000WO-US32678.
XX	
PR	01-DEC-1999; 99WO-US28301.
PR	01-DEC-1999; 99WO-US28634.
PR	02-DEC-1999; 99WO-US28551.
PR	02-DEC-1999; 99WO-US28564.
PR	02-DEC-1999; 99WO-US28565.
PR	09-DEC-1999; 99US-0170262.
PR	16-DEC-1999; 99WO-US30095.
PR	20-DEC-1999; 99WO-US30911.
PR	20-DEC-1999; 99WO-US30999.
PR	30-DEC-1999; 99WO-US31243.
PR	06-JAN-2000; 2000WO-US00277.
PR	06-JAN-2000; 2000WO-US00376.
PR	11-FEB-2000; 2000WO-US03566.
PR	18-FEB-2000; 2000WO-US04341.
PR	18-FEB-2000; 2000WO-US04342.

PR	22-FEB-2000;	2000OMO-US04414.
PR	24-FEB-2000;	2000OMO-US04914.
PR	24-FEB-2000;	2000OMO-US05004.
PR	01-MAR-2000;	2000OMO-US05601.
PR	20-MAR-2000;	2000OMO-US07377.
PR	21-MAR-2000;	2000OMO-US07532.
PR	30-MAR-2000;	2000OMO-US08439.
PR	17-MAY-2000;	2000OMO-US13705.
PR	22-MAY-2000;	2000OMO-US14042.
PR	30-MAY-2000;	2000OMO-US14941.
PR	02-JUN-2000;	2000OMO-US15264.
PR	10-NOV-2000;	2000OMO-US30873.
XX		
PA	(GETH )	GENENTECH INC.
XX		
XX	Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;	
PI	Gerritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;	
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;	
XX		
DR	WP1: 2001-408281/43.	
DR	P-PSDB; AAU12352.	
XX		
PT	Isolated, secretory and transmembrane PRO polypeptide used to detect	
PT	other PRO polypeptides, link bioactive molecules to cells expressing	
PT	PRO polypeptides, and detect the presence of mammalian tumours e.g.	
PT	lung, breast, prostate, cervical	
XX		
PS	Claim 3; Fig 361; 813pp; English.	
XX		
CC	AA521244-AA521518 encode for novel human secretory and transmembrane	
CC	PRO polypeptides. The PRO polypeptides are useful to detect other	
CC	PRO polypeptides, to link bioactive molecules to cells expressing	
CC	PRO polypeptides, to modulate biological activities of cells expressing	
CC	PRO polypeptides, and to detect the presence of mammalian lung, colon,	
CC	breast, prostate, rectal, cervical or liver tumours by comparing PRO	
CC	polypeptide expression in a cell sample to that in a control sample.	
CC	Some of the 275 sequences are also useful to stimulate the release of	
CC	tumour necrosis factor-alpha (TNF-alpha) from human blood, the	
CC	proliferation or differentiation of chondrocytes, the proliferation or	
CC	gene expression in pericyte cells, the release of proteoglycans from	
CC	cartilage, the proliferation of inner ear utricular supporting cells or	
CC	of T-lymphocytes, the release of a cytokine from peripheral blood	
CC	monocytes (PBMCs), or the proliferation of endothelial cells. Some of	
CC	the PRO polypeptides may modulate glucose or free fatty acid uptake by	
CC	skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide	
CC	to factor VIIa. The PRO polypeptides can be used in assays to identify	
CC	molecules involved in binding interactions. The polynucleotides encoding	
CC	PRO polypeptides can be used to generate probes, antisense RNA/DNA,	
CC	transgenic or knock out animals and can be used in gene therapy.	
CC		
XX		
SO	Sequence 1377 BP; 251 A; 422 C; 472 G; 232 T; 0 other;	
XX		
Query Match	100.0%;	Score 1377; DB 22; Length 1377;
Best Local Similarity	100.0%;	Pred. No. 0;
Matches 1377; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	1	GAC TAGTCTCTTGAGAGTCGTGGAGAGAGAAAGCGAGCCGGCAGAGCGAACCAGAGC 60
DB	1	GACTA GTTCTCTTGAGAGTCTGGGAGAGAGAAAGCGAGCCGGCAGAGCGAACCAGAGC 60
OY	61	TGGGGTGACGAGCAGGGGCAAGGGGGCCCTGTGGCCGGGAGAGAGCGCGGGGGCTGTGACACCA 120
DB	61	TGGGGTGACGAGCAGGGGCAAGGGGGCCCTGTGGCCGGGAGAGAGCGCGGGGGCTGTGACACCA 120
OY	121	CCAACTGAGAGGTCCTCCGAGTATGACAGCGCCCGCGAAGAGAGGCCATCGGGAGCGCGGAGGG 180
DB	121	CCAACTGAGAGGTCCTCCGAGTATGACAGCGCCCGCGAAGAGAGGCCATCGGGAGCGCGGAGGG 180
OY	181	GGGAGCTGGGAGAGAGAGCCCGGGCGTCCGGGGCTCCCGGTGTCAGAGCGCTATGAGAGCCACATCCT 240
DB	181	GGGAGCTGGGAGAGAGAGCCCGGGCGTCCGGGGCTCCCGGTGTCAGAGCGCTATGAGAGCCACATCCT 240
OY	241	CGTCTGCTGCTCTCCGTGGGGCTGTGGCGGCGGGCTCGGCCCCACATGAGAGCAACAAATCC 300

|||||  
Db 241 CGTCTCTGCTCTCTGAGCCCTGGGCGGCGTCCGCCCTGAGACGACCAAGATCCC 300  
QY 301 CAGCCTTCGCCGGGGACCCCGGCTTCCAGGACCGCGGGCCACCATGAGCAGCGG 360  
Db 301 CAGCCTTCGCCGGGGACCCCGGCTTCCAGGACCGCGGGCCACCATGAGCAGCGG 360  
QY 361 CTTCGCCGGGGCGGATGAGCCCGGACGGCGCGGCGCGCGGGGCTCCGGGAGAGA 420  
Db 361 CTTCGCCGGGGCGGATGAGCCCGGACGGCGCGGCGCGGGGCTCCGGGAGAGA 420  
QY 421 AGCGGAGGGGGGAGGGCGGAGCTGCGGGACCTTCGAGGGGAGACCCCGGGCGGAGAGA 480  
Db 421 AGCGGAGGGGGGAGGGCGGAGCTGCGGGACCTTCGAGGGGAGACCCCGGGCGGAGAGA 480  
QY 481 GGGGGAGACCCCGGGGGCCACCGGGGCTGCGGGAGATGCTCGGTCCTCCGCGATCGCG 540  
Db 481 GGGGGAGACCCCGGGGGCCACCGGGGCTGCGGGAGATGCTCGGTCCTCCGCGATCGCG 540  
QY 541 CTTCAGCGCCCAAGCGCTCCGAGACCGCGGGTCCCGCCGCTGACGACCCCTTGCCCTT 600  
Db 541 CTTCAGCGCCCAAGCGCTCCGAGACCGCGGGTCCCGCCGCTGACGACCCCTTGCCCTT 600  
QY 601 CGACCGGCTGCTGCTGTAACGACGAGGACATTAGAGCGGCTCACCGGCAAGTCCACTG 660  
Db 601 CGACCGGCTGCTGCTGTAACGAGGACATTAGAGCGGCTCACCGGCAAGTCCACTG 660  
QY 661 CCAAGTGCCTGGGGTCTACTACTTCCGCTTCATGCAACCGCTACCGGGCCAGCTGCA 720  
Db 661 CCAAGTGCCTGGGGTCTACTACTTCCGCTTCATGCAACCGCTACCGGGCCAGCTGCA 720  
QY 721 GTTTGATCTGTGTAAGAAATGCGGATCCATTGCTCTTTCTTCCAGTTTTTTCGGGGGTG 780  
Db 721 GTTTGATCTGTGTAAGAAATGCGGATCCATTGCTCTTTCTTCCAGTTTTTTCGGGGGTG 780  
QY 781 GCCCAAGCCAGCCCTCGCTCGGGGGGGCCATGCTGAGGCTGAGGACCAAGT 840  
Db 781 GCCCAAGCCAGCCCTCGCTCGGGGGGGCCATGCTGAGGCTGAGGACCAAGT 840  
QY 841 GTGGGTCAGAGTGGGTGTGGGTGACTCATTTGGCATTTATGCCAGATCAAGACAGACAG 900  
Db 841 GTGGGTCAGAGTGGGTGTGGGTGACTCATTTGGCATTTATGCCAGATCAAGACAGACAG 900  
QY 901 CACCTTCTCCGGAATTTGTGTGTAACCTGCGACAGCTCCCGACTTTTGTGTAAGT 960  
Db 901 CACCTTCTCCGGAATTTGTGTGTAACCTGCGACAGCTCCCGACTTTTGTGTAAGT 960  
QY 961 CCCACTGCAAAAGTGAAGTCTCATGCTCATCTCTAGAGGAGGGGTGAGGCTGACACCA 1020  
Db 961 CCCACTGCAAAAGTGAAGTCTCATGCTCATCTCTAGAGGAGGGGTGAGGCTGACACCA 1020  
QY 1021 GGTTCATCCAGAGAGGCTGGCCGCCCTGGAATATTTGTGAATGACTAGAGAGTGGGTAGA 1080  
Db 1021 GGTTCATCCAGAGAGGCTGGCCGCCCTGGAATATTTGTGAATGACTAGAGAGTGGGTAGA 1080  
QY 1081 GCACCTCTCCCTCTGCTGCTGCTGCGCAAGAAATGGAACAGTGGCTGTGCATCAGGCTCG 1140  
Db 1081 GCACCTCTCCCTCTGCTGCTGCTGCGCAAGAAATGGAACAGTGGCTGTGCATCAGGCTCG 1140  
QY 1141 GCAGCATAGGGGAGTGGCTGATTTCTGCCCAAGACAGAGAGATGCTGTGCTGGCAA 1200  
Db 1141 GCAGCATAGGGGAGTGGCTGATTTCTGCCCAAGACAGAGAGATGCTGTGCTGGCAA 1200  
QY 1201 GTGTAAGTCCCAAGTTGCTGTGCTCAGAGAGCCACAGGTGGGGTGTCTCTTCTGTCAG 1260  
Db 1201 GTGTAAGTCCCAAGTTGCTGTGCTCAGAGAGCCACAGGTGGGGTGTCTCTTCTGTCAG 1260  
QY 1261 CTCTGCTTCTCTGGAATCTCCCAACCCCTCTGCTCTGCGGCGCGGCTTTTCTCAGA 1320  
Db 1261 CTCTGCTTCTCTGGAATCTCCCAACCCCTCTGCTCTGCGGCGCGGCTTTTCTCAGA 1320  
QY 1321 GATCACTCAATAAAGCTAGAACCTCTATAAAAA 1377  
Db 1321 GATCACTCAATAAAGCTAGAACCTCTATAAAAA 1377

Db 1321 GATCACTCAATAAAGCTAGAACCTCTATAAAAA 1377  
RESULT 7  
AAC58626  
ID AAC58626 standard; cDNA: 1377 BP.  
XX AAC58626;  
AC  
XX 29-JAN-2001 (first entry)  
DE Human PRO344 protein UNQ303 encoding cDNA SEQ ID NO:240.  
XX  
XX Human; immune related disease; diagnosis; antiinflammatory; cardiant;  
KW dermatological; antihypertic; antineumatic; immunosuppressive;  
KW haemostatic; antithyroid; antidiabetic; noctropic; neuroprotective;  
KW antineumatic; hepatotropic; virucide; antiporistic; antiallergic;  
KW antineumatic; systemic lupus erythematosus; rheumatoid arthritis;  
KW osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;  
KW idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;  
KW systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;  
KW autoimmune thrombocytopenia; immune-mediated renal disease;  
KW demyelinating disease; hepatobiliary disease; Whipple's disease;  
KW inflammatory bowel disease; gluten-sensitive enteropathy;  
KW autoimmune disease; immune-mediated skin disease; allergic disease;  
KW immunological disease; transplantation associated disease;  
KW graft rejection; graft-versus-host-disease; ss.  
OS Homo sapiens.  
XX  
XX WO200053758-A2.  
PD 14-SEP-2000.  
XX  
PF 02-MAR-2000; 2000WO-US05841.  
XX  
PR 08-MAR-1999; 99WO-US05028.  
PR 10-MAR-1999; 99US-0123618.  
PR 12-MAR-1999; 99US-0123957.  
PR 23-MAR-1999; 99US-0125775.  
PR 12-APR-1999; 99US-0128849.  
PR 20-APR-1999; 99WO-US08615.  
PR 28-APR-1999; 99US-0131445.  
PR 04-MAY-1999; 99US-0132371.  
PR 14-MAY-1999; 99US-0134287.  
PR 02-JUN-1999; 99WO-US12252.  
PR 23-JUN-1999; 99US-0141037.  
PR 20-JUL-1999; 99US-0144758.  
PR 26-JUL-1999; 99US-0145638.  
PR 28-JUL-1999; 99US-0146222.  
PR 01-SEP-1999; 99WO-US20111.  
PR 08-SEP-1999; 99WO-US20594.  
PR 13-SEP-1999; 99WO-US20944.  
PR 15-SEP-1999; 99WO-US21090.  
PR 15-SEP-1999; 99WO-US21547.  
PR 03-OCT-1999; 99WO-US23089.  
PR 29-OCT-1999; 99US-0162506.  
PR 29-NOV-1999; 99WO-US28214.  
PR 30-NOV-1999; 99WO-US28313.  
PR 30-NOV-1999; 99WO-US28409.  
PR 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30999.  
PR 30-DEC-1999; 99WO-US31274.  
PR 05-JAN-2000; 2000WO-US00219.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.



PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX  
 PA (GENTECH) GENENTECH INC.  
 PI Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Matanabe CK, Wood WI, Yan M;  
 XX WPI: 2000-572271/53.  
 DR P-FSDB; AAB33461.  
 XX  
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 PS  
 PS Claim 23; Fig 95; 309pp; English.  
 XX  
 CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthritis,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,  
 CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 SQ Sequence 1377 BP; 251 A; 423 C; 471 G; 232 T; 0 other;  
 Query Match 96.3%; Score 1326; DB 21; Length 1377;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1376; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 421 AGCGAGGCGCGGAGGCGCGGAGCTGCGGAGACCTGAGAGGAGACCCCGGCGCGAGAGGA 480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 481 GCGGAGACCGCGCGGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 481 GCGGAGACCGCGCGGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 541 CTTGAGGCGCAAGGCGTCCGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 541 CTTGAGGCGCAAGGCGTCCGAGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 601 CGACCGGCTGCTGTGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 601 CGACCGGCTGCTGTGAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 661 CCAGGTGCTGGGGTCTACTACTTCCGCGGTCATGCGGCTACACCGGCTACCGGGCCAGCTGCA 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 661 CCAGGTGCTGGGGTCTACTACTTCCGCGGTCATGCGGCTACACCGGCTACCGGGCCAGCTGCA 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 721 GTTGTATCTGTGTAAGATGCGAATCCATTCCTCTTCCAGTTTTCGGGGGGTG 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 721 GTTGTATCTGTGTAAGATGCGAATCCATTCCTCTTCCAGTTTTCGGGGGGTG 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 781 GCCCAAGCCAGCCTCGCTCTGCGGGGGGCGCATGCTGAGAGCTGAGAGCCAGCAAGT 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 781 GCCCAAGCCAGCCTCGCTCTGCGGGGGGCGCATGCTGAGAGCTGAGAGCCAGCAAGT 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 841 GTGGGTGAGGTGGGTGGGTGGGTGACATCATTTGCGATCATGCGACATCAAGACAGACAG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 841 GTGGGTGAGGTGGGTGGGTGGGTGACATCATTTGCGATCATGCGACATCAAGACAGACAG 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 901 CACCTTCCTCCGATTTTGGGTGCTACTCCGACTGCGACAGCTCCCGAGCTTGTGTTAGTG 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 901 CACCTTCCTCCGATTTTGGGTGCTACTCCGACTGCGACAGCTCCCGAGCTTGTGTTAGTG 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 961 CCCACTGCAAGTAGCTCATGCTCTCATCTCTGAAAGAGAGGAGGTGAGGCTGCAACCA 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 961 CCCACTGCAAGTAGCTCATGCTCTCATCTCTGAAAGAGAGGAGGTGAGGCTGCAACCA 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1021 GGTATATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 1021 GGTATATCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1081 GCACCTCTCCGCTGCTGCTGCTGCTGCAAGAGATGGAACAGTGGCTCTGCTGATGAGTGTG 1140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 1081 GCACCTCTCCGCTGCTGCTGCTGCTGCAAGAGATGGAACAGTGGCTCTGCTGATGAGTGTG 1140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1141 GCACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 1141 GCACATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1201 GTGTAAGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 1201 GTGTAAGTCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1261 CTTGCTCTCTCTGATGATCTCCCAACCCCTCTGCTCTGAGGCGGCGCTTTTCTCAGA 1320  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 1261 CTTGCTCTCTCTGATGATCTCCCAACCCCTCTGCTCTGAGGCGGCGCTTTTCTCAGA 1320  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 1321 GATCACTCAATTAACCTTAAGAACCTCTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1377  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 1321 GATCACTCAATTAACCTTAAGAACCTCTATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1377  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 RESULT 8  
 AAX24684  
 ID AAX24684 standard; cDNA; 1347 BP.  
 XX  
 XX AAX24684;  
 AC  
 XX 21-JUN-1999 (first entry)  
 DT  
 XX Human adipocyte-specific protein zs1g39 cDNA.  
 DE

KW	Adipocyte-specific protein; zslg39; human; fatty acid metabolism;
KW	energy balance; nutrition; antimicrobial; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	198..929
FT	/tag= a
FT	sig_peptide
FT	198..251
FT	/tag= b
FT	/note= "alternatively nucleotides 198-242"
FT	mat_peptide
FT	252..926
FT	/tag= c
FT	/note= "alternatively nucleotides 243-926"
XX	
PX	WO9910492-A1.
PD	04-MAR-1999.
XX	
PE	26-AUG-1998; 98WO-US17724.
XX	
PR	26-AUG-1997; 97US-0056983.
PA	(ZIMO ) ZYMOGENETICS INC.
PI	Humes JM, Shepard FO;
PI	WPI; 1999-204665/17.
DR	P-PSDB; AAM97984.
XX	
PT	Zslg39 protein - used to modulate fatty acid metabolism
PS	Claim 16; 109-111; 132pp; English.
XX	
CC	This isolated polynucleotide encodes human adipocyte-specific
CC	protein zslg39 (AAM97984). Claimed polynucleotides comprise
CC	nucleotides 243-962, 252-962, 285-482, 285-485, 285-485, 285-488,
CC	285-491, 285-491, 491-926 of this isolated polynucleotide.
CC	Novel zslg39 polypeptides were initially identified by querying an
CC	EST database for secretory signal sequences characterised by an
CC	upstream methionine start site, a hydrophobic region of approximately
CC	13 amino acids and a cleavage site. A single EST sequence was
CC	discovered, and the novel polypeptide encoded by the full-length
CC	cDNA allowed the identification of a homologue relationship with
CC	adipocyte complement related protein Acrp30 and adipocyte secreted
CC	protein apml. A full-length clone was obtained from a lung tissue
CC	library. The zslg39 gene maps to the 11q23.3 region. Expression
CC	vectors, cultured cells and a method of producing zslg39 polypeptide
CC	are claimed, as well as probes and primers (useful in diagnostic
CC	applications), and a method for modulating free fatty acid
CC	metabolism by administering a zslg39 polypeptide. The zslg39
CC	polypeptide may also be used in organ preservation, for
CC	cryopreservation, for surgical pretreatment to prevent injury due
CC	to ischaemia and/or inflammation, and as an antimicrobial agent,
CC	promoting lysis or phagocytosis of infectious agents.
XX	
SQ	Sequence 1347 BP: 235 A; 421 C; 465 G; 226 T; 0 other:
Query Match	94.8%; Score 1305; DB 20; Length 1347;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1305; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	AGGAGCAACACAGACTGTGGGTGCAGCGCAGAGGCGGGGCCCTTGGCCGGGAGAAGCG 103
DB	15 AGGAGCAACACAGACTGTGGGTGCAGCGCAGAGGCGGGGCCCTTGGCCGGGAGAAGCG 74
OY	CGGGGCGTGAGACACACCACAATGTGAGGGTCGCGAGTAGCAGCGCCCCCGAAGAGAGCCA 163
DB	75 CGGGGCGTGAGACACACCACAATGTGAGGGTCGCGAGTAGCAGCGCCCCCGAAGAGAGCCA 134
OY	TGGGGGAACCGGGAGGGGGAACTGCGAAGAGACCCCAGCGTCCGGGCTCCGGGTCCACAC 223

[illegible]





DE Human secreted protein related coding sequence SEQ ID NO: 105.  
 XX Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;  
 KM INTERCEPT 258; coronary disorder; olfactory disorder;  
 KM neurological disorder; pulmonary disorder; immunological disorder;  
 KM developmental disorder; kidney disorder; ss.  
 OS Homo sapiens.  
 XX MO200078808-A1.  
 XX PD 28-DEC-2000.  
 XX PF 19-JUN-2000; 2000MO-US16883.  
 XX PR 18-JUN-1999; 99US-0336536.  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX Leiby KR, McKay C, Bossone S;  
 XX WPI; 2001-050109/06.  
 XX DR New nucleic acids for treating diseases and disorders, e.g.  
 XX PT atherosclerosis, infection, autoimmune diseases, obesity, ear  
 XX PT disorders, brain disorders, tumors, diabetes, arthritis, multiple  
 XX PT sclerosis and asthma -  
 XX PS Disclosure: Page 272; 332pp; English.  
 XX CC The present invention provides the protein and coding sequences of the  
 CC human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,  
 CC TANGO 281 and INTERCEPT 258. These are useful in the treatment of  
 CC coronary, pulmonary, olfactory, immunological, neurological,  
 CC developmental and kidney disorders.  
 XX SQ Sequence 1338 BP; 229 A; 422 C; 460 G; 227 T; 0 other;  
 XX  
 Query Match 77.6%; Score 1068; DB 22; Length 1338;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1288; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 537 CGCCTTACGCGCAAGCGCTCCGAGAGCGGGGCTCTCCGCGCTGTGACGACCCCTTGC 596  
 DB 497 CGGCCTTACGCGCGCAAGCGCTCCGAGAGCGGGGCTCTCCGCGCTGTGACGACCCCTTGC 556  
 QY 597 CCTTCGACCGCGCTGTGTGAACGAGCGAGACATTAACGAGCGCGCTCACCGGCAAGTTCA 656  
 DB 557 CCTTCGACCGCGCTGTGTGAACGAGCGAGACATTAACGAGCGCGCTCACCGGCAAGTTCA 616  
 QY 657 CCTGCAGGTGCTGGGGTCTACTTCTGCGCTGATGACCGCTCTACCGGGCGACGC 716  
 DB 617 CCTGCAGGTGCTGGGGTCTACTTCTGCGCTGATGACCGCTCTACCGGGCGACGC 676  
 QY 717 TGCAGTTGATCTGTGAAGAAATGCGAATCATTCGCTCTTCTTCCAGTTTTCGGGG 776  
 DB 677 TGCAGTTGATCTGTGAAGAAATGCGAATCATTCGCTCTTCTTCCAGTTTTCGGGG 736  
 QY 777 GGTGGCCCAAGCGACCTCTGCTCTGCGGGGGGGCCATGCTGAGGCTGAGGCTGAGGAC 836  
 DB 737 GGTGGCCCAAGCGACCTCTGCTCTGCGGGGGGGCCATGCTGAGGCTGAGGCTGAGGAC 796  
 QY 837 AAGTGTGGGTGAGGTGGGTGTGGGTGACTATATGCAATATGCAATATGCAATATGCAAT 896  
 DB 797 AAGTGTGGGTGAGGTGGGTGTGGGTGACTATATGCAATATGCAATATGCAATATGCAAT 856  
 QY 897 ACAGACCTTCTCCGAAATTTCTGCTGTAATCTCCGATGCGACAGCTCCGAGCTTGTGCT 956  
 DB 857 ACAGACCTTCTCCGAAATTTCTGCTGTAATCTCCGATGCGACAGCTCCGAGCTTGTGCT 916  
 QY 957 AGTGCCCAATGCAAGTGAAGTCAATCTCACTCTCTAGAAAGAGGAGGTGTGAGGCTGACA 1016  
 DB 917 AGTGCCCAATGCAAGTGAAGTCAATCTCACTCTCTAGAAAGAGGAGGTGTGAGGCTGACA 976  
 QY 1017 ACCAGTATCTCAGAGAGGCTGGCCCCCTGGAATATGTGAATACATAGGAGGTGGGG 1076  
 DB 977 ACCAGTATCTCAGAGAGGCTGGCCCCCTGGAATATGTGAATACATAGGAGGTGGGG 1036  
 QY 1077 TAGACACTCTCCGCTCTGCTGCTGCAAGAAATGGAACAGTGGCTGCTGCAATCAG 1136  
 DB 1037 TAGACACTCTCCGCTCTGCTGCTGCAAGAAATGGAACAGTGGCTGCTGCAATCAG 1096  
 QY 1137 TCTGACAGATGGGCAAGTGGCTGATTTCTGCCAAGACGAGAGTGTGCTGTGCTG 1196  
 DB 1097 TCTGACAGATGGGCAAGTGGCTGATTTCTGCCAAGACGAGAGTGTGCTGTGCTG 1156  
 QY 1197 GCAAGTGAAGTCCCGCAAGTCTCTGCTGCTGCAAGAGCCACGCTGGGGTGTCTTCT 1256  
 DB 1157 GCAAGTGAAGTCCCGCAAGTCTCTGCTGCTGCAAGAGCCACGCTGGGGTGTCTTCT 1216  
 QY 1257 GGTCTCTGCTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGAT 1316  
 DB 1217 GGTCTCTGCTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGATCTCTGAT 1276  
 QY 1317 CAGAGATCACTCAATTAACCTTAAGAACCTTC 1347  
 DB 1277 CAGAGATCACTCAATTAACCTTAAGAACCTTC 1307

RESULT 12  
 AAF45000 standard; CDNA; 1338 BP.  
 AAF45000;  
 28-MAR-2001. (first entry)  
 Human secreted protein related coding sequence SEQ ID NO: 107.  
 DE Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;  
 KM INTERCEPT 258; coronary disorder; olfactory disorder;  
 KM neurological disorder; pulmonary disorder; immunological disorder;  
 KM developmental disorder; kidney disorder; ss.  
 XX







PR	08-NOV-2000;	2000US-247505P
PR	09-NOV-2000;	2000US-2486642P
PR	16-NOV-2000;	2000US-249824P
PR	21-NOV-2000;	2000US-252824P
PR	08-DEC-2000;	2000US-254305P
PR	18-DEC-2000;	2000US-256448P
XX		
PA	(INCYTE -) INCYTE GENOMICS INC.	
XX		
PI	Yue H, Yao MG, Gandhi AR, Baughn MR, Swarnakar A, Walla NK;	
PI	Sanjanmalwa M, Thornton M, Elliott VS, Lu Y, Gietzen KJ, Burford N;	
PI	Ding L, Hatfield AA, Tang YT, Bandman O, Warren RC, Honchell CD;	
PI	Lu DAM, Thangavelu K, Lee S, Xu Y, Yang J, Lai PG, Tran B;	
PI	Ison CH, Duggan BM, Sapperstein SK;	
XX		
XX	WPI; 2002-519296/55.	
DR	P-PSDB; AAO21663.	
XX		
PT	Human secreted proteins and polynucleotides for diagnosing, treating or	
PT	preventing disorders of cell proliferative, cardiovascular,	
PT	developmental, neurological and autoimmune/inflammatory disorders -	
XX		
XX	Claim 5; Page 194-195; 229pp; English.	

CC The invention relates to an isolated human secreted protein (SCP)  
CC polypeptide from 63 fully defined protein sequences given in the  
CC specification. The polypeptide is useful for the diagnosing/treating of a  
CC disease with decreased/overexpression of SCP. Examples of disorders  
CC associated with abnormal expression of SCP include a cell proliferative  
CC disorder e.g. arteriosclerosis, cancers; autoimmune/inflammatory  
CC disorder, AIDS, allergies, anaemia, asthma; cardiovascular disease e.g.  
CC congestive heart failure, ischemic heart disease; developmental disorder  
CC e.g. renal tubular acidosis, hypothyroidism; neurological disorder e.g.  
CC Alzheimer's disease, dementia, Parkinson's disease, epilepsy or stroke.  
CC The SCP polynucleotide and polypeptide are further useful for analysing  
CC the proteome of a tissue or a cell type. The polynucleotide is useful for  
CC creating knockin humanised animals (pigs) or transgenic animals (mice or  
CC rats) to model human disease, and for somatic or germline gene therapy,  
CC and further for generating hybridisation probes useful in mapping the  
CC naturally occurring genomic sequence. This polynucleotide sequence  
CC represents the DNA of a human secreted protein of the invention.

50 Sequence 3248 BP; 565 A; 1058 C; 946 G; 679 T; 0 other;

Query Match 912:	66.2%	Score 912:	DB 24;	Length 3248;
Best Local Similarity	100.0%	Pred. Nc.	0;	
Matches 912, Conservative	0;	Mismatches	0;	Gaps 0;

QY	437	CCGGGAGCTGCCGGGAACTCCGAGGGGAGACCCGGGGCCGGAGGAGAGGCGGGACCCGGGGG	496
Db	2329	CCGGGAGCTGCCGGGAACTCCGAGGGGAGACCCGGGGCCGGAGGAGAGGCGGGACCCGGGGG	2388
QY	497	CCGACCGGGGCTGCGCGGGGAGTGCCTGCAGTCCGATCCGACTTCCAGCGCCAAAGGC	556
Db	2389	CCGACCGGGGCTGCGCGGGGAGTGCCTGCAGTCCGATCCGACTTCCAGCGCCAAAGGC	2448
QY	557	TCCGAGAGCCGGGTCCTCCGCGCTCTGACGCACCCCTTGCCCTTGACACCGCGTGTGGTG	616
Db	2449	TCCGAGAGCCGGGTCCTCCGCGCTCTGACGCACCCCTTGCCCTTGACACCGCGTGTGGTG	2508
QY	617	AACGACGAGGACATTAGACAGCCGCTACCGGGCAAGTTCACCTGCGAGAGTGCCTGGGTC	676
Db	2509	AACGACGAGGACATTAGACAGCCGCTACCGGGCAAGTTCACCTGCGAGAGTGCCTGGGTC	2568
QY	677	TACTACTTCGCGCGTCAATGACCAACCGTCCACCGGGGACCTCGACGTTTGATCTGGTAG	736
Db	2569	TACTACTTCGCGCGTCAATGACCAACCGTCCACCGGGGACCTCGACGTTTGATCTGGTAG	2628
QY	737	AATGGCAATTCATTCGCTCTTCTTCACAGTTTTCGGGGGGGTGGCCCAACCAACGCTCG	796
Db	2629	AATGGCAATTCATTCGCTCTTCTTCACAGTTTTCGGGGGGGTGGCCCAACCAACGCTCG	2688
QY	797	CTCTCGGGGGGGGCGCAATGTAAGGCTTGAGCCTTAGAGCAACCAATGTGGGTCTAGGTGGT	856

Db	2669	CTCTCGGGGGGGGCATGTGAGGCTGAGGCTGAGGACCAAGTGTGGGTGCAGGTGGT	2748
QY	857	GTGGGTGACTACATTTGGCATCTATGCCAGCATCAAGACAGACAGCACTTCTCCGATT	916
Db	2749	GTGGGTGACTACATTTGGCATCTATGCCAGCATCAAGACAGACAGCACTTCTCCGATT	2808
QY	917	CTGGGTGCTCCGACTGGCAGCGTCCCACGCTTTTGCTTGTAGTGCCCACTGCAAAGTGAG	976
Db	2809	CTGGGTGCTCCGACTGGCAGCGTCCCACGCTTTTGCTTGTAGTGCCCACTGCAAAGTGAG	2868
QY	977	CTCATGCTCTCACTCTAGAAAGAGGGTGTAGGCTGACAAACGAGTCATTCAGAGAGGC	1036
Db	2869	CTCATGCTCTCACTCTAGAAAGAGGGTGTAGGCTGACAAACGAGTCATTCAGAGAGGC	2928
QY	1037	TGGCCCCCTGGAAATTTGTGAATGACTAGGGAGGTGGGATGAGCACTCCGTCCTGC	1096
Db	2929	TGGCCCCCTGGAAATTTGTGAATGACTAGGGAGGTGGGATGAGCACTCCGTCCTGC	2988
QY	1097	TGCTGGCAGAAATGGGAAAGTAGTGGCTGTGCGCATCAGTCTGGCAGCATGGGGCAGTG	1156
Db	2989	TGCTGGCAGAAATGGGAAAGTAGTGGCTGTGCGCATCAGTCTGGCAGCATGGGGCAGTG	3048
QY	1157	GCTGGATTTCTGCCAAGACCCAGAGAGTGTGCTGTGCTGGCAAGTGAATGCCCCAGT	1216
Db	3049	GCTGGATTTCTGCCAAGACCCAGAGAGTGTGCTGTGCTGGCAAGTGAATGCCCCAGT	3108
QY	1217	TGCTGTGGTCCAGAGGCCACAGTGGGGTGTCTCTTCGCGTCCCTGCTGGTCTCTGGAT	1276
Db	3109	TGCTGTGGTCCAGAGGCCACAGTGGGGTGTCTCTTCGCGTCCCTGCTGGTCTCTGGAT	3168
QY	1277	CTCTCCCAACCCCTCTGTGCTCTGTGGGGCGGGCCCTTTCTCAGAGATCACTCAATAAAC	1336
Db	3169	CTCTCCCAACCCCTCTGTGCTCTGTGGGGCGGGCCCTTTCTCAGAGATCACTCAATAAAC	3228
QY	1337	TAAAGACCTCA 1348	
Db	3229	TAAAGACCTCA 3240	

## RESULT 15

ID AAS62228 standard; cDNA; 764 BP.

AC AAS62228;

DT 14-FEB-2002 (first entry)

DE CDNA sequence #15 encoding novel human secreted protein.

KM Human secreted protein; hyperproliferative disorder; autoimmune disorder;  
KM immune deficiency disorder; blood disorder; inflammatory disorder;  
KM infectious disorder; gene therapy; antimicrobial; hepatotropic;  
KM immunosuppressive; antineumatic; ss.

OS Homo sapiens.

PN WO200177291-A2.

PD 18-OCT-2001.

PF 29-MAR-2001; 2001WO-US10485.  
yy

PR 06-APR-2000; 2000US-195604P.  
XY

PA (GEMY ) GENETICS INST INC.  
XX

PI Wong CG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;  
PI Culbertson V, Garbarino TD.

DR WPI; 2002-010900/01.

PT New polynucleotides encoding secreted proteins useful for treating e.g.



PT asthma, HIV and Crohn's disease -  
 XX  
 PS Claim 1; Page 79; 391pp; English.  
 CC The present invention relates to the isolation of novel cDNA sequences  
 CC which encode human secreted proteins. The cDNA sequences have been  
 CC derived from a variety of human tissues. The invention also provides  
 CC a method for producing proteins from these polynucleotide sequences.  
 CC The proteins are useful for identifying compounds that modulate their  
 CC activity and production, and the cell is also useful for identifying  
 CC compounds that modulate expression of the polynucleotide sequences  
 CC encoding the secreted proteins. The sequences of the invention are  
 CC useful for treating diseases such as hyperproliferative disorders  
 CC (e.g. cancer), immune deficiency disorders (e.g. severe combined  
 CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple  
 CC sclerosis), blood disorders (e.g. thrombocytopenia), inflammatory  
 CC disorders (e.g. arthritis) and infectious disorders (e.g. hepatitis).  
 CC The polynucleotide sequences of the invention are also useful in gene  
 CC therapy. AAS62214-AAS62838 represent the cDNA sequences of the  
 CC invention that encode for novel human secreted proteins.  
 XX  
 SO Sequence 764 BP; 136 A; 225 C; 229 G; 174 T; 0 other;

Query Match 55.4%; Score 763; DB 24; Length 764;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-275;  
 Matches 763; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 585 ACGACCCCTTGCCTTGACCGCGTGTGTAACGAGACGACATTACGACGCCCTCA 644  
 DB 1 ACGGACCCCTTGCCTTGACCGCGTGTGTAACGAGACGACATTACGACGCCCTCA 60  
 QY 645 CCGGCAAGTTACCTGCGAGGTGGGTGCTACTACTTCCCGCTCATCCACCGCT 704  
 DB 61 CCGGCAAGTTACCTGCGAGGTGGGTGCTACTACTTCCCGCTCATCCACCGCT 120  
 QY 705 ACCGGGCCAGCCCTGCAGTTGATGTAAGAAATGGCGAATTCCTTTCTTCC 764  
 DB 121 ACCGGGCCAGCCCTGCAGTTGATGTAAGAAATGGCGAATTCCTTTCTTCC 180  
 QY 765 AGTTTTTGGGGGGTGGCCCAAGCCAGCTCTCGGGGGGGCCATGGTAGGCTGG 824  
 DB 181 AGTTTTTGGGGGGTGGCCCAAGCCAGCTCTCGGGGGGGCCATGGTAGGCTGG 240  
 QY 825 AGCTTAGAGACCAAGTGGGTGAGGTGGGTGAGTACATTTGGCATTTATGCA 884  
 DB 241 AGCTTAGAGACCAAGTGGGTGAGGTGGGTGAGTACATTTGGCATTTATGCA 300  
 QY 885 GCATCAAGACAGACAGCACTTCTCCGATTTCTGCTGTAATCGACTGCGACAGCTCC 944  
 DB 301 GCATCAAGACAGACAGCACTTCTCCGATTTCTGCTGTAATCGACTGCGACAGCTCC 360  
 QY 945 CAGTCTTTGCTTACTGCTGCAATGAGTCAATGCTCTCACTCTAGAGAGGCT 1004  
 DB 361 CAGTCTTTGCTTACTGCTGCAATGAGTCAATGCTCTCACTCTAGAGAGGCT 420  
 QY 1005 GTGAGGCTGACACACAGGTATCCAGAGGGCTGGCCCCCTGGAAATTTGTAATGACT 1064  
 DB 421 GTGAGGCTGACACACAGGTATCCAGAGGGCTGGCCCCCTGGAAATTTGTAATGACT 480  
 QY 1065 AGGGAGGTGGGTAGAGCACTCTCCGCTCTCTGCTGCAAGAAATGGGAACAGTGCTG 1124  
 DB 481 AGGGAGGTGGGTAGAGCACTCTCCGCTCTCTGCTGCAAGAAATGGGAACAGTGCTG 540  
 QY 1125 TCTGGGATCAGGCTGCGAGCATGGGGCAGTGGCTGATTTCTGCCAAGACAGAGGAG 1184  
 DB 541 TCTGGGATCAGGCTGCGAGCATGGGGCAGTGGCTGATTTCTGCCAAGACAGAGGAG 600  
 QY 1185 TGTGCTGTGCTGGAAGTGAAGTCCCAAGTGTGCTGCTGCAAGAGCCACAGTGGGG 1244  
 DB 601 TGTGCTGTGCTGGAAGTGAAGTCCCAAGTGTGCTGCTGCAAGAGCCACAGTGGGG 660  
 QY 1245 TGTCTCTCTCTGCTGCTCTCTCTCTGATTCCTCCACCCCTCTGCTCTGAGGAGC 1304

DB 661 TGTCTCTCTCTGCTGCTCTCTCTCTGATTCCTCCACCCCTCTGCTCTGAGGAGC 720  
 QY 1305 CGGCCCTTTCTCAGAGATCACTCAATTAACCTTAAGAACCTC 1347  
 DB 721 CGGCCCTTTCTCAGAGATCACTCAATTAACCTTAAGAACCTC 763

Search completed: June 21, 2003, 12:53:40  
 Job time : 373 secs

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## OM nucleic - nucleic search, using sw model

Run on: June 21, 2003, 11:35:55 ; Search time 3716 Seconds

(without alignments)  
10784.328 Million cell updates/sec

Title: US-09-944-944-41

Perfect score: 1377  
Sequence: 1 gactagtcctcttgagctc.....aaaaaaaaaaaaaaaaa 1377

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

GenEmbl:\*  
1: gb\_da:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_da:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_mus:\*  
34: em\_htg\_pln:\*  
35: em\_htg\_rtd:\*  
36: em\_htg\_mam:\*  
37: em\_htg\_vrt:\*  
38: em\_sy:\*  
39: em\_htgo\_hum:\*  
40: em\_htgo\_mus:\*  
41: em\_htgo\_other:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1377	100.0	1377	6	AX464228
2	1305	94.8	1337	6	AF329841
3	1305	94.8	1347	6	AR138193
4	1136	82.5	1370	9	BC029485
5	1050	76.3	1068	9	HSB009283
6	908	65.9	191362	9	AP003396
7	908	65.9	219574	9	AP002956
8	736	53.4	182429	2	AP001557
9	562	40.8	198902	2	AP001156
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## ALIGNMENTS

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LOCUS  
DEFINITION Sequence 361 from Patent W00140466.  
ACCESSION AX464228  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
Baker, K.P., Beresini, M., DeForge, L., Desnoyers, L., Filvaroff, E.,  
Gao, W.O., Gerlitsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,  
Sherwood, S., Smith, Y., Stewart, T.A., Tamas, D., Watanabe, C.K.,

Pred. No. is the number of results predicted by chance to have a



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ORGANISM Unknown.  
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AUTHORS Sheppard, P.O. and Humes, J.M.  
TITLE Adipocyte-specific protein homologs  
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location/Qualifiers  
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ORGANISM Homo sapiens.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 1370)
JOURNAL Direct Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: gcgaps-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcdexall.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
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 REFERENCE 1  
 Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,  
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 Published Only in Database (2002)  
 2 (bases 1 to 191362)  
 Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P.,  
 Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.  
 Direct Submission  
 Submitted (12-MAR-2001) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suenho-chou, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9111. Fax: 81-45-503-9170  
 This work was done in collaboration with Aral, Y., Kubo, T. and  
 Ohki, M.  
 National Cancer Center Research Institute  
 Cancer Genomic Division  
 5-1-1, Tsukiji, Chuo-ku, Tokyo, JAPAN  
 zip: 104-0045  
 phone: 81-3-3542-2511 ex 4752, fax: 81-3-3542-0688 e-mail:  
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OY	1220	TCTGCTCAGAGAGCCACGCTGGGGTGTCTCTCTCTGCTGCTCTGCTCTGCTGATCT	1279
Db	5602	TCTGCTCAGAGAGCCACGCTGGGGTGTCTCTCTCTGCTGCTCTGCTCTGCTGATCT	5543
OY	1280	CCCCACCCCCCTGCTGCTGCTGGGGCGGGCCCTTTTCAGAGATCAGTCAATTAACCTAA	1339
Db	5542	CCCCACCCCCCTGCTGCTGCTGGGGCGGGCCCTTTTCAGAGATCAGTCAATTAACCTAA	5483
OY	1340	GAACCTC 1347	
Db	5482	GAACCTC 5475	
RESULT 7	AP002956/C	219574 bp DNA linear PRI 15-AUG-2002	
LOCUS	AP002956/C	Homo sapiens genomic DNA, chromosome 11q clone:RI105H09, complete	
DEFINITION	sequence.		
ACCESSION	AP002956		
VERSION	AP002956.1	GI:22255355	
KEYWORDS	HTG.		
SOURCE	Homo sapiens DNA, clone:RI105H09.		
ORGANISM	Homo sapiens		
REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
REFERENCE	2 (bases 1 to 219574)		
AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
REFERENCE	2 (bases 1 to 219574)		
AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
REFERENCE	2 (bases 1 to 219574)		
AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
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AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
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AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
REFERENCE	2 (bases 1 to 219574)		
AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
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AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
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AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
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AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
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AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
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TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
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AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
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AUTHORS	Hattori,M., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T.,		
TITLE	1-7-22 Suehito-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan		
JOURNAL	(E-mail:hattori@esc.riken.go.jp, url:http://hgp.gsc.riken.go.jp/,		
REFERENCE	2 (bases 1 to 219574)		

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zip: 104-0045
phone: +81-3-3542-2511 ex4752, fax: +81-3-3542-0688 e-mail:
yara@enc.go.jp.
FEATURES
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        /db_xref="taxon:9606"
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Matches 908; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      980 ATGCTCTCACTCCTTAAGGAAGAGAGGAGTGTGAGGCTGACAAACAGGTCACTCCAGAGGGCTGG 1039
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 OY 1340 GAACCCCTC 1347  
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RESULT 8  
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 DEFINITION Homo sapiens chromosome 11 clone RP11-680A7 map 11q23, WORKING  
 ACCESSION AP001557  
 VERSION AP001557.3 GI:11094164  
 KEYWORDS HTG: HTGS PHASE1; HTGS DRAFT.  
 SOURCE Homo sapiens DNA, clone:RP11-680A7.  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 182429)  
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 Homo sapiens 182,429 genomic DNA of 11q23  
 2 (bases 1 to 182429)  
 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,  
 Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 Direct Submission  
 Submitted (29-MAR-2000) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail:hattori@gsc.riken.go.jp, URL:http://hqp.gsc.riken.go.jp/,  
 Tel:81-45-503-9111, Fax:81-45-503-9170)  
 On Nov 3, 2000 this sequence version replaced gi:8117391.

COMMENT  
 ----- Genome Center  
 Center: RIKEN Genomic Sciences Center(GSC)  
 Center code: RIKEN  
 Web site: http://hqp.gsc.riken.go.jp/  
 Contact: hattori@gsc.riken.go.jp  
 ----- Project Information  
 Center project name: Humdrat11  
 Center clone name: RP11-680A7  
 ----- Summary Statistics  
 Sequencing vector: PCR products; 100% of reads  
 Chemistry: Dye-terminator ET-amersham; 100% of reads  
 Assembly program: Phrap; version 0.990329  
 Consensus quality: 175597 bases at least Q40  
 Consensus quality: 178555 bases at least Q30  
 Consensus quality: 179768 bases at least Q20  
 Insert size: 180429; sum-of-contigs  
 Quality coverage: 9.01x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of  
 21 contigs. The true order of the pieces is not known and their  
 order in this sequence record is arbitrary. Gaps between the  
 contigs are represented as runs 'N', but the exact sizes of the gaps  
 are unknown. This record will be updated with the finished sequence  
 as soon as it is available and the accession number will be  
 preserved

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 30208 30107 contig of 30107 bp in length  
 54357 contig of 24150 bp in length  
 54458 69839 contig of 15382 bp in length  
 69940 84048 contig of 14109 bp in length  
 84149 95177 contig of 11029 bp in length  
 95278 107763 contig of 12486 bp in length  
 107864 119057 contig of 11194 bp in length  
 119158 128134 contig of 8977 bp in length  
 128235 136903 contig of 8669 bp in length  
 137004 145887 contig of 8884 bp in length  
 145988 153199 contig of 7212 bp in length  
 153200 159565 contig of 6266 bp in length  
 159566 163580 contig of 3915 bp in length  
 163581 163680 contig of 100 bp in length  
 163681 165152 contig of 1472 bp in length  
 165153 165252 contig of 100 bp in length  
 165253 166901 contig of 1649 bp in length  
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 167002 170460 contig of 3459 bp in length  
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DRAFT SEQUENCE, 42 unordered pieces.
ACCESSION AP001156
VERSION   AP001156.2 GI:8118724
KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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          Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
          Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
          Homo sapiens 198,902 genomic DNA of 11q23
          Published only in Database (2000)
          2 (bases 1 to 198902)
          Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
          Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
          Direct Submission
          Submitted (10-FEB-2000) Masahira Hattori, The Institute of Physical
          and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
          Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
          Japan (E-mail:hattori@gsc.riken.go.jp,
          URL:http://hnp.gsc.riken.go.jp/, Tel:81-42-778-9923,
          Fax:81-42-778-9924)
          On May 31, 2000 this sequence version replaced gi:6997842.
COMMENT
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hnp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: Humpdraft11
Center clone name: Rpl11-657A24
----- Summary Statistics
Sequencing Vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329

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Consensus quality: 171788 bases at least Q40  
 Consensus quality: 184443 bases at least Q30  
 Consensus quality: 191295 bases at least Q20  
 Insert size: 194802: sum-of-contigs  
 Quality coverage: 4.12x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 42 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

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 20728 31817 contig of 11090 bp in length  
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 41232 49745 contig of 8514 bp in length  
 49846 59457 contig of 9612 bp in length  
 59358 66804 contig of 7247 bp in length  
 66905 73970 contig of 7066 bp in length  
 74071 81007 contig of 6937 bp in length  
 81008 87320 contig of 6213 bp in length  
 87421 93250 contig of 5830 bp in length  
 93251 97965 contig of 4615 bp in length  
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 98066 102941: contig of 4876 bp in length  
 102942 103041: gap of 100 bp  
 103042 109017: contig of 5976 bp in length  
 109018 109117: gap of 100 bp  
 109118 113391: contig of 4274 bp in length  
 113392 113491: gap of 100 bp  
 113492 118783: contig of 5292 bp in length  
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 169852 172048: contig of 2097 bp in length  
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 175433 177914: contig of 2482 bp in length  
 177915 178014: gap of 100 bp  
 178015 179875: contig of 1861 bp in length  
 179876 179975: gap of 100 bp  
 179976 181604: contig of 1629 bp in length  
 181605 181704: gap of 100 bp  
 181705 183951: contig of 2247 bp in length  
 183952 184051: gap of 100 bp  
 184052 185927: contig of 1876 bp in length  
 185928 186027: gap of 100 bp  
 186028 187870: contig of 1843 bp in length  
 187871 187970: gap of 100 bp  
 187971 189591: contig of 1621 bp in length  
 189592 189691: gap of 100 bp  
 189692 191169: contig of 1478 bp in length  
 191170 191269: gap of 100 bp  
 191270 192527: contig of 1258 bp in length  
 192528 192627: gap of 100 bp  
 192628 194288: contig of 1661 bp in length  
 194289 194388: gap of 100 bp  
 194389 195658: contig of 1270 bp in length  
 195659 195758: gap of 100 bp  
 195759 197707: contig of 1949 bp in length  
 197708 197807: gap of 100 bp

Sequence updated (26-May-2000).

NOTE: This is a 'working draft' sequence. It currently consists of 42 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 20627: contig of 20627 bp in length  
 20628 20727: gap of 100 bp  
 20728 31817: contig of 11090 bp in length  
 31818 31917: gap of 100 bp  
 31918 41131: contig of 9214 bp in length  
 41132 41231: gap of 100 bp  
 41232 49745: contig of 8514 bp in length  
 49746 49845: gap of 100 bp  
 49846 59457: contig of 9612 bp in length

59458 59557: gap of 100 bp  
 59558 66804: contig of 7247 bp in length  
 66805 66904: gap of 100 bp  
 66905 73970: contig of 7066 bp in length  
 73971 74070: gap of 100 bp  
 74071 81007: contig of 6937 bp in length  
 81008 81107: gap of 100 bp  
 81108 87320: contig of 6213 bp in length  
 87321 87420: gap of 100 bp  
 87421 93250: contig of 5830 bp in length  
 93251 93350: gap of 100 bp  
 93351 97965: contig of 4615 bp in length  
 97966 98065: gap of 100 bp  
 98066 102941: contig of 4876 bp in length  
 102942 103041: gap of 100 bp  
 103042 109017: contig of 5976 bp in length  
 109018 109117: gap of 100 bp  
 109118 113391: contig of 4274 bp in length  
 113392 113491: gap of 100 bp  
 113492 118783: contig of 5292 bp in length  
 118784 118883: gap of 100 bp  
 118884 124241: contig of 5358 bp in length  
 124242 124341: gap of 100 bp  
 124342 129766: contig of 5425 bp in length  
 129767 129866: gap of 100 bp  
 129867 135473: contig of 5607 bp in length  
 135474 135573: gap of 100 bp  
 135574 140585: contig of 5012 bp in length  
 140586 140685: gap of 100 bp  
 140686 144027: contig of 3342 bp in length  
 144028 144127: gap of 100 bp  
 144128 147923: contig of 3796 bp in length  
 147924 148023: gap of 100 bp  
 148024 152461: contig of 4438 bp in length  
 152462 152561: gap of 100 bp  
 152562 155444: contig of 2883 bp in length  
 155445 155544: gap of 100 bp  
 155545 158721: contig of 3177 bp in length  
 158722 158821: gap of 100 bp  
 158822 162903: contig of 4082 bp in length  
 162904 163003: gap of 100 bp  
 163004 166121: contig of 3118 bp in length  
 166122 166221: gap of 100 bp  
 166222 169851: contig of 3630 bp in length  
 169852 172048: contig of 2097 bp in length  
 172049 172148: gap of 100 bp  
 172149 175332: contig of 3184 bp in length  
 175333 175432: gap of 100 bp  
 175433 177914: contig of 2482 bp in length  
 177915 178014: gap of 100 bp  
 178015 179875: contig of 1861 bp in length  
 179876 179975: gap of 100 bp  
 179976 181604: contig of 1629 bp in length  
 181605 181704: gap of 100 bp  
 181705 183951: contig of 2247 bp in length  
 183952 184051: gap of 100 bp  
 184052 185927: contig of 1876 bp in length  
 185928 186027: gap of 100 bp  
 186028 187870: contig of 1843 bp in length  
 187871 187970: gap of 100 bp  
 187971 189591: contig of 1621 bp in length  
 189592 189691: gap of 100 bp  
 189692 191169: contig of 1478 bp in length  
 191170 191269: gap of 100 bp  
 191270 192527: contig of 1258 bp in length  
 192528 192627: gap of 100 bp  
 192628 194288: contig of 1661 bp in length  
 194289 194388: gap of 100 bp  
 194389 195658: contig of 1270 bp in length  
 195659 195758: gap of 100 bp  
 195759 197707: contig of 1949 bp in length  
 197708 197807: gap of 100 bp

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FEATURES          * 197808 198902: contig of 1095 bp in length.
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  /db_xref="taxon:9606"
  /chromosome="11"
  /map="11q23"
  /clone="RP11-657A24"
misc_feature
  1..20627
  /note="assembly_fragment"
misc_feature
  20728..31817
  /note="assembly_fragment"
misc_feature
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  /note="assembly_fragment_clone_end:SP6 vector_side:right"
misc_feature
  41232..49745
  /note="assembly_fragment"

Query Match          40.8%; Score 562; DB 2; Length 198902;
Best Local Similarity 99.8%; Pred. No. 9.7e-291;
Matches 612; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 AGAATGGCGAATCCATTGCTCTTCTTCAGTTTTCGGGGGCGGCCCAAGCCAGCCT 794
DB 194389 AGAATGGCGAATCCATTGCTCTTCTTCAGTTTTCGGGGGCGGCCCAAGCCAGCCT 194448
QY 795 CGCTCTCGGGGGGGGCGCATGCTGAGGCTGAGCCCTGAGACCACTGCTGGGCGAGGTGG 854
DB 194449 CGCTCTCGGGGGGGGCGCATGCTGAGGCTGAGACCACTGAGTGGGCTGAGGTGG 194508
QY 855 GTGTGGGTGACTACATTGGCACTATATGCGCAGCATCAGACAGACACACTTCTCCGAT 914
DB 194509 GTGTGGGTGACTACATTGGCACTATATGCGCAGCATCAGACAGACACACTTCTCCGAT 194568
QY 915 TTCTGTGTACTCCGACATGCGACAGCTCCCAAGTCTTTGCTTATAGTCCCACTGCAAAAGTG 974
DB 194569 TTCTGTGTACTCCGACATGCGACAGCTCCCAAGTCTTTGCTTATAGTCCCACTGCAAAAGTG 194628
QY 975 AGCTCATGCTCTCACTCTAGAGAGAGGCTGAGGCTGAGACCACTGCTATCCAGAGAG 1034
DB 194629 AGCTCATGCTCTCACTCTAGAGAGAGGCTGAGGCTGAGACCACTGCTATCCAGAGAG 194688
QY 1035 GCTGGCCCCCTGGAATATTTGTAATGACTAGAGAGTGGGGTAGAGCACTCTCCGCTCT 1094
DB 194689 GCTGGCCCCCTGGAATATTTGTAATGACTAGAGAGTGGGGTAGAGCACTCTCCGCTCT 194748
QY 1095 GCTGTGGCAAGATGGGAACAGTGTCTGTGTGATCAGTCTGCGACATGCGAGATGGGCGAG 1154
DB 194749 GCTGTGGCAAGATGGGAACAGTGTGTGTGTGATCAGTCTGCGACATGCGAGATGGGCGAG 194808
QY 1155 TGGCTGATTTCTGCGCAAGACAGAGAGTGTGTGTGCTGCGCAAGTGTAGTCCGCCCA 1214
DB 194809 TGGCTGATTTCTGCGCAAGACAGAGAGTGTGTGTGCTGCGCAAGTGTAGTCCGCCCA 194868
QY 1215 GTTGTCTGTGTCCAGAGACCCAGAGTGGGGTGTCTCTCTGCTCTCTGCTCTCTG 1274
DB 194869 GTTGTCTGTGTCCAGAGACCCAGAGTGGGGTGTCTCTCTGCTCTCTGCTCTCTG 194928
QY 1275 ATTCCTCCCCACCTCTCTGCTCTGCGGGGCGGCCCTTTTCTCAAGATCACTCAATATA 1334
DB 194929 ATTCCTCCCCACCTCTCTGCTCTGCGGGGCGGCCCTTTTCTCAAGATCACTCAATATA 194988
QY 1335 CCTAAGAACCTTC 1347
DB 194989 CCTAAGAACCTTC 195001

RESULT 10
HMM2D92F04 441 bp mRNA linear PRI 29-AUG-1998
DEFINITION Homo sapiens full length insert cDNA clone ZD92F04.
ACCESSION AF086482.1 GI:3483827
VERSION AF086482.1
KEYWORDS FLI_CDNA.

```

```

SOURCE            Homo sapiens.
ORGANISM          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE         1 (bases 1 to 441)
AUTHORS           Woessner,U., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J.,
                  March,C., Bowles,L., Wylie,T., Bowers,Y., Steptoe,M., Theising,B.,
                  Geisel,S., Allen,M., Underwood,K., Chappell,J., Person,B.,
                  Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
                  Schurk,R., Riller,E., Kohn,S., Swaller,T., Behymer,K., Hillier,L.,
                  Wilson,R. and Waterston,R.
TITLE             Full Clone Sequencing of the Longest Available Member from Each
                  Unigene Cluster
JOURNAL           2 (bases 1 to 441)
REFERENCE         Waterston,R.
AUTHORS           Direct Submission
JOURNAL           Submitted (24-AUG-1998) Department of Genetics, Washington
                  University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT           SUBMITTED BY:
                  Genome Sequencing Center
                  Department of Genetics
                  Washington University
                  St. Louis MO 63108, USA
                  http://genome.wustl.edu/gsc
                  mailto:est@watson.wustl.edu

```

NOTICE: This sequence represents the full insert of this cDNA. NO attempt has been made to verify whether this corresponds to the full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

The location of this clone is unknown.

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  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone="IMAGE:356959"
  /clone_lib="Soares_fetal_heart_NbH19M"
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Best Local Similarity 100.0%; Pred. No. 8.4e-221;
Matches 432; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 917 CTGATGTAATCTCGATGACAGCTCCCAAGTCTTGTAGTGTCCCACTGCAAGTAGAG 976
DB 1 CTGATGTAATCTCGATGACAGCTCCCAAGTCTTGTAGTGTCCCACTGCAAGTAGAG 60
QY 977 CTGATGTAATCTCGATGACAGCTCCCAAGTCTTGTAGTGTCCCACTGCAAGTAGAG 1036
DB 61 CTGATGTAATCTCGATGACAGCTCCCAAGTCTTGTAGTGTCCCACTGCAAGTAGAG 120
QY 1037 TGGCCCCCTGGAATATTTGTAATGACTAGAGAGTGGGGTAGAGCACTCTCCGCTCTG 1096
DB 121 TGGCCCCCTGGAATATTTGTAATGACTAGAGAGTGGGGTAGAGCACTCTCCGCTCTG 180
QY 1097 TGTGTGCAAGATGGGAACAGTGTGTGTGATCAGTCTGCGACATGCGAGGCGAGTG 1156
DB 181 TGTGTGCAAGATGGGAACAGTGTGTGTGATCAGTCTGCGACATGCGAGGCGAGTG 240
QY 1157 GCTGATTTCTGCGCAAGACAGAGAGTGTGTGTGCTGCGCAAGTGTAGTCCGCCAGT 1216
DB 241 GCTGATTTCTGCGCAAGACAGAGAGTGTGTGTGCTGCGCAAGTGTAGTCCGCCAGT 300

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```

* 163685 163784: gap of 100 bp
* 163785 165216: contig of 1432 bp in length
* 165217 165316: gap of 100 bp
* 165317 166657: contig of 1341 bp in length
* 166658 166757: gap of 100 bp
* 166758 168507: contig of 1550 bp in length
* 168508 168407: gap of 100 bp
* 168408 170030: contig of 1623 bp in length
* 170031 170130: gap of 100 bp
* 170131 171725: contig of 1595 bp in length
* 171726 171825: gap of 100 bp
* 171826 173038: contig of 1213 bp in length.

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## FEATURES

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 Best Local Similarity 99.7%; Pred.No.6.3e-136;  
 Matches 394; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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QY 626 GCACATTCAGAGCCGCTCACCAGCAAGTTACCTCCAGAGTGCCTGGGCTACTACTTC 685
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DB 166779 GCACATTCAGAGCCGCTCACCAGCAAGTTACCTCCAGAGTGCCTGGGCTACTACTTC 166838
QY 686 GCCGTCATGCGACCGCTGTACCGGGCCAGCCCTGCAGTTTGATCTGGTGAAGATGGCGAA 745
    |||||||
DB 166839 GCCGTCATGCGACCGCTGTACCGGGCCAGCCCTGCAGTTTGATCTGGTGAAGATGGCGAA 166898
QY 746 TCACATTCGCTCTTTTCTTCCAGTTTTC-6GGGGGTGGGCCCAAGCCAGCCTGCTTCGGG 804
    |||||||
DB 166899 TCACATTCGCTCTTTTCTTCCAGTTTTC-6GGGGGTGGGCCCAAGCCAGCCTGCTTCGGG 166958
QY 805 GGGGGCCATGAGGAGGTGAGGAGCCAGAGACCAATGTGGGGAGAGTGGGGGTGGGAGCA 864
    |||||||
DB 166959 GGGGGCCATGAGGAGGTGAGGAGCCAGAGACCAATGTGGGGAGAGTGGGGGTGGGAGCA 167018
QY 865 CTACATTCGATCTATGCGCAGCATCAGACAGACAGACAGACCTTCTCCGATTTCTGGTGA 924
    |||||||
DB 167019 CTACATTCGATCTATGCGCAGCATCAGACAGACAGACAGACCTTCTCCGATTTCTGGTGA 167078
QY 925 CTCGACATGCGACACACTCCCAAGTCTTGTCTTAGTCCCACTGCAAAATGAGCTATGCT 984
    |||||||
DB 167079 CTCGACATGCGACACACTCCCAAGTCTTGTCTTAGTCCCACTGCAAAATGAGCTATGCT 167138
QY 985 CTCACCTCCTAGAGAGAGGAGGTGTGAGGCTGACAAAC 1019
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DB 167139 CTCACCTCCTAGAGAGAGGAGGTGTGAGGCTGACAAAC 167173

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RESULT 12  
 AK055132  
 LOCUS  
 DEFINITION Homo sapiens cDNA FLJ30570 fis, clone BRAHM2005998, weakly similar  
 to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (BC 3.4.24.-).  
 ACCESSION AK055132  
 VERSION AK055132.1 GI:16549793  
 KEYWORDS oligo capping; fis (full insert sequence).  
 SOURCE Homo sapiens brain cDNA to mRNA, clone\_l1b:BRAHM2  
 clone:BRAHM2005998.

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

## REFERENCE

1

Suzuki,O., Sasaki,N., Aotsuka,S., Shoji,T., Ichihara,T.,  
 Shiohata,N., Matsumoto,K., Hirano,M., Sano,S., Nomura,R.,  
 Yoshikawa,Y., Matsumura,Y., Moriya,S., Chiba,E., Momiyama,H.,  
 Onogawa,S., Kaeriyama,S., Satoh,N., Matsunawa,H., Takahashi,E.,  
 Katsoka,R., Kuga,N., Kuroda,A., Satoh,I., Kamata,K., Takami,S.,  
 Terashima,Y., Watanabe,M., Sugiyama,T., Irie,R., Otsuki,T.,  
 Sato,H., Ota,T., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,  
 Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,  
 Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,  
 Wagaitsuma,M., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,  
 Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,  
 Nagahari,K., Masuko,Y., Nagai,K. and Isogai,T.

## TITLE

NEO human cDNA sequencing project

## REFERENCE

2 (bases 1 to 2288)

## AUTHORS

Isogai,T., Otsuki,T. and Sugiyama,T.

## JOURNAL

Direct Submission

## COMMENT

Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,  
 Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 (E-mail:genomics@hri.co.jp. Tel:81-438-52-3975. Fax:81-438-52-3986)  
 NEO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan. cDNA full insert sequencing:  
 Research Association for Biotechnology (RAB); cDNA library  
 construction: Helix Research Institute (HRI) (supported by Japan  
 Key Technology Center etc.); 5'- and 3'-end one pass sequencing: RAB,  
 HRI, and Biotechnology Center. National Institute of Technology and  
 Evaluation; clone selection for full insert sequencing: RAB and  
 HRI.

## FEATURES

Location/Qualifiers

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/protein_id="BAB70859.1"
/db_xref="GI:16549794"
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PDPPPTHCVMHIOVADHAIOLKIALIESVASCLFRLSPPEPLRVCR
VPPPLTNASHILYVSDSVSGEFGHMYAGMARGSCADDERCOLICLIPD
SVCDGRANCADSDERTNSAKFSGCGNLGLGTFSTPTLYQIPQOLCTHRTISVP
AGHSIELQHNFSLEADDECKFDVEYETSSGAFSLGRFCGAEPPLVSSHBL
SVLEFRDHGISGGSATYLAFNATENPCPSSELSCQAGCKGOMQMDWRDCTDS
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ORIGIN

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Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1185 TGTGCTGTGCTGGCACTGTAAGTCCCAAGTGTCTGTGCTCAGAGAGCCACAGGTGGG 1244
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DB 2126 TGTGCTGTGCTGGCACTGTAAGTCCCAAGTGTCTGTGCTCAGAGAGCCACAGGTGGG 2185
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QY 1245 TGTGCTGTGCTGGTCTGCTGCTGATCTCCCAACCCCTGCTGCTGCTGAGG 1304
      |||||||
DB 2186 TGTGCTGTGCTGGTCTGCTGCTGATCTCCCAACCCCTGCTGCTGCTGAGG 2245
      |||||||

QY 1305 GCGCCCTTTTCTCAGAGAT 1323
      |||||||
DB 2246 GCGCCCTTTTCTCAGAGAT 2264
      |||||||

RESULT 13
ARI38211 144 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 28 from patent US 6197930.
DEFINITION ARI38211
ACCESSION ARI38211
VERSION ARI38211.1 GI:14479720
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 144)
AUTHORS Sheppard,P.O. and Humes,J.M.
TITLE Adipocyte-specific protein homologs
JOURNAL Patent: US 6197930-A 28 06-MAR-2001;
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source location/Qualifiers
1..144
/organism="unknown"

BASE COUNT      38 a      41 c      36 g      29 t
ORIGIN

Query Match
Best Local Similarity 100.0%; Score 73; DB 6; Length 144;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 ACTGAGCAGACAAAGATCCCAAGCTCTGCGCGGGACACCGGCTTCAGAGCAGCC 339
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DB 72 ACTGAGCAGACAAAGATCCCAAGCTCTGCGCGGGACACCGGCTTCAGAGCAGCC 131
      |||||||

QY 340 GGGCCACCATGGC 352
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DB 132 GGGCCACCATGGC 144

RESULT 14
ARI38212 144 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 29 from patent US 6197930.
DEFINITION ARI38212
ACCESSION ARI38212
VERSION ARI38212.1 GI:14479721
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 144)
AUTHORS Sheppard,P.O. and Humes,J.M.
TITLE Adipocyte-specific protein homologs
JOURNAL Patent: US 6197930-A 29 06-MAR-2001;
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ORIGIN
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Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 73 CTGAGCAGACAAAGATCCCAAGCTCTGCGCGGGACACCGGCTTCAGAGCAGCCG 132
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QY 341 GGGCCACCATGGC 352
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DB 133 GGGCCACCATGGC 144
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RESULT 15
ARI38214 144 bp DNA linear PAT 16-JUN-2001
LOCUS Sequence 31 from patent US 6197930.
DEFINITION ARI38214
ACCESSION ARI38214
VERSION ARI38214.1 GI:14479723
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 144)
AUTHORS Sheppard,P.O. and Humes,J.M.
TITLE Adipocyte-specific protein homologs
JOURNAL Patent: US 6197930-A 31 06-MAR-2001;
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BASE COUNT      32 a      32 c      37 g      43 t
ORIGIN
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Query Match
Best Local Similarity 100.0%; Score 72; DB 6; Length 144;
Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 AGCATCAAGACAGACAGACCTTCTCGGATTTCTGTGATCTCGACTGGACAGCTCC 60
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QY 944 CCAGTCTTGTCT 955
      |||||||
DB 61 CCAGTCTTGTCT 72
      |||||||
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Job time : 3723 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd

OM protein - protein search, using sw model

Run on: June 13, 2003, 15:49:51 ; Search time 72 Seconds  
(without alignments).  
449.721 Million cell updates/sec

Title: US-09-944-944-42

Perfect score:

Sequence: 1 MRPLVLLGLAGSPPLD.....DSTFSGFLVYSDWHSSPVFA 243

### Scoring table:

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Searched: 908470 seqs, 133250620 residues

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Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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5:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1984.DAT.*
6:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1985.DAT.*
7:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1986.DAT.*
8:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1987.DAT.*
9:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1988.DAT.*
10:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1989.DAT.*
11:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1990.DAT.*
12:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1991.DAT.*
13:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1992.DAT.*
14:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1993.DAT.*
15:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1994.DAT.*
16:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1995.DAT.*
17:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1996.DAT.*
18:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1997.DAT.*
19:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1998.DAT.*
20:	/SIDS2/gcgdata/genseq/genseq_emb1/AA1999.DAT.*
21:	/SIDS2/gcgdata/genseq/genseq_emb1/AA2000.DAT.*
22:	/SIDS2/gcgdata/genseq/genseq_emb1/AA2001.DAT.*
23:	/SIDS2/gcgdata/genseq/genseq_emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1325	100.0	243	20	AAV06481	Human tumour-asso
2	1325	100.0	243	20	AAV18727	Human PRO344 prote
3	1325	100.0	243	20	AAW97984	Human adipocyte-sp
4	1325	100.0	243	21	AAB37461	Human PRO344 prote
5	1325	100.0	243	21	AAV71468	Human PRO344 prote
6	1325	100.0	243	21	AAV93668	Human PRO344 prote
7	1325	100.0	243	21	AAB01318	Amino acid sequenc
8	1325	100.0	243	22	AAU12352	Human PRO344 polyP
9	1325	100.0	243	22	AAB65815	Human TANGO 253 SE
10	1325	100.0	243	22	AAB45593	Human adipocyte co

11	1325	100.0	243	22	AAB49599	Human adipocyte c
12	1323	99.8	243	22	AAB65891	Human secreted pr
13	1321	99.7	243	22	AAB65888	Human secreted pr
14	1321	99.7	243	22	AAB65889	Human secreted pr
15	1321	99.7	243	22	AAB65886	Human secreted pr
16	1271	95.9	243	21	AAV76040	Rat skin cell prot
17	1271	95.9	243	21	AAV55979	Skin cell protein,
18	1271	95.9	243	23	ABW72179	Rat protein isolat
19	1258	94.9	243	22	AAB65870	Murine TANGO 253
20	1256	94.8	228	22	AAB65816	Murine mature TANG
21	1256	94.8	243	22	AAB65839	Murine secreted pr
22	1254	94.6	243	22	AAB65897	Murine secreted pr
23	1254	94.6	243	22	AAB65888	Murine secreted pr
24	1243.5	93.8	242	22	AAB65896	Murine secreted pr
25	1200	90.6	228	22	AAB65821	Murine mature TANGO
26	1183	89.3	220	22	ABG15784	Novel human diapo
27	1048	79.1	201	23	AAO21653	Human secreted pr
28	675	50.9	128	22	AAB65819	Human TANGO 253
29	650	49.1	128	22	AAB65824	Murine TANGO 253
30	478	36.1	151	22	ABG12733	Novel human diapo
31	449.5	33.9	225	23	ABBB0583	Human sbg103026C1
32	442.5	33.4	333	23	ABBB0582	Human sbg103026C1
33	443.5	32.7	247	18	AAW09107	Murine adipocyte c
34	433.5	32.7	247	22	AAE05528	Mouse OBG3 protein
35	433.5	32.7	247	23	ABBO8252	Mouse OBG3 protein
36	425	32.1	244	18	AAW09108	Mouse acrp30 prote
37	424.5	32.0	247	22	AAE05527	Mouse OBG3 protein
38	424.5	32.0	247	23	ABBO8221	Mouse adipoQ protea
39	424	32.0	244	20	AAV71807	Adipose most abund
40	424	32.0	244	21	AAAB30233	Human adipocyte co
41	424	32.0	244	21	AAV71035	Human APM1 (Adipos
42	424	32.0	244	22	AAE05529	Human OBG3 protein
43	424	32.0	244	22	ABB65828	Human adipocyte co
44	424	32.0	244	22	AAAB9592	Human ACBP30 prote
45	424	32.0	244	22	AAAB49598	Human ACBP30 prote

## ALIGNMENTS

XX	RESULT 1
AA06481	
ID	AA06481 standard; Protein: 243 AA.
XX	
AC	AA06481;
XX	
DT	27-SEP-1999 (first entry)
XX	
DE	Human tumour-associated protein PRO344.
XX	
KW	PRO344; UNQ303; cancer; tumour; diagnosis; therapy; human
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	1..15
FT	/note="signal peptide"
FT	16..243
FT	/note="mature protein"
FT	68..215
FT	/note="N-myristoylated"
FT	216..243
FT	/note="N-myristoylated"
XX	
FN	W09935170-A2.
XX	
PD	15-JUL-1999.
XX	
PE	05-JAN-1999;
XX	
PR	99WC-US00106.
XX	
PR	20-NOV-1998;
XX	
PR	05-JAN-1998;
XX	
PR	29-APR-1998;
XX	
PR	98US-0109304.
XX	
PR	98US-0070440.
XX	
PR	98US-0083500.
XX	

PR 22-MAY-1998; 98US-0086414.  
 PR 10-JUN-1998; 98US-0088742.  
 PR 10-NOV-1998; 98US-0107783.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX Botstein D, Goddard A, Gurney AL, Hillan KJ, Lawrence DA;  
 PI Roy MA, Wood WI;  
 XX WPI: 1999-430385/36.  
 DR N-PSDB: AAX87258.  
 XX  
 PT Antibody against proteins expressed in neoplastic cells, useful for  
 PT tumor diagnosis and treatment  
 PS Example 1; Fig 10; 162pp; English.  
 XX  
 CC This sequence represents human PRO344 (UN0303), a protein encoded  
 CC by the novel cDNA clone DNA40592 (see AAX87258). Amplification of  
 CC DNA40592 was observed in primary lung tumours and in primary colon  
 CC tumours, suggesting a significant role in tumour formation and  
 CC growth. Antagonists (e.g. antibodies) directed to PRO344 may have  
 CC use in cancer therapy. The invention identifies 14 genes (see  
 CC AAX87254-67) that are amplified in the genome of tumour cells. Such  
 CC amplification is expected to be associated with overexpression of  
 CC the gene product and to contribute to tumorigenesis. The encoded  
 CC proteins (see AAY06477-90) may be useful targets for the diagnosis  
 CC and/or treatment (including prevention) of certain cancers, and may  
 CC act as predictors of the prognosis of tumour treatment. Antibodies  
 CC that bind the proteins are claimed and used in claimed cancer  
 CC diagnostic kits.  
 CC  
 XX  
 SQ Sequence 243 AA;  
 Query Match 100.0%; Score 1325; DB 20; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGPHHSGGLPGRDGRDGAAG 60  
 DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGPHHSGGLPGRDGRDGAAG 60  
 QY 61 APGKGGGGRGRLPGPRGDPGPRGAGPAGPTGAGCSVPPSAFSAKSESVPPSPD 120  
 DB 61 APGKGGGGRGRLPGPRGDPGPRGAGPAGPTGAGCSVPPSAFSAKSESVPPSPD 120  
 QY 121 APLEFDRLVNEQGHYDAVTKFTQYPGVYFFAVHATVYRASLOFDLVNKGESIASFFQ 180  
 DB 121 APLEFDRLVNEQGHYDAVTKFTQYPGVYFFAVHATVYRASLOFDLVNKGESIASFFQ 180  
 QY 181 FFGGMPKRPASLSGGAMVRLPEEDQVWVQVGVGDIYIGIYASIKTDSFTSGFLVYSDWHSSP 240  
 DB 181 FFGGMPKRPASLSGGAMVRLPEEDQVWVQVGVGDIYIGIYASIKTDSFTSGFLVYSDWHSSP 240  
 QY 241 VFA 243  
 DB 241 VFA 243  
 RESULT 2  
 ID AAY17827 standard; Protein; 243 AA.  
 XX AAY17827;  
 AC AAY17827;  
 XX  
 DT 12-AUG-1999 (first entry)  
 XX  
 DE Human PRO344 protein sequence.  
 XX  
 KW Human; PRO protein; tumour necrosis factor family; TNF; cytokine;  
 XX secreted protein; transmembrane protein; inflammation disorder.  
 OS Homo sapiens.

XX  
 PN WO9928462-A2.  
 XX  
 PD 10-JUN-1999.  
 XX  
 PF 01-DEC-1998; 98WO-US25108.  
 XX  
 PR 25-FEB-1998; 98US-0075945.  
 PR 03-DEC-1997; 97US-0067411.  
 PR 11-DEC-1997; 97US-0069278.  
 PR 11-DEC-1997; 97US-0069334.  
 PR 11-DEC-1997; 97US-0069335.  
 PR 12-DEC-1997; 97US-0069425.  
 PR 16-DEC-1997; 97US-0069696.  
 PR 16-DEC-1997; 97US-0069702.  
 PR 17-DEC-1997; 97US-0069870.  
 PR 17-DEC-1997; 97US-0069873.  
 PR 18-DEC-1997; 97US-0068017.  
 PR 05-JAN-1998; 98US-0070440.  
 PR 09-FEB-1998; 98US-0074086.  
 PR 09-FEB-1998; 98US-0074092.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;  
 PI Yuan J;  
 XX WPI: 1999-371118/31.  
 DR N-PSDB: AAX80052.  
 XX  
 PT Nucleic acids encoding PRO secreted and transmembrane proteins  
 PS Claim 12; Fig 21; 123pp; English.  
 XX  
 CC The present invention describes nucleic acids encoding PRO secreted and  
 CC transmembrane proteins used therapeutically. The PRO proteins have  
 CC cytosstatic, anti-inflammatory, anti-proliferative and immunosuppressive  
 CC activity. The proteins and polynucleotides can be used in therapy,  
 CC identification of homologues, raising antibodies and design of probes  
 CC and primers. They can be used in a range of diseases related to proteins  
 CC that they have homology with, e.g. a PRO protein having homology to  
 CC complement proteins may be used in inflammatory responses.  
 CC  
 XX  
 SQ Sequence 243 AA;  
 Query Match 100.0%; Score 1325; DB 20; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGPHHSGGLPGRDGRDGAAG 60  
 DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGPHHSGGLPGRDGRDGAAG 60  
 QY 61 APGKGGGGRGRLPGPRGDPGPRGAGPAGPTGAGCSVPPSAFSAKSESVPPSPD 120  
 DB 61 APGKGGGGRGRLPGPRGDPGPRGAGPAGPTGAGCSVPPSAFSAKSESVPPSPD 120  
 QY 121 APLEFDRLVNEQGHYDAVTKFTQYPGVYFFAVHATVYRASLOFDLVNKGESIASFFQ 180  
 DB 121 APLEFDRLVNEQGHYDAVTKFTQYPGVYFFAVHATVYRASLOFDLVNKGESIASFFQ 180  
 QY 181 FFGGMPKRPASLSGGAMVRLPEEDQVWVQVGVGDIYIGIYASIKTDSFTSGFLVYSDWHSSP 240  
 DB 181 FFGGMPKRPASLSGGAMVRLPEEDQVWVQVGVGDIYIGIYASIKTDSFTSGFLVYSDWHSSP 240  
 QY 241 VFA 243  
 DB 241 VFA 243  
 RESULT 3  
 AAM97984

ID	AAW97984 standard; Protein; 243 AA.	
XX		
AC	AAW97984;	
XX		
DT	21-JUN-1999 (first entry)	
XX		
DE	Human adipocyte-specific protein zslg39.	
XX		
KW	Adipocyte-specific protein; zslg39; human; fatty acid metabolism; energy balance; nutrition; antimicrobial.	
KW		
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..15
FT		/note= "signal peptide, alternatively the signal peptide comprises residues 1..18"
FT	Protein	16..243
FT		/note= "mature protein, alternatively the mature protein comprises residues 19..243 (specifically claimed in Claim 4)"
FT		
FT	Domain	30..96
FT		/note= "collagen-like domain"
FT	Domain	98..243
FT		/note= "globular domain"
FT	Region	105..109
FT		/note= "beta strand"
FT	Region	128..130
FT		/note= "beta strand"
FT	Region	136..139
FT		/note= "beta strand"
FT	Region	143..146
FT		/note= "beta strand"
FT	Region	164..171
FT		/note= "beta strand"
FT	Region	176..182
FT		/note= "beta strand"
FT	Region	187..200
FT		/note= "beta strand"
FT	Region	204..210
FT		/note= "beta strand"
FT	Region	226..231
FT		/note= "beta strand"
FT	Domain	111..135
FT		/note= "receptor binding domain"
FT	Domain	170..174
FT		/note= "receptor binding domain"
XX		
PN	W09910492-A1.	
XX		
PD	04-MAR-1999.	
XX		
PF	26-AUG-1998; 98WO-US17724.	
XX		
PK	26-AUG-1997; 97US-0056983.	
XX		
PA	(ZYMO ) ZYMOGENETICS INC.	
XX		
PI	Humes JM, Sheppard PO;	
DR	WPI; 1999-204665/17.	
DR	N-PSDB; AAX24684.	
XX		
PT	zslg39 protein - used to modulate fatty acid metabolism	
PS	Claim 1; 111-112; 132pp; English.	
XX		
CC	This polypeptide comprises human adipocyte-specific protein zslg39, a protein that modulates free fatty acid metabolism. zslg39 is a member of a family of proteins having a globular domain and a collagen-like domain capable of dimerisation or oligomerisation. zslg39 polypeptides were initially identified by querying an EST database for secretory signal sequences characterised by an upstream	

CC	methionine start site, a hydrophobic region of approximately 13 amino acids and a cleavage site. A single EST sequence was discovered, and the novel polypeptide encoded by the full-length cDNA allowed the identification of a homologue relationship with adipocyte complement related protein Acyr30 and adipocyte secreted protein apM1. A full-length clone (see AAX2468) was obtained from a lung tissue library. Expression vectors, cultured cells and a method of producing zslg39 polypeptide are claimed, as well as zslg39 radionucleotides, enzymes or fluorochromes, fusion proteins including zslg39 polypeptides, an antibody that specifically binds to an epitope of zslg39, and a method for modulating free fatty acid metabolism by administering a zslg39 polypeptide. The zslg39 polypeptide may also be used in organ preservation, for cryopreservation, for surgical pretreatment to prevent injury due to ischaemia and/or inflammation, and as an antimicrobial agent, promoting lysis or phagocytosis of infectious agents.	
SX	Sequence	243 AA:
SO	Query Match	100.0%; Score 1325; DB 20; Length 243;
	Best Local Similarity	100.0%; Pred. No. 5.3e-103;
	Matches 243; Conservative	0; Mismatches . 0; Indels 0; Gaps 0
OY	1 MRPLVLVLLGLGAAGSPFLDNDKRTSLCPGHNGLPSTPCNHSOGCLPGDGGRDGCATG	60
Dd	1 MRPLLVTLLLGLAASPPDLDDKKISLCPGHNGLPCTPHNSOGLPGDRGRDGCATG	60
OY	61 APGEKGEGRGRLPPRGGDPGRGSGPRGPGECSVPPRSASFSAKSSESRYPPSD	120
Dd	61 APKEGEGRRQLPPRPGRGPGRGSGPRGPGECSVPPRSASFSAKSSESRYPPSD	120
OY	121 APRPEDRVLDVEQGHYDAVTGKFTEQVPVVYFAVAHYRASLPDFLYKNESIASFQG	180
Dd	121 APRPEDRVLTVDNQGHYDAVTGKFTEQVPVVYFAVAHYRASLPDFLVKNESIASFQG	180
OY	181 FFGGPKPRASLSGGMVRLEPPDDWVGVCVDYGITVASITDTSFSGFLYSMDHSSP	240
Dd	181 FFGGPKPRASLSGGMVRLPEPDWWGVGVGDYIGITVASIKTDSFSQFLYSMDHSSP	240
OY	241 VFA 243 	
Dd	241 VFA 243	
RESULT 4		
XX	AAB33461	
ID	AAB33461 standard; Protein; 243 AA.	
XX	AAB33461;	
AC	.	
DE	29-JAN-2001 (first entry)	
XX		
Human PRO344	protein UNQ303 SEQ ID NO:241.	
XX		
Human; immune related disease; diagnosis; antiinflammatory; cardiac; dermatologic; antiarthritic; antifluemantic; immunosuppressive; haematologic; antithyroid; antidabetic; nootropic; neuroprotective; antianemic; hepatotropic; vitruicide; antipsoriatic; antiallergic; antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis; spondylarthropathy; systemic sclerosis; sarcoidosis; idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopenia; immune-mediated renal disease; demyelinating disease; hepatobiliary disease; Whipple's disease; inflammatory bowel disease; gluten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; allergic disease; immunological disease; transplantation associated disease; graft rejection; graft-versus-host-disease.		
OS	Homo sapiens.	
PN	WO200053758-A2.	

XX 14-SEP-2000.  
 PD 02-MAR-2000; 2000WO-US05841.  
 PF 08-MAR-1999; 99WO-US05028.  
 XX 10-MAR-1999; 99US-0123618.  
 PR 12-MAR-1999; 99US-0123957.  
 PR 23-MAR-1999; 99US-0125775.  
 PR 12-APR-1999; 99US-0128849.  
 PR 20-APR-1999; 99WO-US08615.  
 PR 28-APR-1999; 99US-0131445.  
 PR 04-MAY-1999; 99US-0132377.  
 PR 14-MAY-1999; 99US-0134287.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 23-JUN-1999; 99US-0141037.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 PR 28-JUL-1999; 99US-0146222.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 08-SEP-1999; 99WO-US20594.  
 PR 13-SEP-1999; 99WO-US20944.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 15-SEP-1999; 99WO-US21547.  
 PR 05-OCT-1999; 99WO-US23086.  
 PR 29-OCT-1999; 99US-0162506.  
 PR 29-NOV-1999; 99WO-US28214.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 01-DEC-1999; 99WO-US28634.  
 PR 02-DEC-1999; 99WO-US28551.  
 PR 02-DEC-1999; 99WO-US28564.  
 PR 02-DEC-1999; 99WO-US28565.  
 PR 16-DEC-1999; 99WO-US30095.  
 PR 20-DEC-1999; 99WO-US30999.  
 PR 30-DEC-1999; 99WO-US31274.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00277.  
 PR 06-JAN-2000; 2000WO-US00376.  
 PR 11-FEB-2000; 2000WO-US03365.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 18-FEB-2000; 2000WO-US04342.  
 PR 22-FEB-2000; 2000WO-US04414.  
 XX (GETH ) GENENTECH INC.  
 PA Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W;  
 PI Kabakoff RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V;  
 PI Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;  
 XX WPI: 2000-572271/53.  
 DR N-PSDB; AAC58626.  
 XX  
 PT Sixty four PRO polypeptides, useful in the diagnosis and treatment of  
 PT immune related disorders, e.g. systemic lupus erythematosus, rheumatoid  
 PT arthritis, osteoarthritis, thyroiditis and diabetes mellitus -  
 XX  
 PS Claim 33; Fig 96; 309pp; English.  
 XX  
 CC The present invention describes sixty four human PRO proteins which can  
 CC be used in the treatment of immune related diseases. The human PRO  
 CC proteins, anti-PRO antibodies, agonists and antagonists are useful for  
 CC treating and diagnosing immune related disorders. The disorders are  
 CC selected from systemic lupus erythematosus, rheumatoid arthritis,  
 CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,  
 CC systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's  
 CC syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic  
 CC anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,  
 CC immune-mediated renal disease, demyelinating diseases of the central  
 CC and peripheral nervous systems, hepatobiliary diseases, inflammatory  
 CC bowel disease, gluten-sensitive enteropathy and Whipple's disease,  
 CC autoimmune or immune-mediated skin diseases, allergic diseases,

CC immunological diseases of the lung, and transplantation associated  
 CC diseases including graft rejection and graft-versus-host-disease.  
 CC AAC58397 to AAC58578 represent PCR primers and hybridisation probes used  
 CC in the isolation of human PRO sequences. AAC58579 to AAC58642 and  
 CC AAB33414 to AAB33477 represent human PRO polynucleotide and protein  
 CC sequences given in the exemplification of the present invention.  
 XX  
 SQ Sequence 243 AA;  
 XX  
 Query Match 100.0%; Score 1325; DB 21; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 5,3e-103;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPPTFGHNGSOGLPGRDGRDGAAG 60  
 DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPPTFGHNGSOGLPGRDGRDGAAG 60  
 OY 61 APGKGGCGRGLGPRDPPGPRGAGAGTGPAGGECVPPRASFSAKRSESRVPPSD 120  
 DB 61 APGKGGCGRGLGPRDPPGPRGAGAGTGPAGGECVPPRASFSAKRSESRVPPSD 120  
 OY 121 APLEPDRVLVNEQGHYDAVTGKFTQVGVYTYFAVHATVYRASLQFDLVKNGESIASPFQ 180  
 DB 121 APLEPDRVLVNEQGHYDAVTGKFTQVGVYTYFAVHATVYRASLQFDLVKNGESIASPFQ 180  
 OY 181 FFGWMPKRPASLSGGAMVRLPEDDQVWQVGVGYIGIYASIKTSTESGFLVYDWHSSP 240  
 DB 181 FFGWMPKRPASLSGGAMVRLPEDDQVWQVGVGYIGIYASIKTSTESGFLVYDWHSSP 240  
 OY 241 VFA 243  
 DB 241 VFA 243  
 XX  
 RESULT 5  
 AAY71468  
 ID AAY71468 standard; Protein: 243 AA.  
 AC  
 XX AAY71468;  
 XX 08-NOV-2000 (first entry)  
 DE Human PRO344 protein.  
 XX  
 KW PRO344; DNA40592-1242; human; ATCC No: 209492; antiproliferative;  
 KW neoplastic cell growth inhibitor; cytoskeletal; treatment; cancer; tumour;  
 KW breast; prostate; colon; lung; renal; ovarian; central nervous system;  
 KW CNS; leukemia; melanoma; Expressed Sequence Tag; EST; secreted protein;  
 KW extracellular domain; ECD.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 XX Key Location/Qualifiers  
 XX Peptide 1..15  
 FT Modified-site 11..17 /label- Signal\_peptide  
 FT Protein /note- "N-myristoylation site"  
 FT 16..243 /label- Mature\_PRO344\_protein  
 FT Modified-site 68..74 /note- "N-myristoylation site"  
 FT Binding-site 77..80 /note- "Cell attachment sequence"  
 FT Modified-site 216..222 /note- "N-myristoylation site"  
 XX  
 XX WO200032778-A2.  
 XX 08-JUN-2000.  
 PD 30-NOV-1999; 99WO-US28409.  
 PF 01-DEC-1998; 98WO-US25108.  
 PR

PR 16-DEC-1998; 98US-0112850.  
 PR 22-DEC-1998; 98US-0113296.  
 PR 20-JUL-1999; 99US-0144758.  
 PR 26-JUL-1999; 99US-0145698.  
 XX  
 PA (GETH ) GENENTECH INC.  
 PI Chen J, Goddard A, Gurney AL, Hillan K, Napier M, Wood WI;  
 XX WPI: 2000-412325/35.  
 DR N-PSDB; AAD01241.  
 XX  
 PT New composition useful for inhibiting neoplastic cell growth and for  
 PT treating cancers, comprises PRO655, PRO344 or PRO364 polypeptide or  
 PT their antagonists -  
 XX  
 PS Claim 31; Fig 6; 108pp; English.  
 XX  
 CC The present sequence is the human PRO344 protein, encoded by the cDNA  
 CC clone, designated as DNA40592-1242. It is isolated from human foetal  
 CC lung tissue, cDNA library, identified using probes based on a consensus  
 CC sequence DNA34396, derived from secreted protein extracellular domain  
 CC (ECD) expressed sequence tag (EST). This clone is assigned ATCC deposit  
 CC No: 209492. PRO344 functions as a neoplastic cell growth inhibitor and  
 CC is used for treating tumours, using an effective amount of PRO655, PRO364  
 CC and PRO344. This composition is especially useful for treatment of human  
 CC cancers such as breast, prostate, colon, lung, renal, ovarian and CNS,  
 CC leukemia and melanoma.  
 CC  
 XX  
 SQ Sequence 243 AA:  
 Query Match 100.0%; Score 1325; DB 21; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGTGHHGSGQLPRDGRDGDGAPG 60  
 DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGTGHHGSGQLPRDGRDGDGAPG 60  
 QY 61 APGEKGEGRGRLPGPRDPCGRGAGPAGPTGAGGECVPPRSASFSAKRSESRVPPSD 120  
 DB 61 APGEKGEGRGRLPGPRDPCGRGAGPAGPTGAGGECVPPRSASFSAKRSESRVPPSD 120  
 QY 121 APLEPDRVLVNEOGHYDAVTGKFTQVPGVYFFAVHATVYRASLOFDLVKNGESTIASFFQ 180  
 DB 121 APLEPDRVLVNEOGHYDAVTGKFTQVPGVYFFAVHATVYRASLOFDLVKNGESTIASFFQ 180  
 QY 181 FFGGMPKPRASLSGAMVRLPEPDQVWVGVGDYIGIYASIKTDSFGFLVYSDWHSSP 240  
 DB 181 FFGGMPKPRASLSGAMVRLPEPDQVWVGVGDYIGIYASIKTDSFGFLVYSDWHSSP 240  
 QY 241 VFA 243  
 DB 241 VFA 243  
 RESULT 6  
 ID AAY93688 standard; Protein: 243 AA.  
 AC AAY93688;  
 DT 03-OCT-2000 (first entry)  
 DE Amino acid sequence of novel polypeptide PRO344.  
 KM PRO201; PRO292; PRO327; PRO1265; PRO344; PRO343; PRO347; PRO357;  
 KM PRO715; PRO1017; PRO1112; PRO509; PRO853; PRO882; tumour cell;  
 KM tumorigenesis; cancer; neoplastic cell growth; cell proliferation.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers

FT Peptide 1..15  
 FT /note= "signal peptide"  
 FT Modified-site 11..17  
 FT /note= "N-myristoylation site"  
 FT Modified-site 68..74  
 FT /note= "N-myristoylation site"  
 FT Region 77..80  
 FT /note= "cell attachment sequence"  
 FT Modified-site 216..222  
 FT /note= "N-myristoylation site"  
 XX  
 PN WO200037640-A2.  
 XX  
 PD 29-JUN-2000.  
 XX  
 PF 16-DEC-1999; 99WO-US30095.  
 XX  
 PR 22-DEC-1998; 98US-0113296.  
 PR 08-MAR-1999; 99WO-US05028.  
 PR 02-JUN-1999; 99WO-US12252.  
 PR 01-SEP-1999; 99WO-US20111.  
 PR 15-SEP-1999; 99WO-US21090.  
 PR 30-NOV-1999; 99WO-US28313.  
 PR 30-NOV-1999; 99WO-US28409.  
 PR 01-DEC-1999; 99WO-US28301.  
 PR 02-DEC-1999; 99WO-US28565.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Botstein D, Goddard A, Gurney AL, Hillan K, Lawrence DA, Roy MA;  
 PI Wood WI;  
 DR WPI: 2000-452188/39.  
 DR N-PSDB; AAA46907.  
 XX  
 PT New anti-polypeptide antibody useful in the treatment and diagnosis of  
 PT neoplastic cell growth and proliferation -  
 XX  
 PS Claim 61; Fig 10; 220pp; English.  
 CC  
 CC The present sequence represents a novel human polypeptide. The  
 CC specification describes novel polypeptides designated PRO201, PRO292,  
 CC PRO327, PRO1265, PRO343, PRO347, PRO357, PRO715, PRO1017,  
 CC PRO1112, PRO509, PRO853 and PRO882. These genes are amplified in  
 CC the genome of tumour cells. The polypeptides are believed to contribute  
 CC to tumorigenesis. The polypeptides are useful target for the  
 CC identification of certain cancers, and may act as predictors of the  
 CC prognosis of tumour treatment. Antibodies against these polypeptides  
 CC are useful in the treatment and diagnosis of neoplastic cell growth  
 CC and proliferation in mammals.  
 CC  
 XX  
 SQ Sequence 243 AA:  
 Query Match 100.0%; Score 1325; DB 21; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGTGHHGSGQLPRDGRDGDGAPG 60  
 DB 1 MRPLVLLLLGLAAGSPPLDNNKIPSLCPGHPGLPTGTGHHGSGQLPRDGRDGDGAPG 60  
 QY 61 APGEKGEGRGRLPGPRDPCGRGAGPAGPTGAGGECVPPRSASFSAKRSESRVPPSD 120  
 DB 61 APGEKGEGRGRLPGPRDPCGRGAGPAGPTGAGGECVPPRSASFSAKRSESRVPPSD 120  
 QY 121 APLEPDRVLVNEOGHYDAVTGKFTQVPGVYFFAVHATVYRASLOFDLVKNGESTIASFFQ 180  
 DB 121 APLEPDRVLVNEOGHYDAVTGKFTQVPGVYFFAVHATVYRASLOFDLVKNGESTIASFFQ 180  
 QY 181 FFGGMPKPRASLSGAMVRLPEPDQVWVGVGDYIGIYASIKTDSFGFLVYSDWHSSP 240  
 DB 181 FFGGMPKPRASLSGAMVRLPEPDQVWVGVGDYIGIYASIKTDSFGFLVYSDWHSSP 240

OY		241 VFA 243     241 VFA 243	
DB			
RESULT 7			
ID	AAB01318	standard; Protein; 243 AA.	
AC	AAB01318;		
XX			
DT	25-SEP-2000	(first entry)	
XX			
DE	Human PRO344 polypeptide.		
XX			
KW	PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO715; PRO323; PRO299; PRO33; PRO344; PRO347; PRO355; PRO357; PRO361; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human.		
KW			
OS	Homo sapiens.		
FH			
FT	Key	Location/Qualifiers	
FT	Peptide	1..15	
FT		/label= Signal peptide	
FT	Modified-site	11..17	
FT		/note= "N-myristoylation site"	
FT	Modified-site	68..74	
FT		/note= "N-myristoylation site"	
FT	Region	77..80	
FT		/label= Cell attachment sequence	
FT	Modified-site	216..222	
FT		/note= "N-myristoylation site"	
XX			
PN	WO200032776-A2.		
PD			
XX	08-JUN-2000.		
PE			
PR	01-DEC-1999;	99WO-US28301.	
PR			
PR	01-DEC-1998;	98WO-US25108.	
PR	16-DEC-1998;	98US-0112850.	
XX	22-DEC-1998;	98US-0113296.	
PA	(GETH ) GENENTECH INC.		
PI	Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E; Gerlitsen KE, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KM, Kijavlin IJ, Napier MA, Roy MA, Tumas D, Wood WI; WPI: 2000-412324/35. N-PSTDB: AAAA9560.		
FT	New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical and diagnostic agents		
PS	Claim 12; Fig 18; 187pp; English.		
CC	New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources.		
Sequence	243 AA;		
Query Match		100.0%; Score 1325; DB 21; Length 243;	
Best Local Similarity		100.0%; Pred. NO. 5.3e-103;	
Matches 243; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	

QY		MRELVLVLLILGLAAGSPPLDDNKIPSLCPGHPGLPCTPGHNSOGLPGRDGDHDGAPG	60
Dd	1	MRELVLVLLILGLAAGSPPLDDNKIPSLCPGHPGLPCTPGHNSOGLPGRDGDHDGAPG	60
QY	61	APEKEGGEGRGPGLPERGDPGRPRGEAGPAPTGPAECSVPPRSFAFSAKRSERVRPPSD	120
Dd	61	APEKEGGEGRGPGLPERGDPGRPRGEAGPAPTGPAECSVPPRSFAFSAKRSERVRPPSD	120
QY	121	APLPFRVLVNEGHGHDAVTGKFTCOVPEVVYFAVAHYATYRASLOFDLVNKGESTIASPFQ	180
Dd	121	APLPFRVLVNEGHGHDAVTGKFTCOVPEVVYFAVAHYATYRASLOFDLVNKGESTIASPFQ	180
QY	181	FFGWMPRPASLSGGAAMRLPEPDQVMVGVDYIGIYASIKTDSFSGFLVYSDMHSSP	240
Dd	181	FFGWMPRPASLSGGAAMRLPEPDQVMVGVDYIGIYASIKTDSFSGFLVYSDMHSSP	240
QY	241	VFA 243	
Dd	241	VFA 243	
<hr/>			
RESULT 8			
ID	AAU12352	standard; Protein; 243 AA.	
XX	AAU12352;		
DT	24-OCT-2001	(first entry)	
DE			
XX	Human PRO344 polypeptide sequence.		
KW	Human secretory and transmembrane; PRO; mammalian; cancer; lung;		
KM	breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;		
KW	cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;		
XX	adipocyte; A-peptide; factor VIIA; gene therapy.		
OS	Homo sapiens.		
XX	WO200140466-A2.		
PD	07-JUN-2001.		
XX			
Pf	01-DEC-2000; 2000MO-US32678.		
XX			
XX	01-DEC-1999; 99MO-US28301.		
PR	01-DEC-1999; 99MO-US28634.		
PR	02-DEC-1999; 99MO-US28851.		
PR	02-DEC-1999; 99MO-US28564.		
PR	02-DEC-1999; 99MO-US28565.		
PR	09-DEC-1999; 99US-0170262.		
PR	16-DEC-1999; 99MO-US30095.		
PR	20-DEC-1999; 99MO-US30911.		
PR	20-DEC-1999; 99MO-US30999.		
PR	30-DEC-1999; 99MO-US31243.		
PR	06-JAN-2000; 2000MO-US00277.		
PR	06-JAN-2000; 2000MO-US00376.		
PR	11-FEB-2000; 2000MO-US03565.		
PR	18-FEB-2000; 2000MO-US04341.		
PR	18-FEB-2000; 2000MO-US04342.		
PR	22-FEB-2000; 2000MO-US04414.		
PR	24-FEB-2000; 2000MO-US04914.		
PR	24-FEB-2000; 2000MO-US05004.		
PR	01-MAR-2000; 2000MO-US05601.		
PR	20-MAR-2000; 2000MO-US07377.		
PR	21-MAR-2000; 2000MO-US07532.		
PR	30-MAR-2000; 2000MO-US08439.		
PR	17-MAY-2000; 2000MO-US13705.		
PR	22-MAY-2000; 2000MO-US14042.		
PR	30-MAY-2000; 2000MO-US14941.		
PR	02-JUN-2000; 2000MO-US15264.		
DR	10-NOV-2000; 2000MO-US30873.		
XX			

PA (GETH) GENENTECH INC.  
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Geritsen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI: 2001-408281/43.  
 DR N-PSDB: AAS21424.  
 XX Isolated, secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing  
 PT PRO polypeptides, and detect the presence of mammalian tumours e.g.  
 PT lung, breast, prostate, cervical  
 XX Claim 12; Fig 362; 813pp: English.  
 PS  
 XX AAU12172-AAU12446 represent novel human secretory and transmembrane  
 CC PRO polypeptides. The PRO polypeptides are useful to detect other  
 CC PRO polypeptides, to link bioactive molecules to cells expressing  
 CC PRO polypeptides, to modulate biological activities of cells expressing  
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample.  
 CC Some of the 275 sequences are also useful to stimulate the release of  
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
 CC proliferation or differentiation of chondrocytes, the proliferation or  
 CC gene expression in pericyte cells, the release of proteoglycans from  
 CC cartilage, the proliferation of inner ear utricular supporting cells or  
 CC of T-lymphocytes, the release of a cytokine from peripheral blood  
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by  
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify  
 CC molecules involved in binding interactions. The polynucleotides encoding  
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy.  
 CC  
 SQ Sequence 243 AA;

Query Match 100.0%; Score 1325; DB 22; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLVLLGLAASPPDDNKKIPSLCPGHGRLPOTPGHSGGLPGDGRDGRGAG 60  
 DB 1 MRPLVLLVLLGLAASPPDDNKKIPSLCPGHGRLPOTPGHSGGLPGDGRDGRGAG 60  
 QY 61 APGEKGEGRPLPGPRGDPGRGEGAPGPTGPAEGCSVPPRSASFSAKRSESRYPPSD 120  
 DB 61 APGEKGEGRPLPGPRGDPGRGEGAPGPTGPAEGCSVPPRSASFSAKRSESRYPPSD 120  
 QY 121 APLPDRVLYNQGHDVATGKFTCOVPEVYFFAHHATYRASLQDFLVKNESIASFPQ 180  
 DB 121 APLPDRVLYNQGHDVATGKFTCOVPEVYFFAHHATYRASLQDFLVKNESIASFPQ 180  
 QY 181 FFGGMPKPKASLSGGMVRLPEPDQVWVGVDYIGIVASITDSTFSGLVYSDWHSSP 240  
 DB 181 FFGGMPKPKASLSGGMVRLPEPDQVWVGVDYIGIVASITDSTFSGLVYSDWHSSP 240  
 QY 241 VFA 243  
 DB 241 VFA 243

RESULT 9  
 AAB65815  
 ID AAB65815 standard; Protein; 243 AA.  
 XX  
 AC AAB65815;  
 XX  
 DT 28-MAR-2001 (first entry)  
 XX  
 DE Human TANGO 253 SEQ ID NO: 3.

XX Human: mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;  
 KW INTERCEPT 258; coronary disorder; olfactory disorder;  
 KW neurological disorder; pulmonary disorder; immunological disorder;  
 KW developmental disorder; kidney disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200078808-A1.  
 XX  
 PD 28-DEC-2000.  
 XX  
 XX 19-JUN-2000; 2000WO-US16883.  
 XX  
 XX 18-JUN-1999; 99US-0336536.  
 XX  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PA Leiby KR, McKay C, Bossone S;  
 XX  
 DR WPI: 2001-050109/06.  
 XX  
 PT New nucleic acids for treating diseases and disorders, e.g.  
 PT atherosclerosis, infection, autoimmune diseases, obesity, ear  
 PT disorders, brain disorders, tumors, diabetes, arthritis, multiple  
 PT sclerosis and asthma  
 XX  
 PS Claim 9; Page 211-212; 332pp: English.  
 XX  
 XX The present invention provides the protein and coding sequences of the  
 CC human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,  
 CC TANGO 281 and INTERCEPT 258. These are useful in the treatment of  
 CC coronary, pulmonary, olfactory, immunological, neurological,  
 CC developmental and kidney disorders.  
 CC  
 SQ Sequence 243 AA;

Query Match 100.0%; Score 1325; DB 22; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLVLLGLAASPPDDNKKIPSLCPGHGRLPOTPGHSGGLPGDGRDGRGAG 60  
 DB 1 MRPLVLLVLLGLAASPPDDNKKIPSLCPGHGRLPOTPGHSGGLPGDGRDGRGAG 60  
 QY 61 APGEKGEGRPLPGPRGDPGRGEGAPGPTGPAEGCSVPPRSASFSAKRSESRYPPSD 120  
 DB 61 APGEKGEGRPLPGPRGDPGRGEGAPGPTGPAEGCSVPPRSASFSAKRSESRYPPSD 120  
 QY 121 APLPDRVLYNQGHDVATGKFTCOVPEVYFFAHHATYRASLQDFLVKNESIASFPQ 180  
 DB 121 APLPDRVLYNQGHDVATGKFTCOVPEVYFFAHHATYRASLQDFLVKNESIASFPQ 180  
 QY 181 FFGGMPKPKASLSGGMVRLPEPDQVWVGVDYIGIVASITDSTFSGLVYSDWHSSP 240  
 DB 181 FFGGMPKPKASLSGGMVRLPEPDQVWVGVDYIGIVASITDSTFSGLVYSDWHSSP 240  
 QY 241 VFA 243  
 DB 241 VFA 243

RESULT 10  
 AAB49593  
 ID AAB49593 standard; Protein; 243 AA.  
 XX  
 AC AAB49593;  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Human adipocyte complement related protein homolog zs1939.  
 XX  
 DE Human; zacrpf; gene therapy; complement inhibition; C1q domain;

KW adipocyte complement related protein homolog;  
 KW inflammation; hormone secretion; inositol phosphate; arachidonate;  
 KW phospholipase C activation; gastric emptying; neutrophil activation;  
 KW superoxide anion production; antimicrobial; acute vascular injury;  
 KW wound healing; zsig39.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073444-A1.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PE 18-MAY-2000; 2000WO-US13608.  
 XX  
 PR 27-MAY-1999; 99US-0321372.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Pliddington CS, Sheppard FO;  
 XX  
 DR WPI: 2001-061531/07.  
 XX  
 PT Novel adipocyte complement related protein homolog, ZACRP5, useful for  
 PT diagnosing and treating inflammation, vascular injury microbial  
 PT infections, and in wound healing  
 XX  
 PS Disclosure; Fig 1; 121pp; English.  
 XX  
 CC The present invention relates to human adipocyte complement related  
 CC protein homolog, zacrp5 protein and coding sequence (see ABA49590 and  
 CC AAC90045). ZACRP5 has a carboxyl-terminal C1q domain. The zacrp5 gene is  
 CC located on human chromosome 16. zacrp5 gene and protein are useful for  
 CC diagnosing and treating inflammations, for determining arterial  
 CC remodeling, for modulating calcium ion concentration, hormone  
 CC secretion, DNA synthesis or cell growth, inositol phosphate turnover,  
 CC arachidonate release, phospholipase C activation, gastric emptying, human  
 CC neutrophil activation or ADCC capability and superoxide anion production.  
 CC zacrp5 gene and protein are also useful as antimicrobial applications,  
 CC preferably against bacteria and virus, for complement inhibition, for  
 CC treating acute vascular injury, and for wound healing. The present  
 CC sequence is human adipocyte complement related protein homolog, zsig39  
 CC protein. This protein was used in a sequence homology alignment with  
 CC zacrp5 protein.  
 CC  
 XX  
 SQ Sequence 243 AA;  
 Query Match 100.0%; Score 1325; DB 22; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRPLVLLLLGLAAGSPPLDNNKTPSLCPGHPGLPGTPGHHGSGGLPGRDGRDAPG 60  
 DB 1 MRPLVLLLLGLAAGSPPLDNNKTPSLCPGHPGLPGTPGHHGSGGLPGRDGRDAPG 60  
 QY 61 APGKGGGRGRLPGPRGDPGRGEAGPAGTGPAGCSVPPRAFAKRSSESVPPSPD 120  
 DB 61 APGKGGGRGRLPGPRGDPGRGEAGPAGTGPAGCSVPPRAFAKRSSESVPPSPD 120  
 QY 121 APLEFDRVLVNEOGHYDAVTGKFTQVPGYVFAVHAATVYRASLQDFLVNKGESIASFFQ 180  
 DB 121 APLEFDRVLVNEOGHYDAVTGKFTQVPGYVFAVHAATVYRASLQDFLVNKGESIASFFQ 180  
 QY 181 PFGGWPKPASLSGAMVRLPEDDQVWVQGVGYDITGIVASIKTDTSTSGFLVYSDMHSSP 240  
 DB 181 PFGGWPKPASLSGAMVRLPEDDQVWVQGVGYDITGIVASIKTDTSTSGFLVYSDMHSSP 240  
 QY 241 VFA 243  
 DB 241 VFA 243

ID ABA49599 standard; Protein: 243 AA.  
 XX  
 AC ABA49599;  
 XX  
 DT 13-MAR-2001 (first entry)  
 XX  
 DE Human adipocyte complement related protein homolog zsig39.  
 XX  
 DE Human; zacrp6; gene therapy; complement inhibition; C1q domain;  
 KW adipocyte complement related protein homolog;  
 KW inflammation; hormone secretion; inositol phosphate; arachidonate;  
 KW phospholipase C activation; gastric emptying; neutrophil activation;  
 KW superoxide anion production; antimicrobial; acute vascular injury;  
 KW wound healing; zsig39.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200073446-A2.  
 XX  
 PD 07-DEC-2000.  
 XX  
 PE 22-MAY-2000; 2000WO-US14024.  
 XX  
 PR 27-MAY-1999; 99US-0321262.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Pliddington CS, Sheppard FO;  
 XX  
 DR WPI: 2001-061532/07.  
 XX  
 PT Novel adipocyte complement related protein homolog, ZACRP6, useful as  
 PT modulators of neurotransmission and for treating disseminated  
 PT intravascular coagulation, arteriosclerosis and acute vascular injury  
 XX  
 PS Disclosure; Fig 1; 119pp; English.  
 XX  
 CC The present invention relates to human adipocyte complement related  
 CC protein homolog, ZACRP6 protein and coding sequence (see ABA49596 and  
 CC AAC90051). ZACRP6 has a carboxyl-terminal C1q domain. The zacrp6 gene is  
 CC located on human chromosome 21q. zacrp6 gene and protein are useful for  
 CC diagnosing and treating inflammations, for determining arterial  
 CC remodeling, for modulating calcium ion concentration, hormone  
 CC secretion, DNA synthesis or cell growth, inositol phosphate turnover,  
 CC arachidonate release, phospholipase C activation, gastric emptying, human  
 CC neutrophil activation or ADCC capability and superoxide anion production.  
 CC zacrp6 gene and protein are also useful as antimicrobial applications,  
 CC preferably against bacteria and virus, for complement inhibition, for  
 CC treating acute vascular injury, disseminated intravascular coagulation,  
 CC arteriosclerosis and for wound healing. The present sequence is human  
 CC adipocyte complement related protein homolog zsig39. This protein was  
 CC used in a sequence homology comparison with ZACRP6 protein.  
 CC  
 XX  
 SQ Sequence 243 AA;  
 Query Match 100.0%; Score 1325; DB 22; Length 243;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-103;  
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRPLVLLLLGLAAGSPPLDNNKTPSLCPGHPGLPGTPGHHGSGGLPGRDGRDAPG 60  
 DB 1 MRPLVLLLLGLAAGSPPLDNNKTPSLCPGHPGLPGTPGHHGSGGLPGRDGRDAPG 60  
 QY 61 APGKGGGRGRLPGPRGDPGRGEAGPAGTGPAGCSVPPRAFAKRSSESVPPSPD 120  
 DB 61 APGKGGGRGRLPGPRGDPGRGEAGPAGTGPAGCSVPPRAFAKRSSESVPPSPD 120  
 QY 121 APLEFDRVLVNEOGHYDAVTGKFTQVPGYVFAVHAATVYRASLQDFLVNKGESIASFFQ 180  
 DB 121 APLEFDRVLVNEOGHYDAVTGKFTQVPGYVFAVHAATVYRASLQDFLVNKGESIASFFQ 180  
 QY 181 PFGGWPKPASLSGAMVRLPEDDQVWVQGVGYDITGIVASIKTDTSTSGFLVYSDMHSSP 240  
 DB 181 PFGGWPKPASLSGAMVRLPEDDQVWVQGVGYDITGIVASIKTDTSTSGFLVYSDMHSSP 240



DB 181 FFGGMPKPKASLSGGAMVRLPEPDQWVGVGDYIGIYASIKTDSFSGFLVYSDWHSSP 240  
QY 241 VFA 243  
DB 241 VFA 243

## RESULT 12

AAB65891

ID AAB65891 standard; Protein: 243 AA.

AAB65891;

28-MAR-2001 (first entry)

Human secreted protein related protein SEQ ID NO: 108.

Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;

INTERCEPT 258; coronary disorder; olfactory disorder;

neurological disorder; pulmonary disorder; immunological disorder;

developmental disorder; kidney disorder.

Homo sapiens.

WO200078808-A1.

28-DEC-2000.

19-JUN-2000; 2000WO-US16883.

18-JUN-1999; 99US-0336536.

(MILL-) MILLENNIUM PHARM INC.

Leiby KR, McKay C, Bossone S;

WPI; 2001-050109/06.

New nucleic acids for treating diseases and disorders, e.g.

atherosclerosis, infection, autoimmune diseases, obesity, ear

disorders, brain disorders, tumors, diabetes, arthritis, multiple

sclerosis and asthma -

Disclosure; Page 274; 332pp; English.

The present invention provides the protein and coding sequences of the

human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,

TANGO 281 and INTERCEPT 258. These are useful in the treatment of

coronary, pulmonary, olfactory, immunological, neurological,

developmental and kidney disorders.

Sequence 243 AA:

Query Match 99.8%; Score 1323; DB 22; Length 243;

Best Local Similarity 99.6%; Pred. No. 7.8e-103;

Matches 242; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAASPLDDNKIPSLCPGHPGLPCTPGHNSOGLPGHDGRDGDAG 60  
DB 1 MRPLVLLLLGLAASPLDDNKIPSLCPGHPGLPCTPGHNSOGLPGHDGRDGDAG 60  
QY 61 AGEKGEGRPLPGRGDPGRGEPAGPTGPAEGCVPPRSASFSAKRSRVPSPD 120  
DB 61 AGEKGEGRPLPGRGDPGRGEPAGPTGPAEGCVPPRSASFSAKRSRVPSPD 120  
QY 121 APLPDRVLVNEQGHYDAVTGKFTQVPGVYFAVAHATYRASLQFDLVKNESIASFQ 180  
DB 121 APLPDRVLVNEQGHYDAVTGKFTQVPGVYFAVAHATYRASLQFDLVKNESIASFQ 180  
QY 181 FFGGMPKPKASLSGGAMVRLPEPDQWVGVGDYIGIYASIKTDSFSGFLVYSDWHSSP 240  
DB 181 FFGGMPKPKASLSGGAMVRLPEPDQWVGVGDYIGIYASIKTDSFSGFLVYSDWHSSP 240

QY 241 VFA 243  
DB 241 VFA 243

## RESULT 13

AAB65888

ID AAB65888 standard; Protein: 243 AA.

AAB65888;

28-MAR-2001 (first entry)

Human secreted protein related protein SEQ ID NO: 102.

Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;

INTERCEPT 258; coronary disorder; olfactory disorder;

neurological disorder; pulmonary disorder; immunological disorder;

developmental disorder; kidney disorder.

Homo sapiens.

WO200078808-A1.

28-DEC-2000.

19-JUN-2000; 2000WO-US16883.

18-JUN-1999; 99US-0336536.

(MILL-) MILLENNIUM PHARM INC.

Leiby KR, McKay C, Bossone S;

WPI; 2001-050109/06.

New nucleic acids for treating diseases and disorders, e.g.

atherosclerosis, infection, autoimmune diseases, obesity, ear

disorders, brain disorders, tumors, diabetes, arthritis, multiple

sclerosis and asthma -

Disclosure; Page 270-271; 332pp; English.

The present invention provides the protein and coding sequences of the

human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,

TANGO 281 and INTERCEPT 258. These are useful in the treatment of

coronary, pulmonary, olfactory, immunological, neurological,

developmental and kidney disorders.

Sequence 243 AA:

Query Match 99.7%; Score 1321; DB 22; Length 243;

Best Local Similarity 99.6%; Pred. No. 1.1e-102;

Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAASPLDDNKIPSLCPGHPGLPCTPGHNSOGLPGHDGRDGDAG 60  
DB 1 MRPLVLLLLGLAASPLDDNKIPSLCPGHPGLPCTPGHNSOGLPGHDGRDGDAG 60  
QY 61 AGEKGEGRPLPGRGDPGRGEPAGPTGPAEGCVPPRSASFSAKRSRVPSPD 120  
DB 61 AGEKGEGRPLPGRGDPGRGEPAGPTGPAEGCVPPRSASFSAKRSRVPSPD 120  
QY 121 APLPDRVLVNEQGHYDAVTGKFTQVPGVYFAVAHATYRASLQFDLVKNESIASFQ 180  
DB 121 APLPDRVLVNEQGHYDAVTGKFTQVPGVYFAVAHATYRASLQFDLVKNESIASFQ 180  
QY 181 FFGGMPKPKASLSGGAMVRLPEPDQWVGVGDYIGIYASIKTDSFSGFLVYSDWHSSP 240  
DB 181 FFGGMPKPKASLSGGAMVRLPEPDQWVGVGDYIGIYASIKTDSFSGFLVYSDWHSSP 240  
QY 241 VFA 243

Db 241 VFA 243

RESULT 14  
AAB65889  
ID AAB65889 standard; Protein: 243 AA.  
XX  
AC AAB65889;  
XX  
DT 28-MAR-2001 (first entry)  
XX  
DE Human secreted protein related protein SEQ ID NO: 104.  
XX  
KW Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;  
KW INTERCEPT 258; coronary disorder; olfactory disorder;  
KW neurological disorder; pulmonary disorder; immunological disorder;  
KW developmental disorder; kidney disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200078808-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 19-JUN-2000; 2000WO-US16883.  
XX  
PR 18-JUN-1999; 99US-0336536.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Leiby KR, McKay C, Bossone S;  
XX  
DR WPI: 2001-050109/06.  
XX  
PT New nucleic acids for treating diseases and disorders, e.g.  
PT atherosclerosis, infection, autoimmune diseases, obesity, ear  
PT disorders, brain disorders, tumors, diabetes, arthritis, multiple  
PT sclerosis and asthma  
XX  
PS Disclosure; Page 271-272; 332pp; English.  
XX  
CC The present invention provides the protein and coding sequences of the  
CC human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,  
CC TANGO 281 and INTERCEPT 258. These are useful in the treatment of  
CC coronary, pulmonary, olfactory, immunological, neurological,  
CC developmental and kidney disorders.  
XX  
SQ Sequence 243 AA;

Query Match 99.7%; Score 1321; DB 22; Length 243;  
Best Local Similarity 99.6%; Pred. No. 1.le-102;  
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNRKTPSLCPGHPGLPGTPGHHSQGLRGDRGDRDAPG 60  
DB 1 MRPLVLLLLGLAAGSPPLDNRKTPSLCPGHPGLPGTPGHHSQGLRGDRGDRDAPG 60  
QY 61 APGEKGGGRGRLGPRGDPGPRGEGAPAGPTGAGGCSVPPRSAFSAKSESSESVPPSPD 120  
DB 61 APGEKGGGRGRLGPRGDPGPRGEGAPAGPTGAGGCSVPPRSAFSAKSESSESVPPSPD 120  
QY 121 APLEFDVLYNEQGHYAVTGKFTCOVPGYVFAVHATVYRASLQDFLVNNGESIASFFQ 180  
DB 121 APLEFDVLYNEQGHYAVTGKFTCOVPGYVFAVHATVYRASLQDFLVNNGESIASFFQ 180  
QY 181 FFGGMPKPAASLSGAMVRLPEPDQVWVQVGVGDIIGIYASIKTDSTSGFLVYSMDHSSP 240  
DB 181 FFGGMPKPAASLSGAMVRLPEPDQVWVQVGVGDIIGIYASIKTDSTSGFLVYSMDHSSP 240  
QY 241 VFA 243  
DB 241 VFA 243

Db 241 VFA 243

RESULT 15  
AAB65890  
ID AAB65890 standard; Protein: 243 AA.  
XX  
AC AAB65890;  
XX  
DT 28-MAR-2001 (first entry)  
XX  
DE Human secreted protein related protein SEQ ID NO: 106.  
XX  
KW Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;  
KW INTERCEPT 258; coronary disorder; olfactory disorder;  
KW neurological disorder; pulmonary disorder; immunological disorder;  
KW developmental disorder; kidney disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200078808-A1.  
XX  
PD 28-DEC-2000.  
XX  
PF 19-JUN-2000; 2000WO-US16883.  
XX  
PR 18-JUN-1999; 99US-0336536.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Leiby KR, McKay C, Bossone S;  
XX  
DR WPI: 2001-050109/06.  
XX  
PT New nucleic acids for treating diseases and disorders, e.g.  
PT atherosclerosis, infection, autoimmune diseases, obesity, ear  
PT disorders, brain disorders, tumors, diabetes, arthritis, multiple  
PT sclerosis and asthma  
XX  
PS Disclosure; Page 272-273; 332pp; English.  
XX  
CC The present invention provides the protein and coding sequences of the  
CC human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,  
CC TANGO 281 and INTERCEPT 258. These are useful in the treatment of  
CC coronary, pulmonary, olfactory, immunological, neurological,  
CC developmental and kidney disorders.  
XX  
SQ Sequence 243 AA;

Query Match 99.7%; Score 1321; DB 22; Length 243;  
Best Local Similarity 99.6%; Pred. No. 1.le-102;  
Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MRPLVLLLLGLAAGSPPLDNRKTPSLCPGHPGLPGTPGHHSQGLRGDRGDRDAPG 60  
DB 1 MRPLVLLLLGLAAGSPPLDNRKTPSLCPGHPGLPGTPGHHSQGLRGDRGDRDAPG 60  
QY 61 APGEKGGGRGRLGPRGDPGPRGEGAPAGPTGAGGCSVPPRSAFSAKSESSESVPPSPD 120  
DB 61 APGEKGGGRGRLGPRGDPGPRGEGAPAGPTGAGGCSVPPRSAFSAKSESSESVPPSPD 120  
QY 121 APLEFDVLYNEQGHYAVTGKFTCOVPGYVFAVHATVYRASLQDFLVNNGESIASFFQ 180  
DB 121 APLEFDVLYNEQGHYAVTGKFTCOVPGYVFAVHATVYRASLQDFLVNNGESIASFFQ 180  
QY 181 FFGGMPKPAASLSGAMVRLPEPDQVWVQVGVGDIIGIYASIKTDSTSGFLVYSMDHSSP 240  
DB 181 FFGGMPKPAASLSGAMVRLPEPDQVWVQVGVGDIIGIYASIKTDSTSGFLVYSMDHSSP 240  
QY 241 VFA 243  
DB 241 VFA 243

Search completed: June 13, 2003, 16:00:38  
Job time : 73 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 21, 2003, 14:32:46 ; Search time 202 Seconds

(without alignments)  
1816.694 Million cell updates/sec

Title: US-09-944-944-41

Perfect score: 2540  
Sequence: 1 gactagttctcttgagctc.....aaaaaaaaaaaaaaaa 1377

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 1816940

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -STAR=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi
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-MODE=LOCAL -OUTFMT=ptc -NOR=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGOQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELXT=7
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Database :

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23: /SIDS2/gcgcdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1325	52.2	243	20	AAV06481	Human tumour-assoc
2	1325	52.2	243	20	AAV17827	Human PRO344 prote
3	1325	52.2	243	20	AAW97984	Human adipocyte-sp
4	1325	52.2	243	21	AAW33461	Human PRO344 prote
5	1325	52.2	243	21	AAV71468	Human PRO344 prote
6	1325	52.2	243	21	AAV93688	Amino acid sequenc
7	1325	52.2	243	21	AAAB01318	Human PRO344 polyp
8	1325	52.2	243	22	AAU12352	Human TANGO 253 SE
9	1325	52.2	243	22	AAAB4593	Human adipocyte co
10	1325	52.2	243	22	AAAB4599	Human adipocyte co
11	1325	52.2	243	22	AAAB5891	Human secreted pro
12	1323	52.1	243	22	AAAB5888	Human secreted pro
13	1321	52.0	243	22	AAAB5889	Human secreted pro
14	1321	52.0	243	22	AAAB5890	Human secreted pro
15	1321	52.0	243	22	AAV76040	Rat skin cell prot
16	1271	50.0	243	22	AAV55979	Skin cell protein,
17	1271	50.0	243	23	ABW72179	Rat protein isolat
18	1258	49.5	243	22	AAAB5820	Murine TANGO 253 S
19	1256	49.4	228	22	AAAB5816	Human mature TANGO
20	1256	49.4	243	22	AAAB5899	Murine secreted pr
21	1256	49.4	243	22	AAAB5897	Murine secreted pr
22	1254	49.4	243	22	AAAB5898	Murine secreted pr
23	1254	49.4	243	22	AAAB5896	Murine mature TANG
24	1243.5	49.0	242	22	AAAB5821	Novel human diagno
25	1200	47.2	220	22	ABG12724	Human secreted pro
26	1183	46.6	220	22	AAO21663	Human TANGO 253 C1
27	1048	41.3	201	23	AAAB5819	Murine TANGO 253 C
28	675	26.6	128	22	AAAB5824	Human colon cancer
29	650	25.6	95	22	AAAG74016	Novel human diagno
30	518	20.4	95	22	ABG12723	Human sbp1033026C1
31	480.5	18.9	151	22	ABAB80583	Murine adipocyte c
32	449.5	17.7	225	23	ABAB80583	Murine adipocyte c
33	446	17.6	333	23	AAW09107	Mouse OB33 protein
34	433.5	17.1	247	18	AAW09107	Mouse OB33 protein
35	433.5	17.1	247	22	AAE05528	Mouse adipocyte co
36	433.5	17.1	247	22	ABW08222	Mouse adipocyte co
37	427	16.8	289	23	ABW72306	Rat protein isolat
38	425	16.7	244	18	AAW09108	Human adipocyte co
39	424.5	16.7	247	23	AAE05527	Mouse OB33 protein
40	424.5	16.7	247	23	ABW08221	Mouse adipocyte co
41	424	16.7	244	20	ABW21807	Adipose most abund
42	424	16.7	244	21	AAW30233	Human adipocyte co
43	424	16.7	244	21	AAV71035	Human APW1 (Adipos
44	424	16.7	244	22	AAE05529	Human OB33 protein
45	424	16.7	244	22	AAAB5828	Human adipocyte co

## ALIGNMENTS

RESULT 1  
AAV06481 standard; Protein; 243 AA.

AAV06481;

27-SEP-1999 (first entry)

Human tumour-associated protein PRO344.

PRO344; UNQ303; cancer; tumour; diagnosis; therapy; human.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..15

Protein /note="signal peptide" 16..243 /note="mature protein"



















OY		347 CATGCGACGCAGGGCTTCCGGGCCGCAATGGCAGGACCAGCGCACGGCCGGCCGGG	408
Dd		41 HtSGlySerGelngIyLeurProGIYAgaSPeGYArGaSPelYArGaSPeLYAlalAProGLY	60
OY		407 GCTCCGGGAGAAMAAGCGAAGGGCCGGAGCCGGGACTGCCGGACCTCGAGGGAGCCC	466
Dd		61 ALaPPrOGlYglUbLySgLIylugLiyGAyrPGrOGLYleUrProGlYProlAArgIAspPro	80
OY		467 GGCGCCGCGAGGAGAGCGGGACCCCCGGGGGCCAACCGGGGTTCGCGGGAGTGCTGGTG	528
Dd		81 GLYPROHAgELYglUnlaagLYPROlaagLYPRoThGLIPRolaagLYaLucYSerVal	1000
OY		527 CCTCCGCGATTCCGCTTCAGCGCGCAAAGCCGCTCGAGAGCCGGGTGCCCTCCGCTYGAC	586
Dd		101 PROPrARgsERlalaphESERallaySaRGserGIuseRaRYalPROPPropRoSeRAsp	1200
OY		587 GCACCCCTTGCCCTTCGACCGCGGTGCTGGTAACAAGACAGAGCATTAACAAGCCGCTAC	648
Dd		121 AlApRoleUrpRheASpaRYalLeuvaIASnGLUGnlghISTryAsPaLaVaIThr	1400
OY		647 GGCAGATTCACCTGCCAGGTGCCTGGGGTCTACTACTCGCCGCTCATGCGCACCGTCTAC	706
Dd		141 GlYLysPhetHrcYsgLnvalPRogLYalTYTyTRphebaIValaHSalsatHrrvaITyr	1600
OY		707 CGGSCCAGCCTCAGTTGATCTGTGAAGAATGGCGAAATCCATNGCCTTTCTTCAG	766
Dd		161 ArGalasErlengInlpHeaspLeuvaiLYsaSnGLYgiUseRIIEalasErphEphegn	1800
OY		767 TTTTTCGGGGGGTGGCCCAAGCAGCGCTGCTCGGGGGGGGCCAMTAGGAGAGCTCGAG-828	
Dd		181 PhEPheGelyELtyTPRoplysPRoaLasElLenSerGlyALametyVALargLEgn	2000
OY		827 CCGTAGAGCAAGTGtggGTgcAGtgGGTgtGGTGactAcATPgGCATcTAATGCCAGC	886
Dd		201 PRoGiuaSpGINvAITRpYaIGlnVAlgLYaIgLYASPtyrILlegilyIEtyRYalaser	2200
OY		887 ATCAAGACAGACAGACACCTTCCCGGATTTCTGGSTACTCCGACGTGGACAGCTCCCA	946
Dd		221 IIElySTRhpSPSetHRphEsERGlyPhELEuVAITrsERasPIRHISserSerPro	2400
OY		947 GTCTTTGCTN 955       	
Dd		241 ValpheaIIa 243	
RESULT 10			
ID	AAB49593	standard; Protein; 243 AA.	
XX	AAB49593;		
AC	13-MAR-2001	(first entry)	
DT			
DE	Human adipocyte complement related protein homolog zslj39.		
KW	Human; znrf5; gene therapy; complement inhibition; Clq domain; adipocyte complement related protein homolg; inflammation; hormone secretion; inositol phosphate; arachidonate; phospholipase c activation; gastric emptying; neutrophil activator; superoxide anion production; antimicrobial; acute vascular injury; wound healing; zsij39.		
KX	Homo sapiens.		
OS			
PB	WO200073444-A1.		
PD	07-DEC-2000.		
PF	18-MAY-2000; 2000MO-USJ13608.		
PR	27-MAY-1999; 99US-0321372.		
RZ	(ZYMO ) ZYMOMENTICS INC.		

PI	Piddington CS, Sheppard PO:
DR	WPI: 2001-061531/07.
XX	
PT	Novel adipocyte complement related protein homolog, ZACRP5, useful for
PR	diagnosing and treating inflammation, vascular injury microbial
PP	infections, and in wound healing -
PS	Disclosure; Fig 1; 121pp; English.
CC	
XX	The present invention relates to human adipocyte complement related
CC	protein homolog, zacrps protein and coding sequence (see AAB49590 and
CC	AAC90045). ZACRP5 has a carboxyl-terminal C1q domain. The zacrps gene is
CC	located on human chromosome 16. zacrps gene and protein are useful for
CC	diagnosing and treating inflammations, for determining arterial
CC	remodelling, for modulating calcium ion concentration, hormone
CC	secretion, DNA synthesis or cell growth, inositol phosphate turnover,
CC	arachidonate release, phospholipase C activation, gastric emptying, human
CC	neutrophil activation or ADPC capability and superoxide anion production.
CC	Zacrp5 gene and protein are also useful as antimicrobial applications,
CC	preferably against bacteria and virus, for complement inhibition, for
CC	treating acute vascular injury, and for wound healing. The present
CC	sequence is human adipocyte complement related protein homolog, zs1g39
CC	protein. This protein was used in a sequence homology alignment with
CC	zacrps protein.
XX	
SQ	Sequence 243 AA;
	Alignment Scores:
	Pred. No.: 5.37e-86 Length: 243
	Score: 1325.00 Matches: 243
	Percent Similarity: 100.00% Conservative: 0
	Best Local Similarity: 100.00% Mismatches: 0
	Query Match: 52.17% Indels: 0
	DB: 22 Gaps: 0
US-09-944-944-41 (1-1377) x AAB49593 (1-243)	
OY	227 ATGAGGCACCTCCTCGTCTGTGTCCTGGGCGTGCGCGCGGCTGCCCACTGGAC 286
Db	1 MetArgProLeuLeuValLeuLeuLeuLeuLeuGlyLeuAlaIlaaglySerProProLeuAsp 20
OY	287 GACAACAAGATCCCAGCGCTGCGCCCGGGGACCCCCGGGCTTCCAGGGACGCGGGGCAC 346
Db	21 AspAsnLysIleProSerLeucySProGlyHisPProGlyLeuProGlyThrProGlyHis 40
OY	347 CATGGCACCGCAGGGCTTGGCCGGCGCCGCATGGCGCGACGGCCGACGCGCGCCGGG 406
Db	41 HisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyAlaProGly 60
OY	407 GCTCCGGGAGAAGAAAGCGAAGGCGGGGAAGCCGGGACATCGCGGACTCGAGGGGACCCC 466
Db	61 AlaProGlyGlyIuyluSglyGluGlyGlyArgProGlyLeuProGlyProArgGlyAspPro 80
OY	467 GGCGCCGAGAGAGGCGGGGACC CGCGGGGCCACCGGGGCTGCCGGGAGTTGCTCGGTG 526
Db	81 GlyProArgGlyIuyluIaGlyProAlaGlyProAlaGlyProAlaGlyIuCySerVal 100
OY	527 CTTCGCGATCGCGCTTCAAGCGCCAAGCGCTCCGAGACCGGGTGCCTCGCGCTTGAC 586
Db	101 ProProArgSerAlaPheSerAlaLysArgSerGIuSerAtGvalProProProSerAsp 120
OY	587 GCACCTTGCCCTTGACCGCGCTGGTGGAACGACGAGGAATTACGAGCCGCTACC 646
Db	121 AlaProLeuProPheAspArgValLeuValuValasngluGlnGlyHisTyrAspAlaValThr 140
OY	647 GGCAGATTACCTGCGCAGGTGCTGGGGGTCTACTCTTCCGCGSCATATGCCACGCTTAC 706
Db	141 GlyLyserPheThrcySeluValaIProGlyValTytyrPheAlaValaHIsAlaThrValTyr 160
OY	707 CGGGCAGCCTGCATGTTGATGTGGTAAGAAATGGCGAATGCATTCCTTTCTTCCAG 766
Db	161 ArgAlaSerLeuGlnIlePheAspLeuValLysAsnGlyIuSerIleAlaSerPhePheGln 180

OY		767	TTTTTGGGGGGGTGGCCCAAGGCACGCTCGCTGGGGGGGCCATGCTGAGCGTGAG	826
Dd		181	PhePheGlyGlyTTPProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGlu	200
OY		827	CCTAAGACACAAAGTGTGGGTCCAGGTGGGTGGGTGCATCAATTGGCATCTATGCGCAC	886
Dd		201	ProGlnAspGlnValTrpValGlnValGlyValGlyAspTYrIleGlyIleTYrAlaSer	220
OY		887	ATCAAGACAGACAGCACCCTTCGCGGATTTGTGTACTCCGACGTGCAGACAGCTCCCA	946
Dd		221	IleIleSThrAspSerThrPheSerGlyPheLeuValTYrSerAspPrpHisSerPro	240
OY		947	GTCCTTGCT	955
Dd		241	ValPheAla	243
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XX	AAC	AAB49599:		
XX	DT	13-MAR-2001	(first entry)	
DE	DE	Human adipocyte complement related protein homolog zsig39.		
KW	KW	Human; zacrpf; gene therapy; complement inhibition; C1q domain;		
KM	KM	adipocyte complement related protein homolog;		
KV	KV	inflammation; hormone secretion; inositol phosphate; arachidonate;		
KW	KW	phospholipase C activation; gastric emptying; neutrophil activation;		
KM	KM	superoxide anion production; antimicrobial; acute vascular injury;		
KW	KW	wound healing; zsig39.		
OS	XX	Homo sapiens.		
XX	PN	MO200073446-A2.		
PD	PD	07-DEC-2000.		
XX	XX			
PF	XX	22-MAY-2000; 2000OWO-US14024.		
XX	XX			
PR	XX	27-MAY-1999; 99US-0321262.		
XX	PA	(Zymo ) ZYMOGENETICS INC.		
PI	PI	Pliddington CS, Sheppard PO;		
DR	XX			
PT	PT	WPI; 2001-061532/07.		
XX	XX			
PS	PS			
XX	XX			
Disclosure: Fig 1; 119pp; English.				
CC	CC	The present invention relates to human adipocyte complement related		
CC	CC	protein homolog, ZACRP6 protein and coding sequence (see AAB49596 and		
CC	CC	AAC90051). ZACRP6 has a carboxyl-terminal C1q domain. The zacrpf gene is		
CC	CC	located on human chromosome 21q. zacrpf gene and protein are useful for		
CC	CC	remodeling and treating inflammations, for determining arterial		
CC	CC	remodelling, for modulating calcium ion concentration, hormone		
CC	CC	secretion, DNA synthesis or cell growth, inositol phosphate turnover,		
CC	CC	arachidonate release, phospholipase C activation, gastric emptying, human		
CC	CC	neutrophil activation or ADCC capability and superoxide anion production.		
CC	CC	zacrpf gene and protein are also useful as antimicrobial applications,		
CC	CC	preferably against bacteria and virus, for complement inhibition, for		
CC	CC	treating acute vascular injury, disseminated intravascular coagulation,		
CC	CC	arteriosclerosis and for wound healing. The present sequence is human		
CC	CC	adipocyte complement related protein homolog zsig39. This protein was		
XX	XX	used in a sequence homology comparison with ZACRP6 protein.		

[illegible]







```

Db      141 GlyylsPhehrCysGlnValProGlyValTyrPhealValHisAlaThrValTyr 160
Oy      707 CGGGCCAGCCTGCAGTTGATCTGTGTAAGAAATGCGCAATCCATTGCCTTCTTCCAG 766
Db      161 ArgAlaSerLeuGlnPheAspLeuValIysAsnGlyIleuAlaSerPheGln 180
Oy      767 TTTTTCGGGGGGGCGCCCAAGCCAGCTCGCTCTCGGGGGGGCCATGCTAGAGCTGAG 826
Db      181 PheheGlyGlyTyrProIysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGln 200
Oy      827 CCTAGAGACCAAGTGTGGTGCAGTGGTGGTGGTACTTACATTGGCATTAAGCCAGC 886
Db      201 ProGlnAspGlnValITrpValGlnValGlyAspTyrIleGlyIleTyrAlaSer 220
Oy      887 ATCAAGACAGACAGACACCTTCTCGGATTTCTGTGTTACTCGACTGGACAGCTCCCA 946
Db      221 IleYsthrAspSerThrPheSerGlyPheLeuValTyrSerAspTrpHisSerSerPro 240
Oy      947 GTCTTTGCT 955
Db      241 ValPheAla 243

```

## RESULT 15

AAB65890 standard; Protein; 243 AA.

AAB65890:

28-MAR-2001 (first entry)

Human secreted protein related protein SEQ ID NO: 106.

Human; mouse; secreted protein; TANGO253; TANGO 257; TANGO 281;

INTERCEPT 258; coronary disorder; olfactory disorder;

neurological disorder; pulmonary disorder; immunological disorder;

developmental disorder; kidney disorder.

Homo sapiens.

MO200078808-A1.

28-DEC-2000.

19-JUN-2000; 2000MO-US16883.

18-JUN-1999; 99US-0336536.

(MILL-) MILENNIUM PHARM INC.

Lelby KR, McKay C, Bossone S;

WPI; 2001-050109/06.

New nucleic acids for treating diseases and disorders, e.g.

atherosclerosis, infection, autoimmune diseases, obesity, ear

disorders, brain disorders, tumors, diabetes, arthritis, multiple

sclerosis and asthma

Disclosure; Page 272-273; 332pp; English.

The present invention provides the protein and coding sequences of the

human and murine secreted or transmembrane proteins TANGO 253, TANGO 257,

TANGO 281 and INTERCEPT 258. These are useful in the treatment of

coronary, pulmonary, olfactory, immunological, neurological,

developmental and kidney disorders.

Sequence 243 AA;

Alignment Scores:

Pred. No.: 1.03e-85

Score: 1321.00

Percent Similarity: 99.598

Length: 243

Matches: 242

Conservative: 0

Best Local Similarity: 99.598  
Query Match: 52.01%  
DB: 22  
Gaps: 0

US-09-944-944-41 (1-1377) x AAB65890 (1-243)

```

Oy      227 ATGAGGCACTCTCTGCTGCTGCTCTCTCTGCGGCTGGCGGGCTGCGCCCTGAGC 286
Db      1 MetArgProLeuLeuValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 20
Oy      287 GACAAACAAATCCCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 346
Db      21 AspaAsnYsIleProSerLeuCysProGlyHisProGlyLeuProGlyTyrProGlyHis 40
Oy      347 CATGGACAGCCAGGCTTCCGCGGGCGGATGCGCGGACGCGGACGCGGACGCGGACGCGG 406
Db      41 HisGlySerGlnGlyLeuProGlyArgAspGlyArgAspGlyArgAspGlyArgAspGly 60
Oy      407 GCTCCGGGAGAGAAAGCGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 466
Db      61 AlaProGlyGlnGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 80
Oy      467 GGGCGCGAGAGAGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGGAGGCGG 526
Db      81 GlyProArgGlyGlnAlaGlyProAlaGlyProThrGlyProAlaGlyGlyGlyGlyGly 100
Oy      527 CCTCCGCGATCCGCGCTTCAGGCGCAAGCGCTCCGAGAGCGGAGGCGGAGGCGGAGGCGG 586
Db      101 ProProArgSerAlaPheSerAlaAlaGlyArgSerIleuSerArgValProProProSer 120
Oy      587 GCACCTTGGCCCTTCGACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 646
Db      121 AlaProLeuProPheAspArgValLeuAlaAsnGlnGlnIleHisTyrAspAlaValThr 140
Oy      647 GGCAGTTCACCTGCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 706
Db      141 GlyylsPhehrCysGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyr 160
Oy      707 CGGGCCAGCCTGCAGTTGATCTGTGTAAGAAATGCGCAATCCATTGCCTTCTTCCAG 766
Db      161 ArgAlaSerLeuGlnPheAspLeuValIysAsnGlyIleuAlaSerPheGln 180
Oy      767 TTTTTCGGGGGGGCGCCCAAGCCAGCTCGCTCTCGGGGGGGCCATGCTAGAGCTGAG 826
Db      181 PheheGlyGlyTyrProIysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGln 200
Oy      827 CCTAGAGACCAAGTGTGGTGCAGTGGTGGTGGTACTTACATTGGCATTAAGCCAGC 886
Db      201 ProGlnAspGlnValITrpValGlnValGlyAspTyrIleGlyIleTyrAlaSer 220
Oy      887 ATCAAGACAGACAGACCTTCTCGGATTTCTGTGTTACTCGACTGGACAGCTCCCA 946
Db      221 IleYsthrAspSerThrPheSerGlyPheLeuValTyrSerAspTrpHisSerSerPro 240
Oy      947 GTCTTTGCT 955
Db      241 ValPheAla 243

```

Search completed: June 21, 2003, 16:01:38  
Job time : 212 secs







QY 947 GTCTTGGCT 955  
Db 241 ValPheala 243

## RESULT 5

US-09-336-536-4  
; Sequence 4, Application US/09336536  
; Patent No. 6406884  
; GENERAL INFORMATION:  
; APPLICANT: Leiby, K.  
; APPLICANT: McKay, C.  
; APPLICANT: Bossone, S.  
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
; FILE REFERENCE: 7853-144  
; CURRENT APPLICATION NUMBER: US/09/336, 536  
; CURRENT FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-336-536-4

## Alignment Scores:

Pred. No.: 3,33e-83 Length: 228  
Score: 1256.00 Matches: 228  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 49.45% Indels: 0  
DB: 4 Gaps: 0

US-09-944-944-41 (1-1377) x US-09-336-536-4 (1-228)

QY 272 TCGCCCCCATGAGACGACACAAAGATCCAGCCTCGCCGGGGACACCCGGGCTTCA 331  
Db 1 SerProProLeuaspaspasnlylIleProSerLeuCySProGlyHisProGlyLeuPro 20  
QY 332 GGCACGCGGGGCGGCACCATGAGCAGCAGGCTTGCCTGGGCGCGCATGCGCGAGCGCGC 391  
Db 21 G1YThrProGlyHisHsGlySerGlnGlyLeuProGlyArGaspGlyArg 40  
QY 392 GAGCGCGCGCGCGGCTCCGGGAGAGAAAGCGGCGGAGCGCGGAGCTGCGCGGA 451  
Db 41 AspGlyAlaProGlyAlaProGlyGluGlyGlyLeuGlyArGProGlyLeuProGly 60  
QY 452 CCFGAGGGGACCCCGGCGCGAGAGAGCGGAGCGGAGCGCGGCGCGCGCGCGC 511  
Db 61 ProArgGlyAspProGlyProArgGlyGluAlaGlyProAlaGlyProThrGlyProAla 80  
QY 512 GGGAGTGTCTGGTCCCTCGCGATCCGCTTACGCGCAAGCGCTCCGAGAGCGGCTG 571  
Db 81 GlyGlyCysSerValProProArgSerAlaPheSerAlaLysArgSerGlySerArgVal 100  
QY 572 CCFCCGCGCTGACGACGACCTTGCCTTGACCGGCTGCTGTGAACGAGCAGGACAT 631  
Db 101 ProProProSerAspAlaProLeuProPheAspArgValLeuValAsnGluGlnGlyHis 120  
QY 632 TACGAGCGCGTACCGGCAAGTTCACCTGCAGGTGCTGGGCTTACTTACTTCCGCGTC 691  
Db 121 TyrAspAlaValAlaThrGlyLysPheThrCysGlnValAlaProGlyValYrtyrPheAlaVal 140  
QY 692 CATGCCACGCTACCGGGCGACCTGCATTTGATCTGGTGAAGATGGCAATCCATT 751  
Db 141 HisAlaThrValYrtyrAlaSerLeuGlnPheAspLeuValLysAsnGlyGlnSerIle 160  
QY 752 GCCTCTTCTTCAGTTTTCGGGGGGTGGCCCAAGCCAGCTCGCTTGGGGGGGGCC 811  
Db 161 AlaSerPheGlnPhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAla 180  
QY 812 ATGGTAGGCTGAGCGCTGAGACCAAGTGTGGTGGAGGTGGGTGGGTGACTCAT 871  
Db 181 MetValArgLeuGluProGlyAspGlnValTyrValGlnValGlyAlaGlyAspTyrIle 200

QY 872 GGCATCTATGCACATCAAGACAGACGACCTTTCGGAATTTCTGTACTCCGAC 931  
Db 201 GlyLeuYrAlaSerIleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAsp 220

QY 932 TGGCAGAGTCCCGACGCTTTGCT 955  
Db 221 TrpHisSerSerProValPheala 228

## RESULT 6

US-09-336-536-11  
; Sequence 11, Application US/09336536  
; Patent No. 6406884  
; GENERAL INFORMATION:  
; APPLICANT: Leiby, K.  
; APPLICANT: McKay, C.  
; APPLICANT: Bossone, S.  
; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
; FILE REFERENCE: 7853-144  
; CURRENT APPLICATION NUMBER: US/09/336, 536  
; CURRENT FILING DATE: 1999-06-18  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 228  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-336-536-11

## Alignment Scores:

Pred. No.: 3,64e-79 Length: 228  
Score: 1200.00 Matches: 216  
Percent Similarity: 96.93% Conservative: 5  
Best Local Similarity: 94.74% Mismatches: 7  
Query Match: 47.24% Indels: 0  
DB: 4 Gaps: 0

US-09-944-944-41 (1-1377) x US-09-336-536-11 (1-228)

QY 272 TCGCCCCCATGAGACGACACAAAGATCCAGCCTCGCCGGGGACACCCGGGCTTCA 331  
Db 1 SerProProLeuaspaspasnlylIleProSerLeuCySProGlyHisProGlyLeuPro 20  
QY 332 GGCACGCGGGGCGGCACCATGAGCAGCAGGCTTGCCTGGGCGCGCATGCGCGAGCGCGC 391  
Db 21 G1YThrProGlyHisHsGlySerGlnGlyLeuProGlyArGaspGlyArg 40  
QY 392 GAGCGCGCGCGGCTCCGGGAGAGAAAGCGGCGGAGCGCGGAGCTGCGCGGA 451  
Db 41 AspGlyAlaProGlyAlaProGlyGluGlyGlyLeuGlyArGProGlyLeuProGly 60  
QY 452 CCFGAGGGGACCCCGGCGCGAGAGAGCGGAGCGGAGCGGAGCGGCGCGCGCGC 511  
Db 61 ProArgGlyLysProGlyProArgGlyGluAlaGlyProAlaGlyProThrGlyProAla 80  
QY 512 GGGAGTGTCTGGTCCCTCGCGATCCGCTTACGCGCAAGCGCTCCGAGAGCGGCTG 571  
Db 81 GlyGlyCysSerValProProArgSerAlaPheSerAlaLysArgSerGlySerArgVal 100  
QY 572 CCFCCGCGCTGACGACGACCTTGCCTTGACCGGCTGCTGTGAACGAGCAGGACAT 631  
Db 101 ProProProAlaSpThrProLeuProPheAspArgValLeuLeuAsnGluGlnGlyHis 120  
QY 632 TACGAGCGCGTACCGGCAAGTTCACCTGCAGGTGCTGGGCTTACTTACTTCCGCGTC 691  
Db 121 TyrAspProThrThrGlyLysPheThrCysGlnValAlaProGlyValYrtyrPheAlaVal 140  
QY 692 CATGCCACGCTACCGGGCGACCTGCATTTGATCTGGTGAAGATGGCAATCCATT 751  
Db 141 HisAlaThrValYrtyrAlaSerLeuGlnPheAspLeuValLysAsnGlyGlnSerIle 160  
QY 752 GCCTCTTCTTCAGTTTTCGGGGGGTGGCCCAAGCCAGCTCGCTTGGGGGGGGCC 811

Db 161 AlaserPhepneIntyRPhneglyGlyTrpProLysProAlaSerLeuSerGlyGlyAla 180  
QY 812 ATGTGAGCGCGAGCGCTCGAGACCAAGTGTGGGTGACAGGGGTGGCGGCTACTACTT 871  
Db 181 MetValArgLeuGluProGluAspGlnValTrpAlaGlnValGlyValGlyAspTyrIle 200  
QY 872 GGCACTATAGCCAGCATCAAGACAGACAGACACTTCTCCGATTTCGGTGTACTCCGAC 931  
Db 201 GlyIleTyrAlaSerIleIleTyrThrAspSerThrPheSerGlyPheLeuValTyrSerAsp 220  
QY 932 TGGCACAGCTCCCAAGTCTTGGCT 955  
Db 221 TrpHisSerSerProValPheAla 228

RESULT 7  
US-09-336-536-7  
Sequence 7, Application US/09336536  
Patent No. 6406884  
GENERAL INFORMATION:  
APPLICANT: Leidy, K.  
APPLICANT: McKay, C.  
APPLICANT: Bossone, S.  
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
FILE REFERENCE: 7853-144  
CURRENT APPLICATION NUMBER: US/09/336-536  
NUMBER FILING DATE: 1999-06-18  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-336-536-7

Alignment Scores:  
Pred. No.: 2,42e-41 Length: 128  
Score: 675.00 Matches: 128  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 26.57% Indels: 0  
DB: 4 Gaps: 0

US-09-944-41 (1-1377) x US-09-336-536-7 (1-128)

QY 539 GCCTTACAGCGCCAGAGCGCTCGAGAGCGCGGTGCTCGCGCTGACAGCAACCTTGCC 598  
Db 1 AlapheserAlaLysArgSerGluSerArgValProProPheSerAspAlaProLeuPro 20  
QY 599 TTCGACCGCGTGTGTGAACAGACAGAGGACATTACAGCGCGCTCACCAGGCAAGTTCAC 658  
Db 21 PheAspArgValLeuValAsnGluGlnGlyHisTyrAspAlaValThrGlyLysPheThr 40  
QY 659 TGGCAGGTGCTGGGGTCTACTACTTGCCTCCATGCGCAGCCGCTCTACCGGCGCAGCCTG 718  
Db 41 CysGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyrArgAlaSerLeu 60  
QY 719 CAGTTGATCTGTGAGAAATGCGAATGCATTCGCTCTCTCCAGTTTTCGGGGGG 778  
Db 61 GlnPheAspLeuValLysAsnGlyLysSerIleAlaSerPhePheGlnPheGlyGly 80  
QY 779 TGGCCCAAGCCAGCGCTGCTCTCGGGGGGCGCATGTGTGAGCGTGAAGCTGAGAGCCAA 838  
Db 81 TrpProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGluProGluAspGln 100  
QY 839 GTGGGGTGCAGGTGGGTGGGTGAGTACTACTTGGCATCTATGCGCAGCATCAAGACAGAC 898  
Db 101 ValTrpValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSerIleLysThrAsp 120  
QY 899 AGCACCTTCTCCGAGATTCTGTG 922  
Db 121 SerThrPheSerGlyPheLeuVal 128

RESULT 8

US-09-336-536-14  
Sequence 14, Application US/09336536  
Patent No. 6406884  
GENERAL INFORMATION:  
APPLICANT: Leidy, K.  
APPLICANT: McKay, C.  
APPLICANT: Bossone, S.  
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
FILE REFERENCE: 7853-144  
CURRENT APPLICATION NUMBER: US/09/336-536  
NUMBER FILING DATE: 1999-06-18  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-336-536-14

Alignment Scores:  
Pred. No.: 1,54e-39 Length: 128  
Score: 650.00 Matches: 121  
Percent Similarity: 97.66% Conservative: 4  
Best Local Similarity: 94.53% Mismatches: 3  
Query Match: 25.59% Indels: 0  
DB: 4 Gaps: 0

US-09-944-944-41 (1-1377) x US-09-336-536-14 (1-128)

QY 539 GCCTTACAGCGCCAGAGCGCTCGAGAGCGCGGTGCTCGCGCTGACAGCAACCTTGCC 598  
Db 1 AlapheserAlaLysArgSerGluSerArgValProProPheSerAspAlaProLeuPro 20  
QY 599 TTCGACCGCGTGTGTGAACAGACAGAGGACATTACAGCGCGCTCACCAGGCAAGTTCAC 658  
Db 21 PheAspArgValLeuValAsnGluGlnGlyHisTyrAspProThrThrGlyLysPheThr 40  
QY 659 TGGCAGGTGCTGGGGTCTACTACTTGCCTCCATGCGCAGCCGCTCTACCGGCGCAGCCTG 718  
Db 41 CysGlnValProGlyValTyrTyrPheAlaValHisAlaThrValTyrArgAlaSerLeu 60  
QY 719 CAGTTGATCTGTGAGAAATGCGAATGCATTCGCTCTCTCCAGTTTTCGGGGGG 778  
Db 61 GlnPheAspLeuValLysAsnGlyLysSerIleAlaSerPhePheGlnTyrPheGlyGly 80  
QY 779 TGGCCCAAGCCAGCGCTGCTCTCGGGGGGCGCATGTGTGAGCGTGAAGCTGAGAGCCAA 838  
Db 81 TrpProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGluProGluAspGln 100  
QY 839 GTGGGGTGCAGGTGGGTGGGTGAGTACTACTTGGCATCTATGCGCAGCATCAAGACAGAC 898  
Db 101 ValTrpValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSerIleLysThrAsp 120  
QY 899 AGCACCTTCTCCGAGATTCTGTG 922  
Db 121 SerThrPheSerGlyPheLeuVal 128

RESULT 9

US-08-463-911-2  
Sequence 2, Application US/08463911  
Patent No. 5869330  
GENERAL INFORMATION:  
APPLICANT: Scherer, Philipp E.  
APPLICANT: Lodish, Harvey F.  
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED  
TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA





```
QY 602 GACCGCTGCTGTGAACGAGCAGGACATTACGACCGCTCACCGGCAAGTTCCCTGC 661
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 ThrIlePheTyRAsnGlnGlnAsnHisTyRAspGlySerThrGlyLysPheTyRcys 155
QY 662 CAGTGGCTGGGGCTCACTACTGCGCGCTGACCCACCGCTACCGGGGACCGCTGCAG 721
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 156 AsnIleProGlyLeuTyTyRPheserTyHisIleThrValTyRMetLysAspValLys 175
QY 722 TTTGATCTGTGAAGATGGGATATCCATCCCTCTTCCTCCAGTTTTCGGGGGGTGG 781
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 176 ValSerLeuPheTyRAspLysAspLysAlaValLeuPheThrTyRAspGlnTyRGlInL 194
QY 782 CCCAAGCCAGCGCTGCTCTCGGGGGGGCCATGCTGAGCGTGAAGCTGAGGACCAAGTG 841
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 195 LysAsnValAspGlnAlaSerGlySerValLeuLeuHisIleuGlnValGlyAspGlnVal 214
QY 842 TGGGTGAGAGTG--GGTGGGTGACTACTGATGGCATCTATGGCCAGCATCAAGACAGAC 898
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 215 TrpLeuGlnValTyRgLyAspGlyAspHisAsnGlyLeuTyRAlaAspAsnValAsnAsp 234
QY 899 AGCACCTTCGCCGATTTCTGTGCTACTCGAC 931
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 SerThrPheThrGlyPheLeuLeuTyRHisAsp 245

RESULT 11
US-09-118-408-3
; Sequence 3, Application us/09118408A
; Patent No. 6265544
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
; FILE REFERENCE: 97-30
; CURRENT APPLICATION NUMBER: US/09/118,408A
; EARLIER FILING DATE: 1998-07-17
; EARLIER APPLICATION NUMBER: 60/053,154
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-118-408-3

Alignment Scores:
Pred. No.: 1,66e-23 Length: 247
Score: 428.50 Matches: 101
Percent Similarity: 52.99% Conservative: 32
Best Local Similarity: 40.24% Mismatches: 93
Query Match: 16.87% Indels: 25
DB: 4 Gaps: 8

US-09-944-944-41 (1-1377) x US-09-118-408-3 (1-247)
QY 227 ATGAGGCGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 283
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 LeuGlnAlaLeuLeuPheLeuLeuIleuLeuProSerHisAlaGlnAspAspValThrThr 23
QY 284 GAGCACAACAAGATCCCAAGCTCTGCCCGGGGACACCCCGGC-----CTT 328
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 24 ThrGlnIuLeuAlaProAlaLeuValProProProLysGlyThrCysAlaGlyTrpMet 43
QY 329 CCAGGACGCGCGGCGCCACATGAGCAGCGGCTTGGCGGGGCGCGGATGGCGGCGAGCGC 388
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 44 AlaGlyIleProGlyHisProGlyHisAsnGlyThrProGlyAspAspGlyAlaAsp--- 62
QY 389 CGCGACGCGCGCGCGCGGCTCCGGGAGAGAAAGCAGGCGGAGCGCGGAGCTGCGCG 448
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 -----GlyThrProGlyGluLysGlyGluLysGlyGluLysGlyAspAlaGlyLeuLeu 77
QY 449 GGAACCTGAGAGGAGACCCCGGGCGCGGAGAGAGAGCGGAGACCCCGGGCGCC----- 499
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 78 GlyProLysGlyIuThrGlyAspValAlGlyMetThrGlyAlaGlnGlyProArgGlyPhe 97
```

```
QY 500 -----ACGGGCGCTGCGGGGAGTGCCTGCGCTCGCGATCCGCC 541
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 98 ProGlnThrProGlyAspGlyGluProGlyAlaAlaTyRMetTyRAspVal 117
QY 542 TTCAGCGCAAGCGCTCGAGAGCGGGTGCCTCGCGCTGACGACCGCTTCCTGC 601
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 PheSerVal---GlyLeuGlnThrArgValThrValPro---AsnValProIleArgPhe 135
QY 602 GACCGCTGCTGTGAACGAGCAGGACATTACGACCGCTCACCGGCAAGTTCCCTGC 661
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 ThrIlePheTyRAsnGlnGlnAsnHisTyRAspGlySerThrGlyLysPheTyRcys 155
QY 662 CAGTGGCTGGGGCTCACTACTGCGCGCTGACCCACCGCTACCGGGGACCGCTGCAG 721
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 156 AsnIleProGlyLeuTyTyRPheserTyHisIleThrValTyRMetLysAspValLys 175
QY 722 TTTGATCTGTGAAGATGGGAAATCCATCCCTCTTCCTCCAGTTTTCGGGGGGTGG 781
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 176 ValSerLeuPheTyRAspLysAspLysAlaValLeuPheThrTyRAspGlnTyRGlInL 194
QY 782 CCCAAGCCAGCGCTGCTCTCGGGGGGGCCATGCTGAGCGTGAAGCTGAGGACCAAGTG 841
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 195 LysAsnValAspGlnAlaSerGlySerValLeuLeuHisIleuGlnValGlyAspGlnVal 214
QY 842 TGGGTGAGAGTG--GGTGGGTGACTACTGATGGCATCTATGGCCAGCATCAAGACAGAC 898
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 215 TrpLeuGlnValTyRgLyAspGlyAspHisAsnGlyLeuTyRAlaAspAsnValAsnAsp 234
QY 899 AGCACCTTCGCCGATTTCTGTGCTACTCGAC 931
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 SerThrPheThrGlyPheLeuLeuTyRHisAsp 245

RESULT 12
US-09-506-855-3
; Sequence 3, Application us/09506855
; Patent No. 6448221
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Lasser, Gerald W.
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND
; FILE REFERENCE: 99-12
; CURRENT APPLICATION NUMBER: US/09/506,855
; EARLIER FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-506-855-3

Alignment Scores:
Pred. No.: 1,66e-23 Length: 247
Score: 428.50 Matches: 101
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Best Local Similarity: 40.24% Mismatches: 93
Query Match: 16.87% Indels: 25
DB: 4 Gaps: 8

US-09-944-944-41 (1-1377) x US-09-506-855-3 (1-247)
QY 227 ATGAGGCGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 283
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Db 4 LeuGlnAlaLeuLeuPheLeuLeuIleuLeuProSerHisAlaGlnAspAspValThrThr 23
QY 284 GAGCACAACAAGATCCCAAGCTCTGCCCGGGGACACCCCGGC-----CTT 328
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Db 24 ThrGlnIuLeuAlaProAlaLeuValProProProLysGlyThrCysAlaGlyTrpMet 43
QY 329 CCAGGACGCGCGGCGCCACATGAGCAGCGGCTTGGCGGGGCGCGGATGGCGGCGAGCGC 388
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Db      44 AlaGlyIleProGlyHisAsnGlyThrProGlyArgAsp--- 62
OY      389 CGGACGGCGCCCGGGGCTCCGGAGAGAAAGCGAGGCGGAGCCGGACGTCCG 448
Db      63 -----GlyThrProGlyGlyGlyGlyGlyGlyAspAlaGlyLeu 77
OY      449 GGACCTCGAGGGAGACCCCGCGCGAGAGAGGCGGAGACCCCGCGGGCC----- 499
Db      78 GlyProLysGlyGlyThrGlyAspValGlyMetThrGlyAlaGlyIleProAlaGlyPhe 97
OY      500 -----ACCGGCGCTCCCGGGAGTGGTCCGTCCGCTCCCGCATCCGC 541
Db      98 ProGlnThrProGlyArgLysGlyProGlyGlyAlaAlaGlyMetGlyArgSerAla 117
OY      542 TTCACGCGCAACGCTCCGAGAGCGGAGTGGCTCCGCGCTGACGACGACCCGTGGCTTC 601
Db      118 PheSerVal---GlyLeuGlnThrArgValIleThrPro---AsnValProIleArgPhe 135
OY      602 GACCGCGTCCGCTGTAACGACGACGACATTAACGACGCGCTGACCGGCAAGTTACCTCC 661
Db      136 ThrLysIlePheTyrAsnGlnGlnAsnHisTyrAspGlySerThrGlyLysPheTyrCys 155
OY      662 CAGGCGCTGGGGGTACACTGCTGGCGGCGGCAATGCCAGCTGTACCGGCGGACCGTCCAG 721
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OY      722 TTGATCTGCTGACAGATGCGCAATCCATTCGCTCTTTCTCCAGTTTTCGGGGGGTGG 781
Db      176 ValSerLeuPheTyrLysAspLysAlaValLeuPheThrTyrAspGlnTyrGlnGlu--- 194
OY      782 CCGAAGCCAGGACGCTCGCGGGGGGGGCGCATGCTGAGGCTGAGGCTGAGACACAAAGTG 841
Db      195 LysAsnValAspGlnAlaSerGlySerValLeuLeuHisLeuGlyValGlyAspGlnVal 214
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Db      215 TrpLeuGlnValTyrGlyAspLysAspHisAsnGlyLeuTyrAlaAspAsnValAspAsp 234
OY      899 AGCACCTTCTCGGATTTCTGCTACTCCGAC 931
Db      235 SerThrPheThrGlyPheLeuLeuTyrHisAsp 245

RESULT 13
US-08-463-911-7
Sequence 7, Application US/08463911
Patent No. 5869330
GENERAL INFORMATION:
APPLICANT: Scherer, Philipp E.
APPLICANT: Lodish, Harvey F.
TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
NUMBER OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,911
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH195-05

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: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 861-6240
:
: TELEFAX: (617) 861-9540
:
: INFORMATION FOR SEQ ID NO: 7:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 244 amino acids
:
: TYPE: amino acid
:
: TOPOLOGY: linear
:
: MOLECULE TYPE: protein
:
: DS-08-463-911-7

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DB:	2
Length:	244
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Conservative:	26
Mismatches:	72
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US-09-944-944-41 (1-1377) x US-08-463-911-7 (1-244)

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302 AGCCTCTGCCCGGGGCAC-----CCCGGC----- 325

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Db 51 GLYALAProGLYArgspGLYArgsp-----GLYThrProGLYGLu 64

QY 419 AAAGCGAGGGCGGGAGGCTGCCGGACCTCGAGGGGAC----- 463

Db 65 LysGlyGluLysGlyAspProGlyLeuIleGlyProLysGlyAspIleGlyGluThrGly 84

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Db 124 ThrIlePro--AsnMetProIleArgPheThrLysIlePheTyraSngInGlnAsnHis 142

632 TACGACGCCGTCACCGGCAAGTTCACCTGCCAAGTGGCTCTACTACTTCCGGC 691

Db 143 TyraspGlySerThrGlyLysPheHisCysAsnIleProGlyLeuTyrTrpPheAlaTyr 162

692 CATGCCACCCTCTACCGGGCCAGCCCTGCAGTTTGATCTGCTGAGAGATGGCGATCC-- 748

Db 163 HSIleThrValTyrmettLysAspValLysValSerLeuPhelybLysAspPlysAlamet 182

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Db 183 LeuphethrTyraspGlntYrGlncLuasnasValaspGlnaLa-----SerGlySer 200

809 GCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTG--GGTGTGGGTGAC 865

Db 201 VALLEULEUHSLEUGLNUVALGYSPLNUVALTPREUGLNUVALTYRGYGLUGLYGLU 220

866 TACATTGGCATCTATGCCAGCATCAGACAGACGACCTTCTCCGATTCTGGTGTAAC 925

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QY      692 CATGCCACGCTGTACCGGGCCAGCCTGACGTTGATCTGTGAAGATGGCAATCC--- 748
Db      163 HisIleThrValIlyrMelLysAspValLysValSerLeuPheLysAspLysAlaMet 182
QY      749 ATTGCCCTCTTCTTCAGTTTTCGGGGGTGGCCCAAGCCAGCCTGCTGCGGGGGG 808
Db      183 LeuPheThrTyraSpGlnTyraGlnGluAsnAsnValAspGlnAla-----SerGlySer 200
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Db      201 ValLeuLeuHisLeuGluValGlyAspGlnValIlePheGlnValIleTyraGlyGluGlyGlu 220
QY      866 TACATTGGCATCTATGGCAGACATCAAGACAGACGACCTTCTCCGATTTCTGTGTAC 925
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 Job time : 55.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 21, 2003, 16:06:16 ; Search time:147 Seconds  
(without alignments)  
2027.222 Million cell updates/sec

Title: US-09-944-944-41

Perfect score: 2540

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Searched: 417779 segs, 108206813 residues

Total number of hits satisfying chosen parameters: 835558

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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14:	/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	1325	52.2	243	9	US-09-944-403-42
3	1325	52.2	243	9	US-09-944-896-42
4	1325	52.2	243	9	US-09-944-944-42

5	1325	52.2	243	9	US-09-944-907-42	Sequence 42, Appl
6	1325	52.2	243	9	US-09-944-929-42	Sequence 42, Appl
7	1325	52.2	243	9	US-10-028-072-362	Sequence 362, App
8	1325	52.2	243	9	US-10-121-049-362	Sequence 362, App
9	1325	52.2	243	9	US-10-123-904-362	Sequence 362, App
10	1325	52.2	243	9	US-10-140-470-362	Sequence 362, App
11	1325	52.2	243	9	US-09-796-753-68	Sequence 68, Appl
12	1325	52.2	243	9	US-10-175-746-362	Sequence 362, App
13	1325	52.2	243	9	US-10-176-918-362	Sequence 362, App
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17	1325	52.2	243	9	US-10-142-431-362	Sequence 362, App
18	1325	52.2	243	9	US-10-143-114-362	Sequence 362, App
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35	1325	52.2	243	9	US-10-124-822-362	Sequence 362, App
36	1325	52.2	243	9	US-10-140-925-362	Sequence 362, App
37	1325	52.2	243	9	US-10-160-498-362	Sequence 362, App
38	1325	52.2	243	9	US-09-944-884-42	Sequence 42, Appl
39	1325	52.2	243	9	US-10-121-041-362	Sequence 362, App
40	1325	52.2	243	9	US-10-121-043-362	Sequence 362, App
41	1325	52.2	243	9	US-10-121-047-362	Sequence 362, App
42	1325	52.2	243	9	US-10-123-215-362	Sequence 362, App
43	1325	52.2	243	9	US-10-123-908-362	Sequence 362, App
44	1325	52.2	243	9	US-10-123-908-362	Sequence 362, App
45	1325	52.2	243	9	US-10-123-909-362	Sequence 362, App

#### ALIGNMENTS

RESULT 1  
US-09-944-413-42  
; Sequence 42, Application US/09944413  
; Patent No. US20020156004A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Bolstein, David  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerlitsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Hillan, Kenneth  
APPLICANT: Kljavin, Ivar  
APPLICANT: Napier, Mary  
APPLICANT: Roy, Margaret  
APPLICANT: Tomas, Daniel  
APPLICANT: Wood, William  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P2548PICI  
CURRENT APPLICATION NUMBER: US/09/944,413  
CURRENT FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: 09/866,028  
PRIOR FILING DATE: 2001-05-25

1	PRIOR APPLICATION NUMBER: 60/067, 411
2	PRIOR FILING DATE: December 3, 1997
3	PRIOR APPLICATION NUMBER: 60/069, 334
4	PRIOR FILING DATE: December 11, 1997
5	PRIOR APPLICATION NUMBER: 60/069, 935
6	PRIOR FILING DATE: December 11, 1997
7	PRIOR APPLICATION NUMBER: 60/069, 278
8	PRIOR FILING DATE: December 11, 1997
9	PRIOR APPLICATION NUMBER: 60/069, 425
10	PRIOR FILING DATE: December 12, 1997
11	PRIOR APPLICATION NUMBER: 60/069, 696
12	PRIOR FILING DATE: December 15, 1997
13	PRIOR APPLICATION NUMBER: 60/069, 694
14	PRIOR FILING DATE: December 15, 1997
15	PRIOR APPLICATION NUMBER: 60/069, 702
16	PRIOR FILING DATE: December 15, 1997
17	PRIOR APPLICATION NUMBER: 60/069, 870
18	PRIOR FILING DATE: December 17, 1997
19	PRIOR APPLICATION NUMBER: 60/069, 873
20	PRIOR FILING DATE: December 17, 1997
21	PRIOR APPLICATION NUMBER: 60/068, 017
22	PRIOR FILING DATE: December 18, 1997
23	PRIOR APPLICATION NUMBER: 60/070, 440
24	PRIOR FILING DATE: January 5, 1998
25	PRIOR APPLICATION NUMBER: 60/074, 086
26	PRIOR FILING DATE: February 9, 1998
27	PRIOR APPLICATION NUMBER: 60/074, 092
28	PRIOR FILING DATE: February 9, 1998
29	PRIOR APPLICATION NUMBER: 60/075, 945
30	PRIOR FILING DATE: February 23, 1998
31	PRIOR APPLICATION NUMBER: 60/112, 850
32	PRIOR FILING DATE: December 16, 1998
33	PRIOR APPLICATION NUMBER: 60/113, 296
34	PRIOR FILING DATE: December 22, 1998
35	PRIOR APPLICATION NUMBER: 60/146, 222
36	PRIOR FILING DATE: July 28, 1999
37	PRIOR APPLICATION NUMBER: PCT/US98/19330
38	PRIOR FILING DATE: September 16, 1998
39	PRIOR APPLICATION NUMBER: PCT/US98/75108
40	PRIOR FILING DATE: December 1, 1998
41	PRIOR APPLICATION NUMBER: 09/216, 021
42	PRIOR FILING DATE: December 16, 1998
43	PRIOR APPLICATION NUMBER: 09/218, 517
44	PRIOR FILING DATE: December 22, 1998
45	PRIOR APPLICATION NUMBER: 09/254, 311
46	PRIOR FILING DATE: March 3, 1999
47	PRIOR APPLICATION NUMBER: PCT/US99/12252
48	PRIOR FILING DATE: June 22, 1999
49	PRIOR APPLICATION NUMBER: PCT/US99/21090
50	PRIOR FILING DATE: September 15, 1999
51	PRIOR APPLICATION NUMBER: PCT/US99/28409
52	PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
53	PRIOR APPLICATION NUMBER: PCT/US99/28313
54	PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
55	PRIOR APPLICATION NUMBER: PCT/US99/28301
56	PRIOR FILING DATE: December 1, 1999
57	PRIOR APPLICATION NUMBER: PCT/US99/30095
58	PRIOR FILING DATE: December 16, 1999
59	PRIOR APPLICATION NUMBER: PCT/US00/03565
60	PRIOR FILING DATE: February 11, 2000
61	PRIOR APPLICATION NUMBER: PCT/US00/04414
62	PRIOR FILING DATE: February 22, 2000
63	PRIOR APPLICATION NUMBER: PCT/US00/05841
64	PRIOR FILING DATE: March 2, 2000
65	PRIOR APPLICATION NUMBER: PCT/US00/08439
66	PRIOR FILING DATE: March 30, 2000
67	PRIOR APPLICATION NUMBER: PCT/US00/14042
68	PRIOR FILING DATE: May 22, 2000
69	PRIOR APPLICATION NUMBER: PCT/US00/20710
70	PRIOR FILING DATE: July 28, 2000
71	PRIOR APPLICATION NUMBER: PCT/US00/32678
72	PRIOR FILING DATE: December 1, 2000
73	PRIOR APPLICATION NUMBER: PCT/US01/06520

[illegible]



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Db	181	PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGln	200
QY	827	CCTGAGACCAAGTGTGGGTGCAGGTGGGTGGCTACTACATTGGCATCTATGCCAGC	886
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QY	887	ATCAAGACAGACAGCAGCTTCCTCCGATTCTCGTGCTACTCCGACTGGCAGCAGCAGCTCCCCA	946
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QY	947	GTCCTTGCT 955	
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RESULT 3			
US-09-944-896-42			
Sequence 42, Application US/09944896			
Patent No. US20020168715A1			
GENERAL INFORMATION:			
APPLICANT: Baker, Kevin			
APPLICANT: Boistein, David			
APPLICANT: Batton, Dan			
APPLICANT: Ferrara, Napoleone			
APPLICANT: Filvaroff, Ellen			
APPLICANT: Gerritsen, Mary			
APPLICANT: Goddard, Audrey			
APPLICANT: Godowski, Paul			
APPLICANT: Grimaldi, Christopher			
APPLICANT: Gurney, Austin			
APPLICANT: Hillan, Kenneth			
APPLICANT: Kijavlin, Ivar			
APPLICANT: Napier, Mary			
APPLICANT: Roy, Margaret			
APPLICANT: Tumas, Daniel			
APPLICANT: Wood, William			
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NOCLEIC			
TITLE OF INVENTION: ACIDS ENCODING THE SAME			
FILE REFERENCE: P2548P1C1			
CURRENT APPLICATION NUMBER: US/09/944, 896			
CURRENT FILING DATE: 2001-08-31			
PRIOR APPLICATION NUMBER: 09/866, 028			
PRIOR FILING DATE: 2001-05-25			
PRIOR APPLICATION NUMBER: 60/069, 334			
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PRIOR FILING DATE: January 5, 1998			
PRIOR APPLICATION NUMBER: 60/074, 086			

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1  PRIOR FILING DATE: February 9, 1998
2  PRIOR APPLICATION NUMBER: 60/074,092
3  PRIOR FILING DATE: February 9, 1998
4  PRIOR APPLICATION NUMBER: 60/075,945
5  PRIOR FILING DATE: February 25, 1998
6  PRIOR APPLICATION NUMBER: 60/112,850
7  PRIOR FILING DATE: December 16, 1998
8  PRIOR APPLICATION NUMBER: 60/113,296
9  PRIOR FILING DATE: December 22, 1998
10 PRIOR APPLICATION NUMBER: 60/146,222
11 PRIOR FILING DATE: July 28, 1999
12 PRIOR APPLICATION NUMBER: PCT/US99/19330
13 PRIOR FILING DATE: September 16, 1998
14 PRIOR APPLICATION NUMBER: PCT/US99/25108
15 PRIOR FILING DATE: December 1, 1998
16 PRIOR APPLICATION NUMBER: 09/216,021
17 PRIOR FILING DATE: December 16, 1998
18 PRIOR APPLICATION NUMBER: 09/218,517
19 PRIOR FILING DATE: December 22, 1998
20 PRIOR APPLICATION NUMBER: 09/254,311
21 PRIOR FILING DATE: March 3, 1999
22 PRIOR APPLICATION NUMBER: PCT/US99/12252
23 PRIOR FILING DATE: June 22, 1999
24 PRIOR APPLICATION NUMBER: PCT/US99/21090
25 PRIOR FILING DATE: September 15, 1999
26 PRIOR APPLICATION NUMBER: PCT/US99/28409
27 PRIOR FILING DATE: No. US20020168715a1ember 30, 1999
28 PRIOR APPLICATION NUMBER: PCT/US99/28313
29 PRIOR FILING DATE: No. US20020168715a1ember 30, 1999
30 PRIOR APPLICATION NUMBER: PCT/US99/28301
31 PRIOR FILING DATE: December 1, 1999
32 PRIOR APPLICATION NUMBER: PCT/US99/30095
33 PRIOR FILING DATE: December 16, 1999
34 PRIOR APPLICATION NUMBER: PCT/US00/03565
35 PRIOR FILING DATE: February 11, 2000
36 PRIOR APPLICATION NUMBER: PCT/US00/04414
37 PRIOR FILING DATE: February 22, 2000
38 PRIOR APPLICATION NUMBER: PCT/US00/05841
39 PRIOR FILING DATE: March 2, 2000
40 PRIOR APPLICATION NUMBER: PCT/US00/08439
41 PRIOR FILING DATE: March 30, 2000
42 PRIOR APPLICATION NUMBER: PCT/US00/14042
43 PRIOR FILING DATE: May 22, 2000
44 PRIOR APPLICATION NUMBER: PCT/US00/20710
45 PRIOR FILING DATE: July 28, 2000
46 PRIOR APPLICATION NUMBER: PCT/US00/32678
47 PRIOR FILING DATE: December 1, 2000
48 PRIOR APPLICATION NUMBER: PCT/US01/06520
49 PRIOR FILING DATE: February 26, 2001
50 NUMBER OF SEQ ID NOS: 120
51 SEQ ID NO 42
52 LENGTH: 243
53 TYPE: PRT
54 ORGANISM: Homo Sapien
55 US-09-944-896-42
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: Publication No. US20020198147A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Batton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gertlsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P2548P1C1
: CURRENT APPLICATION NUMBER: US/09/944, 907
: PRIOR FILING DATE: 2001-08-31
: PRIOR APPLICATION NUMBER: 09/866, 028
: PRIOR FILING DATE: 2001-05-25
: NUMBER OF SEQ ID NOS: 120
: SEQ ID NO 42
: LENGTH: 243
: TYPE: PRF
: ORGANISM: Homo Sapien
US-09-944-907-42

Alignment Scores:
Pred. No.:      1,01e-57      Length:      243
Score:          1325.00     Matches:      243
Percent Similarity: 100.00%   Conservative:  0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:      52.17%     Indels:       0
DB:               Gaps:       0

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QY      287 GACAACAAGATCCCACGACTTGCCCCGGGGACACCAGGCGCTTCAGAGCACCGGGGAC 346
Db      21 AspAmnLysIleProSerLeucylSproGlyHisProGlyLeuProGlyThrProGlyHis 40
QY      347 CATGGCAGCCAGGGGCTTGGCGGGCGCCCATGGCCGCCACGGCCCGAGAGGGGCCCCGG 406
Db      41 HisGlySerIleInLysLeuProGlyArgAspGlyArgAspGlyArgAspGlyAlaProGly 60
QY      407 GCATCCGGGAGAGAAGAGCGAGGCGAGGCGGAGGCGGAGCTCCGGGACCTCGAGGGAGCCCC 466
Db      61 AlaProGlyGlyIndLysGlyIndLysGlyArgProGlyLeuProGlyProIleGlyAspPro 80
QY      467 GGAGCGCGAGAGAGGCGGGAGCCCGCGGGCCACCGGGCTCCGGGGAGTCTCGGTG 526
Db      81 GlyProArgGlyGlyIndLysGlyProAlaGlyProIleGlyProAlaGlyGlyLysSerVal 1000
QY      527 CATTCCGGCATCGGCTTTCAGAGGCCCAAAGGCTCCAGAGACCSSGGGTGCTCGGCGTGCAC 586
Db      101 ProProArgSerIleAsheSerAlaLysArgSerGlnSerIleArgValProProProSerAsp 1200
QY      587 GCACCTTGACCCCTTCGACCGGCTGCTGGGAACAGACGAGGACATTACAGACGCGGTACC 646
Db      121 AlaProLeuProPheAspArgValIleValAlaAsnGluInGlnIstGlyArgAlaValThr 1400
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Db      141 GlyLysPheThrCysGlnValArgProGlyValTYrTYrPheAlaValAlaHisAlaThrValTYr 1600

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OY 767 TTTTTCGGGGGGTGGCCCAAGCCAGCTCTCTCGGGGGGGGCCATGGTGAAGCTGAG 826
DB 181 PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyAlaMetValArgLeuGln 200
OY 827 CCTGAGGACCAAGTGTGGGTGCAAGTGGGTGACATACATTGGCATTCGCCAC 886
DB 201 ProGluAspGlnValTyrValGlnValGlyValGlyAspTyrIleGlyIleTyrAlaSer 220
OY 887 ATCAAGACAGACAGACACCTTCGCGATTTCGTGCTCTCCAGCTCGACAGCGACGCCCA 946
DB 221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspThrPheSerPro 240
OY 947 GTCTTTGCT 955
DB 241 ValPheAla 243

RESULT 6
US-09-944-929-42
; Sequence 42, Application US/09944929
; Publication No. US20020197612A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kijavini, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548PICI
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: 09/866,028
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 42
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-929-42

Alignment Scores:
Pred. No.: 1,01e-57 Length: 243
Score: 1325.00 Matches: 243
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 52.17% Indels: 0
Gaps: 0
DB: 9

US-09-944-944-41 (1-1377) x US-09-944-929-42 (1-243)
OY 227 ATGAGGCCACTCTCTGCTGCTGCTGCTGCGGCTGCGGCTCGCCCGCCAGTGAC 286
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OY 287 GACAACAGATCCCAAGCTCTGCGCGGGGACCCCGGGCTTCAGAGCAGCGCGGGCAC 346
DB 21 AspAsnLysIleProSerLeuGlyProGlyHisProGlyLeuProGlyThrProGlyHis 40
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OY 347 CATGGCAGCCAGAGGGCTTGCCGGGCGCGATGGCCGGAGCCGCGAGCGCGCGCCGGG 406
DB 41 HisGlySerGlnGlyLeuProGlyLysArgGlyLysArgGlyLysArgGlyLysArgGly 60
OY 407 GCTCCGGGAGAGAAAGGCGAGGCGGAGCGGAGCGGAGCTCCCGGACCTTCAGAGGAGCC 466
DB 61 AlaProGlyGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGly 80
OY 467 GGGCGCGAGAGAGAGGCGGAGCCCGGGGGCCACCGGGGCTCCCGGGGAGTGTCTG 526
DB 81 GlyProArgGlyGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLysGlyLys 100
OY 527 CCTCCGCGATCCGCTTCAGCGCCCAAGCCCTCCGAGAGCGGGGTGCTCCGCGCTGAC 586
DB 101 ProProArgSerAlaPheSerAlaLysArgSerGlySerAlaValProProSerAsp 120
OY 587 GCACCTTGCCCTTCGACCGCGCTGCTGCTGAAGACAGACAGCATTCACGCGCGTAC 646
DB 121 AlaProLeuProPheAspArgValLeuValAsnGlnGlnGlyHisTyrAspAlaValThr 140
OY 647 GGCAGATTACCTGCCAGGTGCTGGGCTCTACTTGGCGGTCCATGCCACCGTCTAC 706
DB 141 GlyLysPheThrCysGlnValAlaProGlyValTyrTyrPheAlaValHisAlaThrValTyr 160
OY 707 CGGGCCAGCCCTGCTGATCTGCTGAAGATGGCGAATCCATTCCTTCTTCAG 766
DB 161 ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyIleAserPhePheGln 180
OY 767 TTTTTCGGGGGGTGGCCCAAGCCAGCTCTCTCGGGGGGGGCCATGGTGAAGCTGAG 826
DB 181 PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyAlaMetValArgLeuGln 200
OY 827 CCTGAGGACCAAGTGTGGGTGCAAGTGGGTGACATACATTGGCATTCATTCGCCAC 886
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DB 221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspThrPheSerPro 240
OY 947 GTCTTTGCT 955
DB 241 ValPheAla 243

RESULT 7
US-10-028-072-362
; Sequence 362, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
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20	PRIOR APPLICATION NUMBER: 60/079665	60
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36	PRIOR APPLICATION NUMBER: 60/082999	60
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67	PRIOR FILING DATE: 1998-05-28	
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71	PRIOR FILING DATE: 1998-06-10	
72	PRIOR APPLICATION NUMBER: 60/088741	
73	PRIOR FILING DATE: 1998-06-10	
74	PRIOR APPLICATION NUMBER: 60/088741	



Db 41 HisGlySerIleGlyLeuProGlyArgAspGlyValArgAspGlyValArgAspGlyValArgProGly 60  
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QY 467 GGGCGCGAGAGAGAGGGGAGCGCGGGGCGCGGGGCGCGGGGCGCGGGGCGCGGGGCGCGGGG 526  
Db 81 GlyProArgGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 100  
QY 527 CCGCCGGAGCG 586  
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Db 121 AlaProIleuProIleuSerGlyGlyGlyArgProIleuProIleuProIleuProIleuProIleu 140  
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QY 707 CGGGCCG 766  
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QY 767 TTTTTCGGGGGGTGGCCCAAGCCAGCGCTCTCGGGGGGGCGCGCATGTGAGGGCTGAG 826  
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QY 887 ATCAAGACAGACAGACACTTCTCCGATTTCTGGTACTCCGACTGGACAGCTGCCA 946  
Db 221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspTrpHisSerSerPro 240  
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RESULT 9  
US-10-123-904-362  
; Sequence 362, Application US/10123904  
; Publication No. US20030022328A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Deforge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Fillardoff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Geriltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Guiney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P3330R1C54  
; CURRENT APPLICATION NUMBER: US/10/123,904  
; PRIOR FILING DATE: 2002-04-16  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 362  
; LENGTH: 243

TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-123-904-362  
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Pred. No.: 1,01e-57 Length: 243  
Score: 1325.00 Matches: 243  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 52.17% Indels: 0  
DB: 9 Gaps: 0  
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QY 227 ATGAGCGACATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 286  
Db 1 MetArgProIleuLeuValIleuLeuLeuGlyLeuAlaIleuGlySerProIleuLeuAsp 20  
QY 287 GACAAAGATCCCGACGCTCTGCGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 346  
Db 21 AspAsnLysIleProSerLeuCysProGlyHisProGlyLeuProGlyThrProGlyHis 40  
QY 347 CATGGCAGCGAGGCTTGGCG 406  
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QY 407 GCTCCGGAGAGAAAGCGAGGGCGGAGCGCGGAGCTGCCGGAGCTCGAGGGAGACCC 466  
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QY 587 GCAACCTTGGCTTGCAGCG 646  
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Db 161 ArgAlaSerIleuGlnPheAspLeuValLysAsnGlyLysSerIleuAlaSerPhePheGln 180  
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Db 181 PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGln 200  
QY 827 CCGAGAGCAAGATGTGGGTGCGAGGTGGGTGGGTGCTACTGATCTATGCGACG 886  
Db 201 ProGlnAspGlnValTyrValGlnValGlnValGlnValGlnValGlnValGlnValGlnVal 220  
QY 887 ATCAAGACAGACAGACACTTCTCCGATTTCTGGTACTCCGACTGGACAGCTGCCA 946  
Db 221 IleLysThrAspSerThrPheSerGlyPheLeuValTyrSerAspTrpHisSerSerPro 240  
QY 947 GCTCTTGCT 955  
Db 241 ValPheAla 243

RESULT 10  
US-10-140-470-362  
; Sequence 362, Application US/10140470  
; Publication No. US20030022331A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen











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QY 647 GGCAAGTTCACCTGCAGGTGGGCTACTACTTGGCGTCCATGCCACGCTTAC 706
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Db 141 GlyLysPheIleValProGlyValTyrPheAlaValHisAlaThrValTyr 160
    |||||||
QY 707 CGGGCCAGCTGCAGTTGATCTGGTGAAGAATGGCAATCCATTGCCCTTCTTCCAG 766
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Db 161 ArgAlaSerLeuGlnPheAspLeuValLysAsnGlyIleAspLeuValSerPheGln 180
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QY 767 TTTTTCGGGGGGTGGCCCAAGCCAGCTGCTCTGGGGGGGCCCATGGTGAAGCTGGAG 826
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Db 181 PhePheGlyGlyTyrProLysProAlaSerLeuSerGlyGlyAlaMetValArgLeuGlu 200
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QY 827 CCTGAGACCAAGTGTGGTGACAGGTGGGTGCTACTACATGGCATCTATGCCAGC 886
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Db 201 ProGlnAspGlnValTyrValGlnValGlyAspTyrIleGlyIleTyrAlaSer 220
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QY 887 ATCAAGACAGACAGCAGCTTCTCCGATTCTGTGTACTCCGACTGCACAGCTCCCA 946
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Db 221 IleLysThrAspSerThrPheSerClyPheLeuValTyrSerAspTyrPheSerSerPro 240
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QY 947 GTCCTTGCT 955
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Db 241 ValPheAla 243

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Search completed: June 21, 2003, 16:41:47  
 Job time : 166 secs

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## ALIGNMENTS

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QY	584	GAGCAGCCCTTGAGCCCTTCGAGCCGGTGTGTGAAGAGAGAGGAGACATTTACAGAGCGCTTC	643
Db	555	GAGCAGCCCTTGAGCCCTTCGAGCCGGTGTGTGAAGAGAGAGGAGACATTTACAGAGCGCTTC	614
QY	644	ACCGGCAAGTTCACTTCGACAGGTGCGTGGGGTCTACTACTTGGCGGTCCATGCAACCGTC	703
Db	615	ACCGGCAAGTTCACTTCGACAGGTGCGTGGGGTCTACTACTTGGCGGTCCATGCAACCGTC	674
QY	704	TACCGGGAGCCAGCGCTGCAAGTTGATTCGTGAAGATAGCGAATCCATTGCTCTTCTTC	763
Db	675	TACCGGGAGCCAGCGCTGCAAGTTGATTCGTGAAGATAGCGAATCCATTGCTCTTCTTC	734
QY	764	CAGTTTTTCGGGGGGGTGGCCCAAGCCAGCGCTCGCTCGGGGGGGGGCCATGGTGAAGCTG	823
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Db	915	CCAGTCTTTGCTTAGTGCCCACTGCAAGTGAAGTCAATGCTCACTCTGAAGAGAGGG	974
QY	1004	TGTGAGGCTGACAACCAAGTCAATCCAGAGAGGAGTGGCCCCCTGGAAATTTGTGAATGAC	1063
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QY	1124	GTCCTCGATCAAGTCTGGCAGCATGGGGAGATGGCTGGATTTCTGCCAAGACCAAGAGA	1183
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QY	1184	GTCGCTGTGGTGGCAAGTGTAAATCCCCCAAGTTGCTGTGTCCAGAGAGCCCAAGGTGGG	1243
Db	1155	GTCGCTGTGGTGGCAAGTGTAAATCCCCCAAGTTGCTGTGTCCAGAGAGCCCAAGGTGGG	1214
QY	1244	GTGCTCTCTTCCTGATCCTGTGCTTCCTGGATCCGCCACCCCTCCTGCTCTGGGG	1303
Db	1215	GTGCTCTCTTCCTGATCCTGTGCTTCCTGGATCCGCCACCCCTCCTGCTCTGGGG	1274
QY	1304	CCGGCCCTTTTCTCAGAGTCACTCAATAAACCATAAGAACCTCA 1348	
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; Sequence 2, Application US/09140804  
; Patent No. 6197930  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Humes, Jacqueline M.  
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS  
; FILE REFERENCE: 97-49  
; CURRENT APPLICATION NUMBER: US/09/140,804  
; CURRENT FILING DATE: 1998-08-26  
; EARLIER APPLICATION NUMBER: 60/056,983  
; EARLIER FILING DATE: 1997-08-26  
; NUMBER OF SEQ ID NOS: 47  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-140-804-2

Query Match 100.0%; Score 1325; DB 4; Length 243;  
Best Local Similarity 100.0%; Pred. No. 9.5e-114;  
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	181	FFGGWPKPASLSGAMRLEPEDQVWVQGVGDYIGIYASIKTDSFSGFLVYSDWHSSP	240
QY	241	VFA	243
DB	241	VFA	243

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